us-10-009-823a-1.rag

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OM protein - protein search, using sw model Run on:

October 26, 2004, 09:04:10 ; Search time 71 Seconds (without alignments) 2536.368 Million cell updates/sec

US-10-009-823A-1 2586 1 MMGSLFIGATGMKTHSTGLG.....NSKSVTTADTWLQKALELKR

score: Title: Perfect :

Sequence:

502

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 Total number of hits satisfying chosen parameters:

2002273 segs, 358729299 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 23Sep04:*

1: geneseqp1980s:*

2: geneseqp2000s:*

4: geneseqp2001s:* geneseqp20028:* geneseqp2003a8:* geneseqp2003bs:* geneseqp20048:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	2 Aab36552 Law	0 Aaw16680	7	0 Abo70780	2 Abj18752	9 Abu22839 Pro	Adk13784	Abb49883	Aaw80991	Adf07897	Abm68268	Abg24709	Abo70969	Abm68266 Ph	Aaw20373 H.	Aaw24645 H.	Aaw20863 H.	Adf07825		3 Aaw73073	. Abo81481	7 Aab01847 Haemo	Aar41723 High	Aar41725	1
o o	ΩĦ	AAB3655	AAW1668	ABU2021	AB07078	ABJ1875	ABU2283	ADK13784	ABB49883	AAW80991	ADF07897	ABM68268	ABG24709	AB070969	ABM68266	AAW20373	AAW24645	AAW20863	ADF07825	AAY51377	AAW7307	AB081481	AAB0184	AAR41723	AAR41725	
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3 AAB01846	6 ABU50020	2 AAW30293	6 ABU38411	6 ABP59933	2 AAW20361	7 ADC01014	8 ADF83256	8 ADK13634		6 ABU30969	6 ABU21223	2 AAW73072	3 AAY51376	6 ABU36440	5 ABB54168	3 AAB01845	3 AAB01844	2 AAW20658	7 ADD48744	
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ALIGNMENTS

Lawsonia intracellularis; flgE; flagellar hook protein; vaccine; intestinal disease; immunogenic; diagnosis; antibacterial; swine; pig; infection; detection; identification. Lawsonia intracellularis flagellar hook protein FlgE SEQ ID NO:1. AAB36552 standard; protein; 486'AA. 07-MAR-2001 (first entry) AAB36552; RESULT 1

Lawsonia intracellularis. WO200069904-A1.

23-NOV-2000.

11-MAY-2000; 2000WO-AU000437.

99US-0133973P. 13-MAY-1999; (PFIZ) PFIZER PROD INC. (AGRI-) AGRIC VICTORIA SERVICES PTY LTD. (PIGR-) PIG RES & DEV CORP.

Ď,

Hasse D, Panaccio M, Rosey EL, Sinistaj M, Ankenbauer RG;

Parsons J;

WPI; 2001-016210/02. N-PSDB; AAC88037.

New immunogenic Lawsonia FlgE peptide, its nucleic acid and antibody, useful in vaccines and diagnosis of Lawsonia infections, particularly in swine.

Claim 13; Page 87-90; 97pp; English.

The present sequence is the Lawsonia intracellularis flagellar hook protein F1gE. The present invention describes an isolated or recombinant polypeptide (1) that comprises, minics or cross-reacts with a B- or T-cell epitope of a F1gE (flagellar hook) polypeptide from a Lawsonia spp. (1) has antibacterial activity, and induces a specific humoral immune response. (1) are used as antigens in vaccines to prevent or treat infection by Lawsonia, in birds and animals, especially pigs, to raise specific antibodies (Ab) and to detect past or present infection. Ab are

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also useful in diagnosis, to detect L. intracellularis or immunologically cross-reactive species, also for identification of epitopes in FlgE. Vectors that contain nucleic acids (II) encoding (I) are also useful in genetic vaccines, and fragments of (II) are useful as primers or probes for detecting L. intracellularis or related microorganisms, in hybridisation or amplification assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATKDLNAWQP 300
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in the nucleotide sequence"
13
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                                                                                                                                                                                                                                                                                                                                                                                     TOSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSSTGSK
                                                                                                                                                                                                                                                                                                                                                      MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTOGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QAGMGAQVGSVRIIFTQGA-------FFQVTLEDKVHYTRAGNFRFTQDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNWWAGAPASAAAIGTDIGKLPSMMPIQT
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                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                  16;
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                                                                                                                                                                                                                                                  Length 486;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                            Score 2484; DB 4;
Pred. No. 9.7e-178;
0; Mismatches 0;
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in the nucleotide i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW16680 standard; protein; 120
                                                                                                                                                                                                                                         Similarity 96.8%; Sonservative
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                                                                                                                                                                                      Sequence 486 AA;
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Misc-difference
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Matches 486;
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LD AAW1
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AC AAW:
XX
DT 20-
XX
C AAW:

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A polypeptide (AAW16680) of Lawsonia intracellularis shows sequence similarity to flagellar basal body rod protein. Its amino acid sequence was deduced from a DNA molecule (AAT69204) obtd. by immunoscreening a Lintracellularis library using sera from vaccinated pigs. Polypeptides (AAW16678-85) of L. intracellularis are vaccine candidates for protection of birds and animals against intestinal diseases, esp. protection of pigs against porcine proliferative enteropathy. They can be administered as recombinant polypeptides or expressed as recombinant vaccines utilising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123
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                                         (GNT)
                                                                                                                                                                                                                                                                                                            Vaccine for treating or preventing Lawsonia intracellularis infection especially in pigs, containing non-pathogenic form of bacterium or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 SLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacterial, fungal or viral vectors. Antibodies raised against the polypeptides may be useful in immunotherapy, diagnosis and detection
  codon
                                          codon
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  degenerate
                                         to degenerate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #5744.
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C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 538; DB 2; I
Pred. No. 1.7e-32;
; Mismatches 12;
                                     "residue 16 corresponds
nucleotide sequence"
 "residue 13 corresponds
nucleotide sequence"
                                                                                                                                                                                                                                                                                                                                                                Claim 26, Page 51-52, 94pp, English.
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                                                                                                                                                            95AU-00006910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.8%;
                                                                                                                                   96WO-AU000767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                   DARATECH PTY LTD.
PIG RES & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 89.2
Matches 107; Conservative
/note=
in the:
16
/note=
in the:
                                                                                                                                                                                                                                           Hasse D;
                                                                                                                                                                                                                                                                      WPI; 1997-310605/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU20217 standard;
                                                                                                                                                                                                                                                                                    N-PSDB; AAT69204.
                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200277183-A2
                                                                                                                                 29-NOV-1996;
                                                                                                         05-JUN-1997.
                                                                                                                                                           30-NOV-1995;
                                                                                                                                                                                                                                         Panaccio M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUN-2003
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                                                                                                                                                                                                                                                                                                                                       components
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(PIGR-)
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The follower relates to an isolated mutter. Actua computation of the follower than t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typnimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at from in clectronic format directly from Form with the properties of the prope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 48141; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Malone C,
Carr GJ,
                                                                          21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072881.
06-MAR-2002; 2002US-0362699P.
2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003-029926/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang L,
Wall D,
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DB 6; Length 414; Query Match

20.5%; Score 529.5; DB 6; Length 4
Best Local Similarity 29.8%; Pred. No. 4.2e-31;
Matches 149; Conservative 72; Mismatches 182; Indels

68 VGSVRIIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGFLNDPSGF 127 121 NLMGYAAGAGGVINTAQTVPLQA---PTNNIAPRATS-KITGQFNL-NAQDKVFAK--- 171 188 YFALLESWKGNGTPPISTSN--YSYAQPMRVYDQQGNSHDITVYFDGAPSSTGSKTFEYL 245 9 8 GATCMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQ 67 6 GLSGLAGASSNLDVIGNNIANANTVGFKÖGRANFADMYANSVATSVN-----TÖLGIGTR 128 TLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANP 97; Gaps

> 원 à g à 원

211 246 VAMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKNWTAFTPTGSATKDLNAWQPAPLVN 305 361 421 334 481 306 GLPOFSANFV----GAGIOPLTLDFGIKSQONMWAGAPASAAAIGTDIGKLPSMMPIQTS 362 SGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSE 422 DGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQ 251 SLGČFAFSIPNTTGGANPQNLTLDL-----482 MNSKSVTTADTMLQKALELK 501 395 ANAQTIKTQQAVDQTLLNLR 414 g à g ద 8 g 8 ò

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Z ABO70780 standard; protein; 471 29-JUL-2004 ABO70780;

RESULT 4

Pseudomonas aeruginosa polypeptide #2955.

Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

Pseudomonas aeruginosa JS6551795-B1.

22-APR-2003

98US-0074788P 18-FEB-1999; 18-FEB-1998; 27-JUL-1998;

(GENO-) GENOME THERAPEUTICS CORP.

ä Bush Deloughery C, Nolling J, Rubenfield MJ,

WPI; 2003-615309/58. N-PSDB; ABD04351.

Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.

Disclosure; SEQ ID NO 19526; 455pp; English

The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostice, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The

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(HARD ) HARVARD COLLEGE
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Best Local Similarity.
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                                                                                                                                                                                                                                                                                      226 IPENSWTWKVLIDGVNPLDPSNKTP-----MSFNVTFDASGQMTSVRA--PDGSTSG 275
                                                                                                                                                                                                                                                                                                                                                           345 IGTDIGKLPSMMPIQTSSGNSTARNGSSSTRRYS------QDGYPQGDLVDVTITSE 395
                                                                                                                                                                                                                                                                                                                  -----ATKDINAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAA 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biofilm formation modulation; biofilm-associated disease; cystic fibrosis; AIDS; middle ear infection; aone; periodontal disease; catheter-associated infection; medical device-associated infection.
                                                                                                                  66 SGVLLSDVSQMFKQGNIDSTNSVLDLAINGNGFFVTSNNGAISYTRAGYFNTDKQDFIVD
                                                                                                                                                                                                     SLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAG
                                                                                                                                                MGAQVGSVRIIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGFLND
                                                                                                                                                                                                                                                                          ---GSKTFEYLV-AMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNWTAFTPTGS---
                                                                                     Gaps
sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html
                                                                                 93;
                                                               Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aeruginosa biofilm formation-related protein #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                           VNQLETSNVDMSREMVNMIIIQRGFQMNSKSVTTADTMLQKALELK 501
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                                                                DB 7;
                                                               Query Match 20.4%; Score 528.5; DB 7; Best Local Similarity 28.5%; Pred. No. 5.9e-31; Matches 150; Conservative 84; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 462 AA
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2001US-0344142P.
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                                           Sequence 471 AA;
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24-OCT-2001;
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Identifying compound capable of modulating biofilm formation by bacteria/bacterial antibiotic resistance, useful for treatment of biofilm associated disease.
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                                                                                                                                                                                                                                                                                                                                                           The invention comprises a method for identifying a compound capable of modulating biofilm. Formation by bacteria. The method of the invention is useful for identifying a compound capable of modulating biofilm formation by bacteria or modulating bacterial antibiotic resistance. The method of the invention is also useful for diagnosing and treating a subject (especially an immunocompromised human) that is affilicted with a biofilm associated disease or disorder, such as: cystic fibrosis; AIDS; middle as infections, anchy periodonical disease, catheter-associated infections and medical device-associated infections. The present amino acid sequence represents a protein that is used in the invention
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   뎚.
Greenberg
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       Lory
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   Whiteley M, Bangera MG,
                                                               WPI; 2003-075601/07.
N-PSDB; ABT14574.
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Antisense; prokaryotic essential gene; cell proliferation; drug design Protein encoded by Prokaryotic essential gene #8366 21-MAR-2002; 2002WO-US009107 Burkholderia mallei WO200277183-A2. 19-JUN-2003 03-OCT-2002 Wang L, Wall D,

.007 00.00.77

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AON HOE

(first entry)

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-0362699P. (ELIT-) ELITRA PHARM INC.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, 2003-029926/02 N-PSDB; ACA26709

Claim 25; SEQ ID NO 50763; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an host cell containing the vector; (3) an isolated polypeptide; (5) producing the polypeptide of its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that the inhibits cellular proliferation; (8) identifying a compound that influences the activity of required for proliferation, or that inhibits cellular proliferation of an order required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies cor a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of surfaction of an organism. The antisense nucleic acids are useful for strains; or (13) identifying the target of a compound that inhibits the confictiving proteins or screening for homologous nucleic acids required for proliferation in cells other than S: aureus, S. typhimurium, confirting proliferation in cells other than S: aureus, S. typhimurium or present aid not form when act of the printed specification, but was obtained confirm electronic format directly from WIPO at the sequences.

Sequence 413 AA;

Query Match
Best Local Similarity 27.2%; Pred. No. 2.2e-29;
Matches 137; Conservative 81; Mismatches 180; Indels 105;

GATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQ

174 F-----NYTDPTS---YNYTTSVQVFDTLGGSQNVNLYFVKSATSGQWEAYAGPAG 221 248 MNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATKDLNAWQPAPLVNGL 307 270 AGVPT-----TNVGQFSFSIPTTGAANPQN 270 477 68 VGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGFLNDPSGF 127 187 417 308 POFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTSSGN---365 -----STARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLAR 128 TLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANP 418 FISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQ 188 YFALLESWKGNGTPPISTSNYSYAQFWRVYDQQGNSHDITVYFDGAPSSTGSKTFEYLVA 222 KTPTDLGS---------VKFSTAGTITGTSTP-----| :| |::: | |: | 391 RNYQANAQTIKTQQTVDQTLINL 413 478 RGFQMNSKSVTTADTMLQKALEL 500 245 ò g 원 ò ઠે 요 ద δ g ઠે ઠે 셤 δ ö

ADK13784 standard; protein; 402 RESULT

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20-MAY-2004 (first entry)

ADK13784;

E. coli iron transport and metabolism protein SEQ ID NO:79.

Escherichia coli; iron transport and metabolism protein; iron transport; iron metabolism; antibacterial. Escherichia coli

WO2004018638-A2.

34-MAR-2004.

21-AUG-2003; 2003WO-US026488.

21-AUG-2002; 2002US-0405331P.

(MINU) UNIV MINNESOTA KAPUR V. GADGIL M. (KAPU/) (GADG/)

Kapur V, Gadgil M;

WPI; 2004-238974/22 N-PSDB; ADK13720. New isolated and purified iron transport and metabolism polypeptides and encoding polymucleotides, useful in identifying potential targets for agents against pathogenic bacteria.

Claim 1; SEQ ID NO 79; 185pp; English

11-APR-2001; 2001WO-FR001118

2000FR-00004629

11-APR-2000;

(INSP) INST PASTEUR

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The present sequence represents an Bscherichia coli iron transport and metabolism protein. Also described: (1) an isolated and purified polynucleotide comprising a nucleic acid sequence encoding an Escherichia coli iron transport and metabolism protein, and (2) an expression cassette comprising a nucleic acid sequence encoding a promoter operably linked to at least one of the polynucleotide sequences of (1). The Escherichia coli iron transport and metabolism proteins have antibacterial activity. The methods and compositions of the present invention are useful in identifying genes and proteins involved in bacterial iron transport and metabolism, and using such as potential targets for agents against pathogenic bacteria.
                                                                                                                                                                                                                             Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---TFSLSFLNS--------MOON------
                                                                                                                                                                                                                            19.0%; Score 491.5; DB 8; 28.8%; Pred. No. 2.8e-28; ive 75; Mismatches 173;
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                                                                                                                                                                                                                                                         143; Conservative
                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                Sequence 402 AA;
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                                                                                                                                                                                                                          Query Match
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245 56 GITQDFTDGTTTNTGRGLDVAISQNGFFRLVDSNGSVFYSRNGQFKLDENRNLVAMQGLQ 115 129 LMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANPY 188 166 209 210 VYIQDSSDPNSIAKT-----AITLEFNANGTL--VDGAMANNIATGAINGAEPA---- 256 70 SVRIIFTQGAFEPGNSVTDLAIGGKGFFQ-VTLEDKVHYTRAGNFRFTQDGFLNDFSGFT 128 246 VAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATKDLNAWQPAPLVN 305 GLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTSSGNS 365 425 276 VAT-----TQNGYKPGDLVSYQINDDGTVVGNYSNEQTQLLGQIVLANFANNEGLA 326 485 69 SGLNAAATWLDVIGNNIANSATYGFKSGTASFADMFA------GS----KVGLGVKVA 55 10 TGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVG 189 FALLESWKGNGTPPISTSN---YSYAQPWRVYDQQGNSHDITVYFDGAPSSTGSKTFEYL ------VTPFSASNADSYNKKGSVTVFDSQGNAHDMSVYF----VKTGDNNWQ--TARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSEDGLR REGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMNSK Gaps Indels 105; :: | : | : | : | TIKTODQILNTLVNLR 387

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Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                        Listeria monocytogenes protein #2587.
                   ABB49883 standard; protein; 411
                                                       (first entry)
                                                                                                                     Listeria monocytogenes
                                                      05-FEB-2002
                                    ABB49883
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WO200177335-A2

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61 THPMSFGSGSKIGALLTDYTAGSPTSTGRNKDAALQGRGFFIAGDNAGGNIVYTRDGSFA 120

57 QGPNQAGMGAQVGSVRIIFIQGAFEPGNSVTDLAIGGKGFFQV--TLEDKVHYTRAGNFR

1 MIQTMYTAISGMNAFQQALSVTSNNIANANTTGYKKGSVVFNDLLYQNTMGSVAGGLYAG 1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQD----LAIGSTGS

9

105;

Conservative

Matches 137;

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Local Similarity

Query Match

115 FTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNL 174

121 VSDNNYLTYQQGKYVMGYATDKNGNVLNGNLQPIQIPLNSAIPGEATKNGSLSGNIPLDW

GDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGA-

------LSVYDNAGGKHKLQVNMKAAT

181 GEK-DIISSE-

175

. 234

294

252 -LKNIQINSTVNG-------GLNLSGLT 276

DLNAWOPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNWWAGAPASAAAIGTDIGKLP 353

211 PDASGNVSYEYEIQM----DGKALTPP-----VTGTLNYNAQGELTNDDA-----

PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATK

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The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see AbA00041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein expressed from the genome sequence of the present invention. Proteins cartibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of vitamin ST. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this in a leterance of the printed specification, but was obtained in a leterance of the printed specification, but was obtained in a leterance of the printed specification, but was obtained in a leterance of the printed specification, but was obtained the printed specification, but was obtained to the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides.
                                                                                                                                                                                                                 Dehoux P;
Cossart P;
                                                                                                                                                                                     Buchrieser C, Frangeul L, Couve E, Rusnick C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart F Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA, Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Chakrabit A, Durant L, Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N, Raduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J, Rose M, Voss H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.7%; Score 484.5; DB 5; Length 411; 27.0%; Pred. No. 9.8e-28; Live 77; Mismatches 188; Indels 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; SEQ ID NO 2588; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-010914/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 411 AA;
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380 DGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFISEDGLRREGNNHYSATLDSG 439 57 QGPN--QAGMGAQVGSVRIIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKV--HYTRAGN 112 476 KFTHATHATSIDVIDSLGTKHAMRIEFYRSGGADWNFRVIVPEPGELVGGSAARPNVFEG 535 180 ASNRISMRANINAGRHADQTAA----IFALDSSAKTPSDGINPVYDSGTNLAQVAEDMGS 208 -----SSTGSKIFEY DLNAWQ-----PAPLVN------GLPQFSANFV------GAGIQPLTL 113 FRFTQDGFLNDPSGFTLM-----GSRISNNPNIKKETLEFIQLDFNDPTVAKSPAK 245 LVAMNPSEDGSAASG----TDSAGLLMSGTWIFSSNGELKNMI-----AFIPIGSAIK 164 TST--ALNAVVNLGDSTDKTQSEANPYFALLESWK--GNGTPPISTSN-----344 --------AIGT-----A 325 DFG-----IKSQQNMW-----348 ----DIGKLPSMMP-----294 500 ADF07897; RESULT 10 음 ઠે 8 ઠે 셤 ઠ 셤 8 셤 ò g ò 셤 ઠે 셤 ठे ద ठे 셤 à 용 ò 셤 This is the amino acid sequence of a Helicobacter pylori FlgE flagellar hook protein that is encoded by an isolated FlgE gene (see AAV99813). FlgE polypeptide is used in a claimed vaccine, which further comprises an adjuvant (a pharmaceutically acceptable form of cholera toxin), and which is used therapeutically as a prophylactic vaccine in mammals (especially humans) infected by H. pylori. It is additionally used to form a composition in the treatment and diagnosis of H. pylori infection, and in eliciting a protective immune response towards both the coccidal and imporpatite elicits an immune response towards both the coccidal and bacillary forms of H. pylori, and also increases protective immune mechanisms locally in the stomach, which is important because systemic immunity only plays a limited role in protection against mucosal 473 323 AVATFSNEDGLVKMGNGEYVPGLSSGDAVYGVAGQNGAGGISGSSLEGSNVDLSREFVNL 382 PLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNM SMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNI NY-------GINQVFSPISDGKGAAIVKDYAVIDSGYIAVSYSDGIVIPVAQL Ø New Helicobacter pylori FlgE polypeptide - useful for inducing protective immune response to H. pylori infection. FlgE; flagellar hook; vaccine; infection; therapy; ulcer. 474 IIIQRGFQMNSKSVTTADTMLQKALEL 500 : | | | | | | : | : : : | mrxgsgfggntkvirvarddnurgivnl 409 pylori FlgE flagellar hook. Claim 2; Page 24-26; 36pp; English. AAW80991 standard; protein; 718 AA. 98WO-SE001093 97SE-00002242 (first entry) Berglindh T, Mellgard WPI; 1999-080888/07. N-PSDB; AAV99813. Helicobacter pylori (ASTR) ASTRA AB Sequence 718 AA; Helicobacter 08-JUN-1998; 12-JUN-1997; WO9856816-A1 12-APR-1999 17-DEC-1998 277 414 383 354 AAW80991 RESULT 9 셤 ઠે à 셤 ઠ

163

235

207

355

324

475 347

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379

655

Proteus mirabilis infection; bacterial infection; antibacterial; Ą. (GENO-) GENOME THERAPEUTICS CORP. ADF07897 standard; protein; 412 05-APR-2000; 2000US-00543681 99US-0128706P Bacterial polypeptide #4010 12-FEB-2004 (first entry) Proteus mirabilis. LKR 502 LKQ 718 immunostimulant. US6605709-B1. 09-APR-1999; 12-AUG-2003

21;

Gaps

9

1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGS----TGS 56

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Query Match
18.7%; Score 483; DB 2; Length 718;
Best Local Similarity 24.9%; Pred. No. 2.8e-27;
Matches 180; Conservative 90; Mismatches 227; Indels 226;

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The invention relates to new Proteus mirabilis polypeptides and polymcleotides. The invention also relates to antibodies against the polypeptides, an method a method for producing the polypeptides, an method of producing the polypeptides, and method for evaluating a compound for the ability to bind a P. mirabilis, and polypeptide and method for screening test compounds for anti-bacterial activity. The polypeptides and polymucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial diagnos or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                                         New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as
                                                                                                                                                                        Disclosure; SEQ ID NO 8182; 870pp; English
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MIVAQRNYQSNAQTIKTQDQILQTLVSMR
                                                                                                                                         biocontrol agents for plants.
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                                             WPI; 2003-895291/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                            N-PSDB; ADF03725
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 412 AA,
               Breton GL;
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239 352 IPLARFISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVN 472 70 SVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDK---VHYTRAGNFRFTQDGFLNDPSG 126 127 FTLMGSRISN----NPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLG---DSTD 179 KTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNG-----ELKNMTAFTPTGSAT 292 353 PSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYN 412 -----SGSTQQKVAESSVSKLAQNGYQAGEFTNFRIEPDGSIMATYSNQQSQVVGQ 323 61 10 TGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVG 69 62 GISQNFKDGSITTTNRPTDVAISGGGFFRI--EDSNGGVFYSRNGEFGKDKNGYLTNNQG SCINDARARANIDTIGNNISNSATYGFKGATVSFADVFA-----GS----GAGLGVKVS KTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSSTGS QTTHKEDP-----KDN-----DSYNFSTNVTTYDSLGNEHNLNLFF-----VKT KDNEWSVYAQDTTTGEPAQDL----GKLVYKDNGVLDETAPKLKNFTTVAYKGS--KDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKL 18.4%; Score 475.5; DB 7; Length 412; 26.7%; Pred. No. 4.7e-27; Indels 127; Gaps iive 81; Mismatches 165; Indels 127; Gaps

ABM68268 standard; protein; 405 AA

RESULT 11 ABM68268

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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms, for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polymorphisms, for gene analysis and for detection/identification of the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter ceponse or sensitivity to toxins and antibiotics produced by P. ceponse or sensitivity to toxins and antibiotics produced by P. ceponse or sensitivity to toxins of the gross are useful for recombinant production of the proteins, particularly toxins and artibacterials useful as insecticides, bactericides and fungicides. The genes in place of the genes and Ab are also useful that are sensitive to P. luminescens and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128
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                                                                                                              Antibacterial; fungicide, insecticide, polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 TGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 SGLNAAAGNLDVIGNNIANAATYGFKSSTVAFSDIFA-----GS----QVGLGVKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danchin A;
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Pred. No. 4.8e-25;
6; Mismatches 174; Indels 127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunst
                                                                            Photorhabdus luminescens protein sequence #1365.
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27.8%; Pre
ative 66;
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(CNRS ) CNRS CENT NAT RECH SCI
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                                    (first entry)
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                                                                                                                                                                                                                     Photorhabdus luminescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taourit S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-148459/14.
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                                                                                                                                                                                 whooping cough.
                                                                                                                                                                                                                                                           WO200294867-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duchaud E, T
Buchrieser C;
                                    20-NOV-2003
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Matches
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16;
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                                                                                                                                                                                                                                                                                                                                                                                                              supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in disgnostics, forersics, gene mapping, identification of mutations are responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 FALLESWKGNGTPPISTSN---YSYAQPWRVYDQQGNSHDITVYFDGAPSSTGSKTFEYL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 VNGLPQFSANFVGAGIQPLTLDFGIKSQONWWAGAPASAAIGTDIGKLPSMMPIQTSSG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :||
258 ING------TISFLNSMQQN------TIGAN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 NIVAT-----TQNGYKPGDLVSYQINDDGTVVGNYSNEQTQLLGQIVLANFANNEG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 IMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANPY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 VAMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKN--MTAFTPTGSATKDLNAWQPAPL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 NSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSEDG 423
                                                                                                                                                                                                                                                                                                                                             10 TGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVG 69
                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 -----VYPFSASNADSYNKKGSVTVFDSQGNAHDMSVYF----VKTGDNNWQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.6%; Score 376.5; DB 4; Length 565;
Best Local Similarity 26.5%; Pred. No. 2e-19;
Matches 125; Conservative 66; Mismatches 160; Indels 121; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETS----NVDMSREM 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ||:|:||| || || || || ||::::
LASEGDNVWSATQSSGVALLGTAGTGNFGTLTNGSIESGIAFLVNVPLNPKL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa polypeptide #3144.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABO70969 standard; protein; 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
                                                                                                                                                                                                                                            Sequence 565 AA;
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Disclosure; SEQ ID NO 19715; 455pp; English
                   Deloughery C,
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         (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                       129 HLNSDGQIVTSNGFAL-----
                                                                                                                                                          segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                          IIIQRGFQMNSKSVTTADTML
                                                                                                                                                                               11.9%;
21.6%;
                   Nolling J,
                                                                                                                                                                             Query Match
Best Local Similarity 21.6%
Matches 108; Conservative
                              2003-615309/58.
                                   N-PSDB; ABD04540.
                                                                                                                                                                     Sequence 269 AA;
                   Rubenfield MJ,
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RESULT 14 ABM68266 g ò The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant or production of P. aeruginosa derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using blochip technology. Sequences ABO67826-ABO84136 represent P aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed 11; 148 160 Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection. 113 ------ 148 353 413 QTADFINPAGLQAIGNNLFLETGSSGAPQVGTPGLNGLGTVAQNTLENSNVNVVEELVNM 241 114 RFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTYAKSPAKTSTALNAVVN 173 234 PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKNMTAFTPTGSATK 293 414 PLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNM 473 1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGFN 60 61 QAGMGAQVGS-VRIIFIQGAFEPGNSVT----DLAIGGKGFFQVTLED-KVHYTRAGNF 69 ELPSGLÓLGTGVRVVGTÓKIFTPGSLQTTEQPLDMAVNGRGFFQVLLPDGTVSYTRDGSF 174 LGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPWRVYDQQGNSHDITVYFDGA 294 DINAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP 354 SMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNI Gaps 93; Indels 254; ; Score 307; DB 7; Length 269; Pred. No. 1.1e-14; 46; Mismatches 93; Indels 2 ä Bush 98US-0094190P 27-JUL-1998;

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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/demplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. Luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes proteins, vectors containing the genes and Ab are also useful the are sensitive to P. luminescens and the proteins are as virulence the properticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. Luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKOOOVVFODLFSQDL----AIGSTGS 56
                                                                                                                                                                                                                                                                                            Antibacterial; fungicide, insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunst F,
                                                                                                                                                                                                                        Photorhabdus luminescens protein sequence #1363.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Frangeul L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; SEQ ID NO 1363; 1205pp; French.
ABM68266 standard, protein, 261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glaser P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECH SCI
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                                                                                                                                                (first entry)
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Best Local Similarity 20.3$
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Photorhabdus luminescens.
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(CNRS: ) CNRS CENT NAT
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                                                                                                                                                                                                                                                                                                                                                                                                                    whooping cough.
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Buchrieser C;
                                                                                                                                                20-NOV-2003
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                                                                        ABM68266;
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57 QGPN--QAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVH-YTRAGNF 113

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114 RFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVN 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKNMTAFTPTGSATK 293
pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (Arcc 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts
                                                                                                                                                                                                                                                                                                                         10 MLRSLYSATSGMLAQQTHIDTTSNNIANVNTTGFKKSRADFNDLFYQAMQYAGTNTSNTT
                                                                                                                                                                                                                                                                                                                                                                                10 ISPDGMEVGLGVRPSAITKMFSQGSFKETENNLDIAITGKGFFQVQLPDGTTAYTRSGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 DINAWOPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP
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                                                                                                                                                                                                                                                                                                  1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPN
                                                                                                                                                                                                                                                                                                                                                                 61 -----QAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLED-KVHYTRAGNF
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 21.0%; Pred. No. 3.1e-13;
Matches 107; Conservative 39; Mismatches 109; Indels 254; Gaps
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                                                                                                                                                                                                            Sequence 271 AA;
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                                                                                                                                                                                                                                                                                                                                                                      410 FYNIPLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSRE 469
                                                      RFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; flagella; associated; flagellum.
        and related polypeptide(s) pylori infection, and to
                                                                                                                  LGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYA@PMRVYDQQGNSHDITVYFDGA
                                                                                                                                                                                234 PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKNWTAFTPTGSATK
                                                                                                                                                                                                                                             294 DENAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a Helicobacter pylori flagella associated protein. The protein may be used in a vaccine to prevent or treat H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori flagella associated protein, 29298130.aa.
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to treat or prevent H.
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                                                                               CEDONGOLTTANGFLIF-----
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useful for vaccines
detect Helicobacter.
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N-PSDB; AAT67783.
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01-APR-1996;
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                                                                                                                                                                                                                                                                          The present sequence is a Helicobacter pylori flagella associated protein, which was found to be homologous to flagellar basal body rod protein following BLAST protein analysis. H. Pylori has been strongly inked to chronic gastrifts and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. Pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are also useful for generating vaccines for immunising subjects against H. Pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. Pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA ragments were bluntended and ligated to unique BexXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BsxXI-cut pMpX vectors; while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts were ligated to each of the 20 pMpX vectors to construct as series of shotgun subclone libraries. The purified DNA samples were then sequenced Note: The ORF/protein reference number for this sequence was obtained from the related specification, W09640893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKNWTAFTPTGSATK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 DLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                       Helicobacter pylori nucleic acid sequences and related proteins - used for diagnostics and therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 SMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNI
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21.0%; Pred. No. 3.1e-13;
.ive 39; Mismatches 109; Indels 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Page 167-168; 235pp; English.
                                          96WO-US018542
                                                                       95US-00561469.
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                                                                                                                                                             WPI; 1997-298052/27.
N-PSDB; AAT77463.
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Best Local Similarity
                                                                                                  (ASTR ) ASTRA AB.
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                                          15-NOV-1996;
                                                                       17-NOV-1995;
            29-MAY-1997.
                                                                                                                                Smith DH;
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QGLQTTSNVIG--QI 182
                                                                                                                                               183 TLANFVNPAGLHSMGDNLFSITNASGDAIVGNPDSQGLGKLRQGFLELSNVRLVEEMTDL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytoplasmic, vaccine, prevention, treatment, infection, identification, binding compound, bacterium, life cycle, activator, bacteria, inhibitor, duodenal ulcer disease, chronic gastritis, diagnosis, envelope, flagella.
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Best Local Similarity 21.0%; Pred. No. 3.2e-13;
Matches 107; Conservative 39; Mismatches 109; Indels 254; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H. pylori flagella-associated membrane protein, 12ge20305orf11.
                                                                                                                                                                                                                     474 IIIQRGFQMNSKSVTTADTMLQKALELKR 502
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                                                                                                                                                                                                                                                               243 ITAQRAYEANSKSIQTADAMLQTVNSLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW20863 standard; protein; 279 AA.
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96US-00630405.
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01-APR-1996;
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239 IQTQRAYEINSKAISTSDQMLQKLTQL 265
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 jejuni flgG protein.

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                                                                                                                                                                                                     Sequence 265 AA;
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                                           294 DLNAWQPAPLVNGLPQFSANFVGAĞIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 PLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNM
                                                                                          RFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVN
                                                                                                                                --PEDTTQ----VN
                                                                                                                                                                 LGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGA
                                                                                                                                                                                                       TDQA-----
                                                                                                                                                                                                                                        234 PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATK
                                                                                                                                                                                                                                                                                                                                                                                          SMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNI
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                     ----QAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLED-KVHYTRAGNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteus mirabilis infection; bacterial infection; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Proteus mirabilis polypeptides and polynucleotides, useful reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or biocontrol agents for plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 8110; 870pp; English.
                                                                                                                                  KLDEQGNLVTSEGYLLI -----PQI ---TL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIIORGFOMNSKSVTTADTMLOKALELKR 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2000; 2000US-00543681
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                                                                                                                                                                                                                                                                                  174 VSVT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-895291/82.
N-PSDB; ADF03653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteus mirabilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 RFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKUMTAFTPTGSATK 293
polypeptides, methods for producing the polypeptides, a method of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polynucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial days or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 MIRSLWIAKTGLDAQQTNMDVISNNLANVSTNGFKRQRAVFEDLLYQTIRQPGAMTSEQT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 NAPSGLOIGTGVRPVATERLHSQGNLAQTNGTRDVAİKGQGFFHVQLPDGTDAYTRDGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 LGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 DLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 PLARFISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
11.1%; Score 286; DB 7; Length 265;
Best Local Similarity 19.7%; Pred. No. 4.2e-13;
Matches 100; Conservative 55; Mismatches 98; Indels 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Basal body rod protein; flgG; flagellum; vaccine; immunogen;
pathogenic bacteria; detection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 QMDQNGQLVTSSGFQIVPA-----ILPETAKKVMV-----
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us-10-009-823a-1.rag

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producible by a transformed host recombinant basal body for protein (1) producible by a transformed host containing an expression vector.

Comprising a nucleic acid selected from; (a) an entire nucleic acid sequence of 1800 base pairs (bp), or the nucleic acid sequence of the protein of 1800 base pairs (bp), and the specification; (b) a nucleic acid sequence of the amino acid sequence of the FlgF protein, a 270 residue sequence, given in the specification; (c) a nucleic acid sequence encoding a functional FlgF basal body rod protein of a flagellum of a strain of Campylobacter; or (d) an immunogenic fragment of an FlgF protein of (a), (b) or (c), and expression means operatively coupled to the nucleic acid molecule for expression by the host of a basal body rod protein of a flagellum of a strain of Campylobacter. (I) is useful in immunological vaccine compositions for in vivo administration to protect of menunological vaccine compositions for in vivo administration protect computations and pathogens that produce basal body rod protein and/or peptide antibodies. The product of the invention has immunostimulatory activity. This sequence of the invention has immunostimulatory activity.
                                                                                                                                                                                                                                                                               Recombinant basal body rod protein producible by a transformed host for use in immunological vaccine compositions for in vivo administration to protect against diseases caused by bacterial pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                          invention describes a novel recombinant basal body rod protein (I)
                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Col 23-26; 28pp; English
                                                      95US-00436748
  95US-00483857
                                                                                                    (CONN-) CONNAUGHT LAB LID
                                                                                                                                                                                                         2000-146875/13.
                                                                                                                                                     Chan VL;
                                                                                                                                                                                                   WPI; 2000-146875,
N-PSDB; AAZ88554
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07-JUN-1995;
                                                                                                                                                        Louie H,
                                                                                                                                                                                                                                                                                                                                                                                                                                        This
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Sequence 263 AA;

FRFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVV 172 NLGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDG 232 293 KDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNWWAGAPASAAAIGTDIGKL 352 412 ---GEQQETQI---GQ 173 413 IPLARFISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVN 472 9 1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPN 1 MARSIHTAATGMVAQQTQIDVTSNNIANVNTAGFKKSRAEFADLMYQVMKYAGTSTSATT 61 QAGMGAQVG-----SVRTIFTQGAFE-PGNSVTDLAIGGKGFFQVTLED-KVHYTRAGN 233 APSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSAT 353 PSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYN Indels 255; Length 263; 9.2%; Score 237.5; DB 3; 18.6%; Pred. No. 1.8e-09; ative 45; Mismatches 115; 121 FTKDNEGNIVNSDGYRL----Conservative Local Similarity les 95; Conserv SVMLP-113 Query Match 138 Matches P ઠે d ò ò g d ઠે ઠે g 8 원 d े

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for
                                                                                                                                                                                                                                                                                                                             DNA encoding Campylobacter flagellum basal body rod proteins - useful f recombinant production of the proteins for use as vaccines against the bacterium, and for its detection, additionally with antibodies raised
                                                                                                                                                       FlgFG operon; flgF protein; flgG protein; basal body rod protein; flagellum; secretory diarrhoea; enteritis; vaccine; therapy.
                         473 MIIIQRGFQMNSKSVTTADTMLQKALELKR 502
                                   AAW73073 standard; protein; 263 AA.
                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 27pp; English.
                                                                                                                                                                                                                                   95US-00436748.
                                                                                                                                                                                Campylobacter jejuni
                                                                                                                                                                                                                                                                   (UTOR ) UNIV TORONTO
                                                                                                                                                                                                                                                                                                    WPI; 1998-593983/50.
N-PSDB; AAV58977.
                                                                                                                                                                                                                                                                                    Louie H, Chan VL;
                                                                                                                                                                                                                                                                                                                                                        with the protein.
                                                                                                                     05-JAN-1999
                                                                                                                                     FlgG protein.
                                                                                                                                                                                                                                  08-MAY-1995;
                                                                                                                                                                                                                                                   08-MAY-1995;
                                                                                                                                                                                                US5827654-A.
                                                                                                                                                                                                                 27-OCT-1998.
                                                                                                    AAW73073;
                                                                   RESULT 20
                                                                            AAW73073
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This sequence represents the Campylobacter figg protein, encoded by the figfs operon of the invention. The figF and figg proteins are basal body rod proteins of the fiagellum of the Campylobacter. The figfs operon and host cells containing it, are useful for the recombinant production of Campylobacter, especially C. jejuni, basal body rod proteins. This bacterium is the cause of secretory diarrhoea and enterties. As such, the peptides produced can be used to raise antibodies, which in turn can be used to detect the presence of the organism diagnosis of the conditions. Additionally, the peptides, and specifically the live vectors (e.g. poxor vaccinia virus) can be used as vaccines against the bacterium, and the antibodies can be used for passive immunisation. The nucleic acids can also be used to detect the presence of the bacterium . 1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPN Indels 253; Length 263; 8.6%; Score 223.5; DB 2; 19.3%; Pred. No. 2e-08; vative 43; Mismatches 115; Conservative Query Match Best Local Similarity Matches 98; Conserv Seguence 263 AA;

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114 RFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVN 173

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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target
                                        233
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                                                                                                                         -----VNSDGYRLLPEMTI-------PEG---- 146
                                                                                                                                                  DLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIXSQQNMWAGAPASAAAIGTDIGKLP 353
                                                                                                                                                                              -----ATAINVATD-GTVS 159
                                                                                                                                                                                                           SMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNI 413
                                                                                                                                                                                                                                    174
                                                                                                                                                                                                                                                               414 PLARFISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNM 473
                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment o pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                           174 LGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGA
                                                                                              234 PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
                                                                    ---DNEGNI-
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                                                                                                                                                                                                                                    160 VMLP------
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                                                                                                                                                                                                                                                                                                                        IIIORGFOMNSKSVTTADTMLOKALELKR 502
                                                                                                                                                                                                                                                                                                                                                ITGORAYEAGSKAITTSDDMLGIVNOLKR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa polypeptide #13656
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                                                                                                                                                                                                                                                                                                                                                                                                                      standard; protein; 2736
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N-PSDB; ABD15052.
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27-JUL-1998;
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components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-860848. Fepresent P. aeruginosa polypepitides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.
                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                 ----LNGTAEPGSTVTLTDGNGNPIGQTTADG-----SGNWSFTPGSQLPNGTVVNVTA 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286
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                                                                                                                                                                                                                                                                                                 72 RIIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGFLNDPSGFTLMG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                248
                                                                                                                                                                                                                                                                                                                                                                SRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTOSEANPYFAL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mature HMW protein; hmw gene; hmwAl; hmwA2; high molecular weight; non-typeable Haemophilus influenzae; NTHi; non-encapsulated; recombinant production; Escherichia coli; antibacterial; vaccine; human disease; otitis media; epiglottitis; pneumonia; tracheobronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TADGSGNWSFTPGIPLPDGTVVNVVARSPSNVDSAPAVITVDGVAPAAP-----VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTG-----SATKDLNAWQPAPLVN-----GLPQFSANFV-----GAGIQPLTLDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1635 GK-----WAFTPATPLANGTVINAL------AQDAAGNNSSPTSATVDSLAPAAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 LESWKGNG--TPPISTSNYSYAQPWRVYDQQGNSHDITVYFDG-APSSTGSKTFEYLVAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SGTMTFS----SNGELKNMTAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 IKSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388 VDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSEDGLRREGNNHYSATLDSGGPEFGLPG
                                                                                                                                                                                                                                     20 GTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQG------PNQAGMGAQVGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae strain 12 mature HWN1A protein, SEQ ID NO:69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T------PLSNGTV-----VNAVAQDAAGNTSGPASTTVDSVAPAA 1759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         497
                                                                                                                                                                                                    212; Indels 142;
                                                                                                                                                                  6.8%; Score 176; DB 7; Length 2736;
22.6%; Pred. No. 0.0021;
ive 56; Mismatches 212; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 TSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMNSKSVTTADTMLQKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae; strain 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB01847 standard; protein; 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 NPSEDGSAASGTDSAGLLM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                          Similarity
                                                                                                                                          Sequence 2736 AA;
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Matches
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The invention relates to the recombinant production of Haemophilus influenzae high molecular weight (HMW) proteins in Escherichia coli. The expression construct used to effect recombinant expression comprises a promoter functional in E. coli (e.g., the T7 promoter) operably Hinked to a modified hmwABC operon from a non-typeable (non-encapsulated) H. colificaters termed hmwABC and hmwABC percent woo hmw gene clusters termed hmwABC and hmwABC each hmwABC operan comprises hmwA, hmw and hmwC genes. The hmwA genes encode the structural HMMA proteins and thmwC genes encode accessory proteins which are responsible for post-translational processing and secretion of the HMWA proteins. The modified hmwABC operon used in the expression construct of the invention contains an A gene modified such that it encodes only the mature HMMA. The invention also discloses hmwA genes (AAAS2175-AS2198) and HMWA proteins (AAB01824-B01849) from the non-typeable H. influenzae strains Joyc, XI, XI, LCDC2, PMHI, 15 and 12. The uncleic acids and vectors are used for the production of recombinant H. influenzae HMW proteins which can be used as vaccines to mediate a humoral or cell-conditions which can be used as vaccines to mediate a humoral or cell-condition and close the mediate and the mediate and close hww genes from other non-typeable can be used to isolate and clone hww genes from other non-typeable strain of H. represents a mature HMWA protein reactions. The present sequence represents a mature HMWA protein reactions. The present sequence represents and our substitution of the present sequence. (Updated on 12-SEP-2003 to standardise of field)
                                                                                                                                                                                                                                                                            Nucleic acid molecule for producing recombinant high molecular weight proteins of Haemophilus which are used as a vaccine to provide protection against Haemophilus induced diseases in humans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - - - - SALTIDAKNVTVNNNITSHKAVSI -----SATSGEITIKTGTTINATTGNVEITAQTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ILGGIESSSGSVTLTATEGALAVSNIS------GNTVTVTAN-SGALTTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.7%; Score 173.5; DB 3; Best Local Similarity 22.8%; Pred. No. 0.00088; Matches 119; Conservative 80; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Fig 28F-Q; 307pp; English.
                                                                                                                                                                        Klein MH;
                      99WO-CA000938.
                                                             98US-00167568
98US-00206942
                                                                                                                        (CONN-) CONNAUGHT LAB LTD
                                                                                                                                                                        Yang Y,
                                                                                                                                                                                                                 2000-303789/26.
                                                                                                                                                                                                                                        N-PSDB; AAA52196.
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                                                                                                                                                                        SM,
                  07-OCT-1999;
                                                               07-OCT-1998;
                                                                                 08-DEC-1998;
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NA
                                                                                                                                                                                                                                                                                                                                                                              HMW; high molecular weight protein; virus; vaccine; influenza; epitope; immunity; haemophilus influenzae.
102 YSNSQVVDFYNIPLARFISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLET
                                                                     876 ----TTEASSHITSAKGQVNLSAQDGSVAGSINAANVTLNTTGTLTTVKGSNINATSGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The isolation and purification of the high molecular weight protein enables the identification of the major protective epitopes of the protein by conventional epitope mapping. These epitopes can then be synthesised using standard techniques and incorporated into fully synthetic or recombinant vaccines. (Updated on 25-MAR-2003 to correct field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRIIFTQGAFEPGNS------VTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGFLND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-typeable haemophilus
                                         356 MPIQTSSGNSTARNGSSSTRRYSQDGYPQGDL--VDVTITSEGKL---QGK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1536;
                                                                                                                        932 VINAKDAELNGAALGNHTVVNATNANGSGSVIATTSS---RVNITG
                                                                                                                                                                       462 SNVDMSREMVNWIIIQRGFQMNSKSVTTADTMLQKALELKR 502
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6.7%; Score 173.5; DB 2;
Best Local Similarity 22.8%; Pred. No. 0.0014;
Matches 119; Conservative 80; Mismatches 222;
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                                                                                                                                                                                                                                                                                                                                                     High molecular weight protein 1 (HMWI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nolecular weight surface proteins exhibit immunogenic properties.
                                                                                                                                                                                                                                                   AAR41723 standard; protein; 1536
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                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae
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26-APR-1994
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24;

Gaps

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1117 -AGLTIDAKNVTVNNNİTSHKAVSİ----SATSGEITTKİGİTINATTGNVEITAQIGS 1170
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synthesised using standard techniques and incorporated into fully synthetic or recombinant vaccines. This sequence is claimed to be the same as that given in AAR41723 (High molecular weight protein 1) although it does differ slightly. (Repeated regions which are possibly incorrect and occur in the corresponding nucleotide coding sequence contribute to these differences). (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 MPIQTSSGNSTARNGSSSTRRYSQDGYPQGDL--VDVTITSEGKL---QGK-----
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                                                                                                                                                                                                                                                           6.7%; Score 173.5; DB 2; Length 1536; 22.8%; Pred. No. 0.0014; ive 80; Mismatches 222; Indels 100;
                                                                                                                                                                                                                                                     Length 1536;
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for this region is LNVSESGEFN. (See comments)."
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immunity; haemophilus influenzae; gene cluster
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N-PSDB; AAQ49508.
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The HMM1 protein encoded by this sequence is useful in a vaccine to protect against disease caused by non-typeable Haemophilus which are not controlled by H. influenzae type b (Hib) vaccines. The encoded protein can also be used as a carrier for protective Hib polysaccharide (in a conjugate vaccin against meningitis) or for other antigens, haptens, etc. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                            New immunogenic high mol. wt. proteins of non typeable Haemophilus
                                                                                                                                                                                                           Claim 2; Page 31; 127pp; English.
                                                                                                                                                                           useful in protective vaccines.
                                                                   Barenkamp SJ, St Geme JW;
               (BARE/) BARENKAMP S J. (SGEM/) ST GEME J W.
                                                                                                     WPI; 1994-316665/39
                                                                                                                          N-PSDB; AAQ72293
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Sequence 1536 AA;

1059 24; 123 2 12 MKTHSTGLGTVSNNIANAN-TIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVGS 71 VRIIFTQGAFEPGNS-----VIDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGFLND 6.7%; Score 173.5; DB 2; Length 1536; 22.8%; Pred. No. 0.0014; Ative 80; Mismatches 222; Indels 100; Gaps Matches 119; Conservative Query Match Best Local Similarity 0907 d ò g

183 124 PSGFTLMGSRISNNPNIKKETLEPIOLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQS ò

238 : | |: | : | |: | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 184 EANPYFALLESWKGNGT----PPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSSTG

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----ILGGIESSSGSVTLTATEGALAVSNIS------GNTVTVTAN-SGALTTLA 1214 | : : | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 239 SKTFEYLVAMNPSEDGSAASGTDSAGLL---MSGTMTFSSNGELKANMTAFTPTGSATKDL 1171

1275 GGTISGNTVN------VTANAGDLTVGNGAE-----INATEGAATLTTSSGKL--- 1316 296 NAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNWWAGAPASAAAIGTDIGKLPSM 356 MPIQISSGNSTARNGSSSTRRYSQDGYPQGDL--VDVTITSEGKL---QGK----

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SNVDMSREMVNWIIIQRGFQMNSKSVTTADTMLQKALELKR 502 1424

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AAB01846 standard; protein; 1536 AA RESULT 26 AAB01846

AAB01846;

(revised)
(first entry) 12-SEP-2003 11-SEP-2000 SASSES

HMW protein; hmw gene; hmwAl; hmwA2; high molecular weight; non-typeable Haemophilus infilenzae; NYH4; non-encapsulated; recombinant production; Escherichia coli; antibacterial; vaccine; human disease; otitis media; epiglottitis; pneumonia; tracheobronchitis; Haemophilus influenzae strain 12 HMW1A protein, SEQ ID NO:67.

Haemophilus influenzae; strain 12.

WO200020609-A2.

13-APR-2000.

99WO-CA000938 07-OCT-1999;

98US-00167568. 98US-00206942. 07-OCT-1998; 08-DEC-1998;

(CONN-) CONNAUGHT LAB LTD.

Klein MH; × Yang Loosmore SM,

Nucleic acid molecule for producing recombinant high molecular weight proteins of Haemophilus which are used as a vaccine to provide protection against Haemophilus induced diseases in humans. 2000-303789/26. N-PSDB; AAA52195

Example 16; Fig 28A-Q; 307pp; English.

The invention relates to the recombinant production of Haemophilus

influenzee high molecular weight (HWW) proteins in Escherichia coli. The

expression construct used to effect recombinant expression comprises a

promoter functional in E. coli (e.g., the T7 promoter) operably linked to

a modified humABC operon from a non-typeable (non-encapsulated) H.

colusters termed hum1ABC and hum2ABC. Each humABC operan comprises humA,

colusters termed hum1ABC and hum2ABC. Each humABC operan comprises humA,

colusters termed hum1ABC and hum2ABC. Each humABC operan comprises humA,

colusters termed hum2ABC and hum2ABC. Each humABC operan comprises humA,

colusters termed hum4ABC operan used the structural HMMA proteins

condition and humABC operan used in the expression construct of

the invention contains an A gene modified such that it encodes only the

condition also discloses humA genes (AAAS2175-AS2199)

and HMMA proteins (AAB01824-B01849) from the non-typeable H. influenzae

the invention contains also discloses humA genes (AAAS2175-AS2199)

and HMMA proteins (AAB01824-B01849) from the non-typeable H. influenzae HMM

conteins which can be used as vaccines to mediate a humoral or cell
conteins which can be used as vaccines to mediate a humoral or cell
conteins which can be used as vaccines to mediate a humoral or cell
conteins which can be used as vaccines to mediate a humoral or cell
conteins which can be used as vaccines to mediate a humoral or cell
conteins which can be used as vaccines to mediate a humoral or cell
conditions by H. influenzae (e.g., otitis media, epiglottitis, pneumonia and

tracheobronchitis). The HMM proteins are also useful as antigens in

immunoassays for detecting antibodies against Heamophilus, HMM proteins

can be used to isolate and clone hum genes from other non-typeable

cracked by H. influenze and clone hum genes from other hym proteins

can be used to isolate and clone hum genes from the ron-typeable

cracked by H. influence and clone hum genes from the present sequence

c

Sequence 1536 AA;

Query Match 6.7%; Score 173.5; DB 3; Length 1536; Best Local Similarity 22.8%; Pred. No. 0.0014; Matches 119; Conservative 80; Mismatches 222; Indels 100; Gaps

1059 12 MKTHSTGLGTVSNNIANAN-TIGYKOOQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVGS 1011 IKAGVDGENSDSDATNNANLTIKTKELKL-----TÖDLNI----SGFNKAEITAKDGS

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1116 1060 DLTIGNTNSADGTNAKKVTFNQVKDSKISADG-HKVTLHSKVE--TSGSNNNTEDSSDNN 71 VRIIFIQGAFEPGNS-----VTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGFLND

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1316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSM 355
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(1) a vector comprising a promoter operably linked to the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic essential gene; cell proliferation; drug design
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Xu HH;
                                                                                                                                                                   184 EANPYFALLESWKGNGT-----PPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSSTG
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PSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQS
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Forsyth RA,
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Yamamoto R,
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-GCT-2001; 2001US-0342223P.
08-FEB-2002; 2002US-00072851.
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Trawick JD,
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encoding a polypeptide whose expression is inhibited by the antisense mucleic acid, (2) a host cell containing the vector; (3) an isolated antisense mucleic acid, (4) an antibody capable of specifically binding the polypeptide of the specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular composition; (7) identifying a gene in an operon required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the activity of against a biological pathway in which a proliferation-required gene or the biological dentifying a gene required for cellular proliferation or the biological corresponds a gene compound that inhibits proliferation of an oraginsm acts; (9) manufacturing an antibiotic; (10) profifing a compound; a servexpresses or underexpresses or (10) profiling a compound; a activity; (11) a culture comprising strains in which the gene product is overxpresses or underexpresses or (10) profiling a compound; a activity; (11) a culture comprising strains in which the cent of the strains is present in a culture or collection of corpanies, or (13) identifying the target of a compound that inhibits the extent or or an activity proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational corrections or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, crequired to the praget prockaryotic essential genes. Note: The sequence data for this corpus and incertly from WIPO at the present data for this corpus and incertion format directly from WIPO at the present sequence is encoded by one of the prace of the present data for this corpus propries. Sequence 3705 AA;

1111 SNGLLINVA 2711 2712 KNDASTAFDFGATVGGAFTGTVN-----LNNSTFDLSGNNTT-VLAQATLKLSSGNL 2762 2477 2403 24; 487 181 376 GMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGFLN 123 DPSG-FILMGSRISNNPNIKKETLEPIOLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKT 2450 IKGGDFTI---SIDNN------GLAGOTNISDGASVT QSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSSTGSKT 242 FEYLVAMNPSEDGSAAS----GT--DSAGLLMSGTWTFS-----SNGEL-----KOMT -----FGIKSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTSSGNSTARNGSSSTRR 2610 QYALAGNSKLIVASINNI.-GASSSVALAGT--GDILSLSGFNGFFGNSVFGSGVLQVT-377 YSQDGYPQGDLVDVTITSEGXLQGKYSNSQVVDFYNIPL----ARFT---SEDGLRREG 429 NNHYSATLDSGGPEFG-LPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMNSKSV GSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQA ------TGNGIFN Indels 191; Gaps DB 6; Length 3705; 284 AFTPTGSATKDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLD-6.7%; Score 172.5; DB 6; 21.7%; Pred. No. 0.0059; ive 58; Mismatches 180; 2404 GNGGELTSTDTLINTGMINVTDGILNLENGGASSISGCL--Query Match
Best Local Similarity 21.7
Matches 119; Conservative 326 2478 ო 63 182 g 셤 ठ d

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This protein comprises the high molecular weight surface protein HWW1 (125 kDa) of non-typeable Haemophilus influenzae strain 12 that has the immunological ability to protect against disease caused by a non-typeable Haemophilus strain and is characterised by at least one surface-exposed B cell epitope that is recognised by monoclonal antibody AD6. The HWW1 and AAT90996). The expressed protein is truncated, starting at residue 42 of the full-length gene product. HWW2 (see AAW30294), HWM3 (see AAW30291) and HWW4 (see AAW30292) have also been identified. A conjugate comprising HWM1 linked to an antigen, hapten or polysaccharide, and a synthetic peptide of 6-150 amino acids corresponding to at least protective epitope of HWM1 are also claimed. HWW proteins, conjugates and be used in vaccines, as immunogens for preparation of antibodies and as antigens for detection of these antibodies. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                      Non-typeable Haemophilus; high molecular weight surface protein; HMW1, hmw1A gene; immunogen; vaccine; otitis media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High molecular weight proteins of non-typeable Haemophilus influenzae useful for vaccine production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.5%; Score 167.5; DB 2; Length 1536;
Best Local Similarity 22.3%; Pred. No. 0.004;
Matches 116; Conservative 81; Mismatches 224; Indels 100; Gaps
                                                                                                                                     Non-typeable Haemophilus high mol.wt. surface protein HMM1.
                                                                                                                                                                                                                                                                                                                                                            /note= "encoded by AAG"
                                                                                                                                                                                                                                                                                           note= "encoded by CTA"
                                                                                                                                                                                                                                                                                                                            'note= "encoded by GAT"
                  AAW30293 standard; protein; 1536 AA
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 66-70; 183pp; English.
                                                                                                                                                                                                                      Haemophilus influenzae; strain 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-00617697
                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US004707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT90994, AAT90996.
                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BARE/) BARENKAMP S J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-503038/46.
                                                                                                                                                                                                                                                                                                                                          Misc-difference 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 1536 AA;
                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barenkamp SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                           WO9736914-A1
                                                                                   17-OCT-2003
14-APR-1998
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                                                  AAW30293
AAW30293
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1171 ----ILGGIESSSGSVTLTATEGALAVSNIS------GNTVTVTATAN-SGALTTLA 1214
                                                                                                                                                                                  1274
                                                                                                                                                                                                                                                                                    | : :| : :| : :| 1317 ----TTEASSHITSAKGOVNLSAQDGSVAGSINAANVTLNTTGTLTTVKGSNINATSGTL 1372
                                                                                                                                                                                                                                       1275 GGTISGNTVN------VTANAGDLTVGNGAE-----INATEGAATLTTSSGKL--- 1316
                                                                                                                                                                                                                                                                                                                                                   1373 VINAKDAELNGAALGNHTVVNATNANGSGSVIATTSS---RVNITG----DLITINGL-- 1423
                                                                                                                                                        295
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                                                                                                                                                                                                              355
                                                                                                                                                                                                                                                                     401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                              296 NAWOPAPLVNGLPOFSANFVGAGIOPLTLDFGIKSQONMWAGAPASAAAIGTDIGKLPSM
                                        124 PSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQS
                                                                                                 184 EANPYFALLESWKGNGT----PPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSSTG
                                                                                                                                                     239 SKTFEYLVAMNPSEDGSAASGTDSAGLL---MSGTMTFSSNGELKNWTAFTPTGSATKDL
                                                                                                                                                                         402 YSNSQVVDFYNIPLARFISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLET
                                                                                                                                                                                                                                                                    356 MPIQTSSGNSTARNGSSSTRRYSQDGYPQGDL--VDVTITSEGKL---QGK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Äξ
                                                                                                                                                                                                                                                                                                                                                                                                  SNVDMSREMVNMIIIQRGFQMNSKSVTTADTMLQKALELKR 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by Prokaryotic essential gene #23938.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID NO 66335; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU38411 standard; protein; 2468 AA
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0042923P.
08-FEB-2002; 2002US-00672881.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-029926/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200277183-A2
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                                                                                                                                                                                                                                                                                                                                                                                 462
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Wall D,
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ABU38411
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The invention relates to an isolated nucleic acid comprising any one

12 MKTHSTGLGTVSNNIANAN-TIGYKQQQVVFQDLFSQDLAIGSTGSQGFNQAGMGAQVGS

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71 VRIIFTQGAFEPGNS-----VTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGFLND 123

23;

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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated oplypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, (7) identifying a compound that influences the activity of dentifying a gene required for cellular proliferation; (8) identifying a gene required for cellular proliferation of the test compound that inhibits proliferation of an organism acts; (8) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene proliferation of an organism acts; (13) identifying the target of a compound that inhibits the proliferation of an organism of an organism or capable of the strains is present in a culture or collection of a complexity of proliferation of an organism. The antisense nucleic acids required for cellular proliferation to solve the capable of the strains or screening for homologous nucleic acids required for cellular proliferation to solve the capable of the capable or and capable or activity or action of an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig.wipo.int/pub/published_pct_sequences
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Sequence 2468 AA;

: | : | :: | :: | :: | 1.18 1387 248 328 IXSQQNMWAGAPASAAAIGTDJGKL-------PSMMPIQTSSGNSTA 367 368 RNGSSSTRRYSQD--GYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSEDGLR 425 191 PTG-----GAGIQPLTLDFG 327 1298 GTVVNAVA---------QDPA-GNTGPQGSTTVDAVAPNTPVVNPSNGNL 1338 ----LNGTAEPGSTVTLTDGNGNPIGQTTADG-----SGNWSFTPGSQLPNGTVVNVTA | : | : | : | : | SDAAGNTSLPAITT----TVDSSLPSIPQVDPSNGSVISGTADAGNTIITDGNGNPIGQV NPSEDGSAASGTDSAGLLM-----SGTWTFS----SGTWTFST 132 SRISHNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANPYFAL 192 LESWKGNG--TPPISTSNYSYAQPMRVYDQQGNSHDITVYFDG-APSSTGSKTFEYLVAM 20 GTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQG------PNQAGMGAQVGSV 72 RIIFIQGAFEPGNSVIDLAIGGKGFFQVILEDKVHYTRAGNFRFIQDGFLNDPSGFTLMG Query Match
6.4%; Score 166; DB 6; Length 2468;
Best Local Similarity 21.9%; Pred. No. 0.01;
Matches 112; Conservative 67; Mismatches 197; Indels 136; -AGNTSGPVSTTVDAVAPATPVIDPSNGVELS 1749 455 REGNNH--YSATLDSGGPEFGLPGTSNYGKLS 1388 249 287 쉱 g ₹ 셤 ઠે 셤 ਨੇ g ઠ g ð g ö ò

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20 GTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQG------PNQAGMGAQVGSV

72 RIIFIQGAFEPGNSVIDLAIGGKGFFQVILEDKVHYTRAGNFRFIQDGFLNDPSGFTLMG 131

132 SRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANPYFAL 191

192 LESWKGNG--TPPISTSNYSYAQPMRVYDQQGNSHDITVYFDG-APSSTGSKTFEYLVAM

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The present invention relates to a method of identifying a compound capable of altering the sensitivity of a microorganism to an antimicrobial agent by employing efflux pumps comprising polypeptides concoded by the following genes: PA1874, PA4142, PA2389, PA1876, PA4143, PA2390 or PA1163. The method is useful for identifying modulators of microbial resistance of an organism in a biofilm. The methods are also useful for identifying genes that encode proteins that play a role in biofilm resistance. The method is particularly useful for screening compounds or discovering compositions that will inhibit biofilm formation and overcome their resistance mechanisms. These methods are particularly useful in medical, industrial or natural settings, where formation of biofilms can have serious negative consequences and result in high costs both in human health and economic terms. The present sequence is a protein shown in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying modulators of microbial resistance of organisms in biofilms, e.g. inhibitor of biofilm formation, by employing expression controls, or efflux pumps containing polypeptides, of genes associated with biofilm resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.4%; Score 166; DB 6; Length 2468; Best Local Similarity 21.9%; Pred. No. 0.01; Matches 112; Conservative 67; Mismatches 197; Indels 136; Gaps
                                                                                                                                                                                                                                                                                                                              Microbial resistance gene PA1874 protein.
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                                                                                 ABP59933 standard; protein; 2468
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                                                                                                                                                                                                                                                                                                                                                                                                       Biofilm; microbial resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-2001; 2001US-0323241P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L8-SEP-2002; 2002WO-US029565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DART-) DARTMOUTH COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-468567/44.
N-PSDB; ACC59398.
                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003041483-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                            28-AUG-2003
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                                                                                                                                                                   ABP59933;
ABENULT 31
ABEN 59333
ID ABEN 59333
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1610
            ---GSGNWSFTPGTPLANGSVINALAQDAAGNNSSPTSATVDSLAPAAPVIDPSNGSVIA 1667
                                                                                                                                              GTAEAGATVILTDGNGNPIGO-----VTADG--SGNWSFTPGTPLSNGTVVNAVAQDA-- 1718
                                        327
                                                                                 367
                                                                                                                           RNGSSSTRRYSQD--GYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSEDGLR 425
                                                                                                                                                                                                                                                                                                                              Cytoplasmic, vaccine, prevention, treatment, infection, identification, binding compound, bacterium, life cycle, activator, bacteria, inhibitor, duodenal ulcer disease, chronic gastritis, diagnosis, envelope.
                                                      PTG-----SATKOLNAWQPAPLVN-----GLPQFSANFV-----GAGIQPLTLDFG
                                                                                  --- PSMMPIQTSSGNSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to
                                                                                                                                                                                                                                                                                                          H. pylori flagella-associated protein 26588588.aa
                                                                                 328 IKSQQNMWAGAPASAAAIGTDIGKL-------
                                                                                                                                                                                REGNNH--YSATLDSGGPEFGLPGTSNYGKLS 455
                                                                                                                                                                                                                                                                                                                                                                                                                  /label= unknown
/note= "encoded by TWA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             by AGS"
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                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                            AAW20361 standard; protein; 124 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label= unknown
NPSEDGSAASGTDSAGLLM---
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96US-00630405.
                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori
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                                                                                                                                                                                                                                                                                      11-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
01-APR-1996;
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249
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                                                                                                                                                                                                                         RESULT 31
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mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. Pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. Pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts
                                                                                                                                                                                                                                                                                                                                                            500
                                                                                                                                                                                                                                                                                                                                                                               63 LGWDEBGKLKFGKIRHKYLETSNVNAGNALTNLILMQRGYSMNARAFGAGDDMIKEAISL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel enterohaemorragic Escherichia coli 0157:H7-specific nucleic acid molecule. A polynucleotide of the invention has anti-bacterial activity. The polypeptide can be used in detection and/or treatment of 0157:H7 infection. The nucleotide sequence of the genome of Enterohaemorragic E coli 0157:H7 was determined. The present sequence represents an E. coli 0157:H7-specific polypeptide of the
                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterohemorragic Escherichia coli 0157:H7-specific nucleic acid molecule and a polypeptide and its use, a polypeptide, a vector and a host cell.
                                                                                                                                                                                                                                                                                       392 ITSEGKLQGKYSNSQVVDFYNIPLARFTSEDGLRREGNNHY---SATLD-----SGGPE
                                                                                                                                                                                                                                                                                                            3 IEENĞVISLAFSNGVVEPVARIGIXAFTNDQGLRKIĞGNLYEMQEGTINGENRPLXGNPI
                                                                                                                                                                                                                                                                                                                                                              443 FGL--PGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMNSKSVTTADTMLQKALEL
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 1058
                                                                                                                                                                                                                                                 11;
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22.6%; Pred. No. 0.036;
ive 71; Mismatches 189; Indels 236;
                                                                                                                                                                                                              Length 124;
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                          6.4%; Score 165.5; DB 2;
32.0%; Pred. No. 0.00016;
tive 24; Mismatches 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC01014 standard; protein; 5291 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enterohaemorragic; anti-bacterial
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                                                                                                                                                                                                              Query Match
Best Local Similarity 32.0%
Matches 39; Conservative
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Best Local Similarity
Matches 145; Conserv
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                                                                                                                                                                           Sequence 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 KK 124
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35;

Gaps

Conservative

This sequence is a H. pylori flagella-associated protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to indentify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by

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968 NISASLGGTYSQTTNVTVTSAVLNSIOVSPADISVAKGNTKAYTAI
Rosa Croda JH
Barocchi M,
                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 4; 59pp; English
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Ko AI, Galvao Reis M,
Matsunaga J, Riley LW,
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                                                                              WPI; 2004-022913/02.
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        GATGMKTH----STGLGTVS-----NNIANANTIGYKQQQVVFQDLFSQDLAI--GSTG
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                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the protein sequence of bacterial immunoglobulin-
like Leptospira protein 2 (BigL2) from Leptospira kirschneri. BigL2 has a molecular weight of 205,000 and comprises 12 tandem repeat sequences of approximately 90 amino acids, with a large C-terminal domain. The repeat regions show over 90% sequence homology to the repeat sequences of other resolated leptospiral Big proteins, BigL1 ADF83254 and BigL3 polypeptides from recombinant or native antigen preparations are immunogenic, inducing an immune response against pathogenic spirochaetes. The invention provides BigL1, BigL2 and BigL3 polypeptides useful in diagnostic, therapeutic and vaccine applications, especially for the diagnostic, therapeutic and vaccine applications, especially for the diagnostic and prevention of infection with Leptospira species in medical and veterinary applications.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49
                                                                                                                                                                      New Bacterial Immunoglobulin-like (Big) polypeptides and nucleic acids, useful as vaccines or for diagnosing, preventing or treating infection diseases caused by Spirochetes e.g. Treponema, Borellia or Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 SDQVAWNSSNSSILQISNLNAVPKREIQSPSSGGLG-----TARITATLEAISSYTDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIGGKGFFQVTLEDKVHYTRAG-NFRFTQDGFLNDPSGFTLMGSRISNNPNIKKETL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            703 FTVSAAVLDSIQVTLEDSPIAKGTST--RAIATGVFSDGSNLNISDQVIMDSSQTNVIQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          818 SVANGLIQ---NFTATGV-----YSDGSNQNLTDSVTWASSNPAVATISNASGTNGKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVNAATLVSIEVSPTNPSVSSGLTVPFTATGVYTDGSNQNLTSQVTWNSSNTNRATISNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 IGATGMKTHSTGLG-TVSNNIANA------NTIGYKQQQVVFQDLFSQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AIGSTGSQGPNQAGMGAQVGSVRTIFTQGAFEPGNSVTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---EPIQLDFNDPT------VAKSPAKTSTALNAVVN-------LGDSTDKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DITVYFDGAPSSTGSKTFEYLVAMNPSEDGSAASGTDSA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       761 GVLETGPKKKLMNSPANG---NSTTGTSRITATLGGVSGYADLTVIAPSLTSIQIDPTHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 PIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         869 TLOTGSTNISASLGATTS-----DPSVLTVT------NATLTSITIAPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GNNHYSATLDSGGPEFGLPGTSNYGKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1013
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   Haake
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.3%; Score 162; DB 8; Length 195
19.3%; Pred. No. 0.015;
tive 80; Mismatches 241; Indels
JH, Siqueira IC,
M, Young TA;
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181

224

760

301

868

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523 SVNAATLVSIEVSPINPSVSSGLTVPFTATGVYTDGSNQNLTSQVTWNSSNTNRATISNA 582
                                                               NGTOGIALGSSVGTTNISATLGAVTSSATTLTVTNAVLNSITITPSLPSVAVGRSLNLTA 642
                                                                                                             643 TGTYSDGSNQDLTTSVAWTSTDSSIVSVDNASGRQGQTTGVAQGNTQISATLGGTSSAIN 702
                                                                                                                                                                                                                                                                                                                                                                       908 SFNIAKGINQDFVATGYYTDGSSRDLTTQVTWNSSNTSTATISNANGTQGRMAAVDTGST 967
                                                                                                                                                                                                                    761 GVLETGPKKKLMNSPANG---NSTTGTSRITATLGGVSGYADLTVIAPSLTSIQIDPTHP 817
                                                                                                                                                                                                                                                PLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNM-----WAGAPASAAAIGTDIGKLPSMM 356
                                                                                                                                                                                                                                                                                                  357 PIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLA 416
                                                                                                                                                                                                                                                                                                                         869 TLQTGSTNISASLGATTS------DPSVLTVT-------NATLTSITIAPTS 907
                                                                                                                                                                                                                                                                                                                                                     RFTSEDGLRRE---------GNNHYSATLDSGGPEFGLPGTSNYGKL 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Helicobacter infection, gastroduodenal disease, gastritis, disease.
                                                                                                                                                             818 SVANGLTQ---NPTATGV----YSDGSNQNLTDSVTWASSNPAVATISNASGTNGKAT
                                                                                                                                                                                             GLLMSG----TMTFSSNGELKNMTAFTPTGSAT-----KDLNAWQPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                       SVN-----QLETSNVDMSREMVNMIIIQRGFQMNSKSVTTADTML 494
                                                                                         ----OSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSH---
                                                                                                                                            -----DITVYFDGAPSSTGSKTFEYLVAMNPSEDGSAASGTDSA-
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                                        -----VAKSPAKTSTALNAVVN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miller C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; protein; 1230 AA.
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97US-00881227.
97US-00902615.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. pylori GHPO 690 protein.
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(HUMA-) HUMAN GENOME SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-542293/46.
N-PSDB; AAX13994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHPO protein;
peptjc ulcer d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIGGKGFFQVTLEDKVHYTRAG-NFRFTQDGFLNDPSGFTLMGSRISNNPNIKKETL--- 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New substantially purified BigL1, BigL2 and BigL3 polypeptides and encoding polynuclectides, useful for diagnosing, preventing or treating Leptospiral infections in humans and other mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a substantially purified polypeptide. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of infection with Leptospira species in humans and other mammals, including those of veterinary importance. The present sequence represents the amino acid sequence the Leptospira kirschneri bacterial-Ig-like (Big) domain containing
                                                                                                                               L. kirschneri bacterial-Ig-like (Big) domain containing protein BigL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 IGATGMKTHSTGLG-TVSNNIANA--------NTIGYKQQQVVFQDLFSQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -AIGSTGSQGPNQAGMGAQVGSVRTIFTQGAFEPGNSVTDL
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                                                                                                                                                        therapy, vaccine; infection; Leptospira; bacterial-Ig-like;
Omain; BigL2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.3%; Score 162; DB 8; Length 1954; 19.3%; Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsunaga J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Siqueira IC,
                                                                                                                                                                                                                                                 /note= "Encoded by AGTA"
                                                    ADK13634 standard; protein; 1954 AA
                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 4; 52pp; English
                                                                                                                                                                                                                                                                                                                             2002US-00147299
                                                                                                                                                                                                                                                                                                                                                     19-SEP-2002; 2002US-00147299
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丐
                                                                                                      (first entry)
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Matches 125, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Croda
                                                                                                                                                                                                                                                                                                                                                                                                       CRODA J H.
SIQUEIRA I C.
MATSUNAGA J.
RILEY L W.
BAROCCHI M A.
                                                                                                                                                                                              Leptospira kirschneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reis MG, LLC
Young T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2004-268783/25.
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                                                                                                                                                                                                                                                                                                                                                                                 KO A I.
REIS M G.
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                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                             19-SEP-2002;
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                                                                                                       17-JUN-2004
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                                                                             ADK13634;
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(RILE/)
(BARO/)
(YOUN/)
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Zyskind JW; Xu HH;

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Ohlsen | Forsyth |

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Haselbeck R, Yamamoto R,

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Malone C,
Carr GJ,
     06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
06-FSB-2002; 2002US-0072851.
06-MAR-2002; 2002US-036269P.
                                                       (ELIT-) ELITRA PHARM INC
                                                                          Zamudio C,
Trawick JD,
                                                                                                      WPI; 2003-029926/02.
N-PSDB; ACA34839.
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                                                                                                                                                                                                                                                                                                                      MNPSEDGSAASGTDSAGLLMSGT--MTFSSNGELK------NMTAFTPTGSATK 293
                                                                                                                                                                                                                                                                                                                                        ----QATTQSGSNGGNSITYNVQQITLTSNGLLNQITTNLKSVNGGNGASGTGSGNGTS 778
                                                                                                                                                                                                                                                                                                                                                                                                                                             SQVVDFYNIPLARFIS---EDGLRR--EGNNHYSATLDS --GGPEFGLPGISNYGKL--S 455
                                                                                                                                                                              596
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                                                                                                                                                                                                                      625
                                                                                                                                                                                                                                        NNPNIKKETLEP-----IQLDFNDPTVAKS-PAKTSTALNAVVNLGDSTDKTQSEANP 187
                                                                                                                                                                                                                                                     247
                                                                                                                                                                                                                                                                                                                                                               DLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP 353
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                                                                                                                                                                                                                                                                                                                                                                                                     354 SMMPIQTSSG-----NSTARNGSSSTR-RYSQDGYPQGDLVDVTITSEGKLQGKYSN 404
                                                                                                                                                                                                                                                                                                                                                                                                                          851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                          GTVSNNIANANTIGYKOOOVV--FODLFSQDLAIGS-TGSGGPNOAGMGAQVGSVRTIFT 76
                         invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also bused for the production of antibodies. The products can also be used forter and diagnosis
                                                                                                                                                                       ----YSSSSGSNNGYTPCNST--NGSNKTSGNNCYEPNKQQNATTATATTDSNLQKVYND
                                                                                                                                                                                                                                                                                 YFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSSTGSKTFEYLVA
                                                                                                                                                                                                                                                                                            ------QNVSNFQQSIQNAFQNQESNIQAWANAIY
                                                                                                                                         Gaps
                  sequence represents a Helicobacter pylori GHPO protein of the
                                                                                                                  Query Match 6.2%; Score 160; DB 2; Length 1230; Best Local Similarity 21.6%; Pred. No. 0.011; Matches 114; Conservative 71; Mismatches 182; Indels 160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded by Prokaryotic essential gene #16496
 Page 301-306; 2054pp; English.
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                                                                                                  Sequence 1230 AA;
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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
conclude a polypeptide whose expression is inhibited by the antisense
conclude acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
contisense nucleic acid; (4) an antibody capable of specifically binding
contisense nucleic acid; (4) an antibody capable of specifically binding
contisense nucleic acid; (4) an antibody capable of specifically binding
contisense nucleic acid; (4) an antibody capable of specifically binding
contisense nucleic acid; (4) an antibody capable of specifically binding
contisense nucleic acid; (4) an antibody capable of specifically binding
contisense nucleic acid; (4) an antibody capable of specifically binding
contisense nucleic acid; (7) identifying a gene polypeptide; (6) inhibiting cellular
contisense nucleic acidity; (1) aciditication or the biological
contisense nucleic acidity; (1) antibody cellular proliferation of an
congound's acitivity; (1) antibody cellular proliferation of an
congound's acitivity; (1) antibody cellular proliferation of an
congound's acitivity; (1) antibody cellular proliferation of
compound's acitivity; (1) antibody cellular proliferation of
congounds; or (3) identifying the target of a compound that inhibits the
confounds; or (13) identifying the target of a compound that inhibits or collection of
conditises or acreening for homologous nucleic acids are useful for
confound a cillular proliferation or solate candidate molecules for rational
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aerucinosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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21.6%; Pred. No. 0.011;
.ive 71; Mismatches 182; Indels 160;
                                                                                                                                                                                                Claim 25; SEQ ID NO 58893; 1766pp; English
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Best Local Similarity 21.6'
Matches 114; Conservative
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353
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                                                                                      294 DLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAIGTDIGKLP
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                                                                                                                                    ----TAYQMLT---
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ABU21223 standard; protein; 3073 AA

Protein encoded by Prokaryotic essential gene #6750.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Zyskind JW; Xu HH; 耳罩 Ohlsen I Forsyth I а, Haselbeck R, Yamamoto R, Malone C, Carr GJ,

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 49147; 1766pp; English.

38

RESULT

the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound, a activity; (11) a culture compising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or owhich each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational detrifying proteins or for screening homologous nucleic acids required for cellular proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryoric essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at first province and province and province and province and province and province of the printed specification, but was obtained in electronic format directly from WIPO at 2328 2439 2388 2214 2274 2614 2674 255 ---AASGTD----SAGLL-----MSGTMTFSSNGELKNMTAFTP--TGSATKDLNAWQ 299 2675 KTYNSVATTMDALNAKIAT-GSTDGVVYDTSAHNKLTL--GGVNATTPVTVANVAAATSD 2731 161 201 400 450 S---TGSQGPNQAGMGAQVGSVR-TIFTQGAFEPGNSVTDLAIG----GKGFFQVTLEDK 104 : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 2389 TPVKVŠN------VANGVANNDAVNVAQLTAMGGTINSSGVVTNSF-VAYDDTTKGSI 4 SLFIGAT-----GMKTHSTGLGTVS-NNIANANTIGYKQQQVVFQDLFSQD----LAIG 2164 SLLEGAVPVTNYIAVSQNVTGGGSTSASNDLNAMAIG------PLAAASGVGALAVG 2215 AGSIAGSDASTAVGTGAAVGSVNSTAIGYSASVGVNSANSLAIGYNSRAQALNSLAIGTE 105 VHYTRAGNFRFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFN---DPTVAKSP 2275 ASATSAGSIAIGYGAFLN-PSATNSMALGL----NSSVSAANAVAIGYNAVADRANÀVS-2555 GAVGAERQIINVANATNSTDAVNLSQLQAMGANVNSSGVVTNAFVAYDDSTKGKVTLGGV KYSNS--QWDFYNI PLARFTSEDGLRREGNNHYSATLDSGGPEFGLP-----GTSN 162 AKTSTALNAVVNLGDSTDKTQS-EANPYFALLESWKGNGTP-------2497 -- NIVNGGGIKYFHANSTLADSSATGTDSVAIGGAANATAANSVALGANSVAGRANAVSV PSMMPI-----QTSSGNSTARNGSSSTRRYSQDGYPQGDLVDV----TITSEGKLQG 202 -PISTSNYSYAQPMRVYDQQGNSHDITV----YFDGAPSSTGSKTFEYLVAMNPSEDGS-6.1%; Score 156.5; DB 6; Length 3073; 22.2%; Pred. No. 0.072; ive 73; Mismatches 228; Indels 187; 314 -FVGAGIQPLTLDFGIKS-----QQNMWAGAPASAAAIGTD-300 PAPLVN--GLPQFSAN-------DOAVNLAQLKAAGLNVDTSGNVTNSFV 2758 451 YGKLSVNQLETS--NVDMSREMVNMII 475 Matches 139; Conservative Local Similarity Sequence 3073 AA; 256 23 353 401 Query Match \$ g δ 임 ઠ ò В ò ద ð D. 8 g Š 엄 $\overset{\circ}{\circ}$ 원 à g ò 셤 ò

32;

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This sequence represents the Campylobacter figF protein, encoded by the figFG operon of the invention. The figF and figG proteins are basal body rod proteins of the flagellum of the Campylobacter. The figFG operon and host cells containing it, are useful for the recombinant production of Campylobacter, especially C. jejuni, basal body rod proteins. This bacterium is the cause of secretory diarrhoea and enteritis. As such, the peptides produced can be used to raise antibodies, which in turn can be used to detect the presence of the organism diagnosis of the conditions. Additionally, the peptides, and specifically the live vectors (e.g. poxor vaccinia virus) can be used as vaccines against the bacterium, and the antibodies can be used for passive immunisation. The nucleic acids can also be used to detect the presence of the bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding Campylobacter flagellum basal body rod proteins - useful for recombinant production of the proteins for use as vaccines against the bacterium, and for its detection, additionally with antibodies raised
                                                                                                                                                          FlgFG operon; flgF protein; flgG protein; basal body rod protein; flagellum; secretory diarrhoea; enteritis; vaccine; therapy.
                 AAW73072 standard; protein; 270 AA.
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                                                                                                                                                                                                                                                                                                                            95US-00436748.
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                                                                                     05-JAN-1999 (first entry)
                                                                                                                                                                                                                 Campylobacter jejuni.
                                                                                                                                                                                                                                                                                                                                                                                                UTOR OTHOROTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-593983/50.
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                                                    AAW73072;
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AAW73072
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54 --TGSQGPNQAGMG-AQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQV--TLEDKVHYT 108
                                                                                                                                                                                                                                                 61 TRDASRFVNTTIDGIPQVSQEYIDFSLGSLKATNNPLDLAMTREDAFYLVQTKDGEVRLT 120
                                                                                                                                1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVV---FQDLFSQ----DLAIGS- 53
6.0%; Score 155; DB 2; Length 270;
30.7%; Pred. No. 0.003;
tive 28; Mismatches 64; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                    109 RAGNFRFTQDGFLNDPSGFTLMGSRISNNP 138
                                                                                                                                                                                                                                                                                                                                    46; Conservative
  Query Match
Best Local Similarity
                                                Matches
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RESULT 40
ABU36440
AAY51376 standard; protein; 270 AA.
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AAY51376;

RESULT 39 AAYS1376
ID AAYS
XX
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This invention describes a novel recombinant basal body rod protein (I) producible by a transformed host containing an expression vector comprising a nucleic acid selected from, (a) an entire nucleic acid sequence of 1800 base pairs (bp), for the nucleic acid sequence of the FigF gene having 810 bp, both given in the specification, (b) a nucleic acid encoding the amino acid sequence of the FigF protein, a 270 residue sequence, given in the specification; (c) a nucleic acid sequence of the figF protein, a 270 residue encoding a functional FigF basal body rod protein of a flaggellum of a strain of Campylobacter; or (d) an immunogenic fragment of an FigF protein of a caid molecule for expression means operatively coupled to protein of a flaggellum of a strain of Campylobacter. (I) is useful in immunological vaccine compositions for in vivo administration to protect against diseases caused by bacterial pathogens that produce basal body rod proteins. (I) are also useful as immunogens, as antigens in immunossays, or for procedures for the detection of antibacterial, campylobacter, basal body rod product of the invention has immunostimulatory activity. This sequence for the invention has immunostimulatory activity. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 --TGSQGPNQAGMG-AQVGSVRIIFTQGAFEPGNSVTDLAIGGKGFFQV--TLEDKVHYT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVV---FQDLFSQ----DLAIGS- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant basal body rod protein producible by a transformed host for use in immunological vaccine compositions for in vivo administration to protect against diseases caused by bacterial pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. MQNGYYQATGGMVTQFNKLDVITNNLANINTSGYKRDDVVIADFKRIFKETQDELPIENH
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                                                                                               Basal body rod protein; flgF; flagellum; vaccine; immunogen; pathogenic bacteria; detection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.0%; Score 155; DB 3; Length 270; Best Local Similarity 30.7%; Pred. No. 0.003; Matches 46; Conservative 28; Mismatches 64; Indels 1
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121 KDGNFQLDDEGYLVNKQGYKVLSSDYFNNP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1a; Col 21-24; 28pp; English
                                                                                                                                                                                                                                                                                      95US-004B3857.
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                 (first entry)
                                                         C. jejuni flgF protein.
                                                                                                                                                              Campylobacter jejuni.
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N-PSDB; AAZ88553.
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                                                                                                                                                                                                                                                                                                                            08-MAY-1995;
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                    04-MAY-2000
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid enoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation or the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, sactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of proliferation of an organism. The antisense nucleic acids are useful for cidentifying proteins or serventing for homological acids required for a compound that inhibits the configuration of an organism or required for antisense nucleic acids required for a configured for a compound that inhibits the configuration of an organism or required for antisense nucleic acids are useful for a configuration of an organism or remaining the remaining for rational action of an organism or remaining for parallement of a compound that inhibits the configuration of an organism or remaining for parallement of a compound that inhibits and the configuration or an organism and the confi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
                                                                                                                                                                                   Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or cellular proliferation to isolate candidate molecules for rational
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Forsyth RA,
                                                                                                                                           Protein encoded by Prokaryotic essential gene #21967
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25; SEQ ID NO 64364; 1766pp; English
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  ABU36440 standard; protein; 2204 AA
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2001US-00815242.
; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
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                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC.
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Trawick JD,
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06-SEP-2001;
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Wall
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Zyskind JW; Xu HH;

5.9%; Score 151.5; Sequence 2204 AA

DB 6; Length 2204;

24; 1570 |: | : | : | : | 1631 LSTTITIPEIPYRYDLSVPIDIPITGTVVATTPNSFTIPGFQIRVLLGPAAVLVNEMIGP 1690 1841 .842 TLNFGVANQGGLNAG------IGNLGSVNIGFVNTGDSNLGIGNLGDLNFGGVNI 1890 1891 GGNNIGIANTGIFDIGLANLGSYNIGLANLGDDNLGPGNAGSYNIGFANFGSDNLGFANT 1950 ---IGPSSGFFHTGAGHVSGFGNFGAGNMSGSGNF------GAGNSGFFNAGGLG 1782 147 148 IQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANPYFALLESWKGNGTPPISTSN 207 322 422 22 1516 NSGSFNTGLG-NTGSTNT----GLFNPGNVNTGVGNTGSINTGSINTGSFNTGSTNTGSFNTGSTNTGSF 1571 NLGDHNTGSFNSGDYNTGYFNAGDYNTGVANTGANTGAFISGNYSNGFFWRGDYQGLIG 208 YSYAQPMRVYDQQGNSHDITVYFDGAPSSTGSKTFEYLVAMNPSEDGSAASG-TDSAGIL 3 GSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTG-----1783 NSGLINFGALQSGLANLGNTISGVYNTSTLDLATPA-FGSGIANIGANLAGLFLDNTGNL MSGTMTFSS-NGELKNMTAFTPTGSATKDLNAWQPAPLVNGLPQFSANFVGAGIQ---PL 378 --SQDGYPQGDLVDVTITSEGKLQGKYSN--SQVVDF----YNIPLARFTSED----TLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTSSGNSTARNGSSSTRRY---56 SQGPNQAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGK-----GFFQV--ed. No. 0.11; Mismatches 220; Indels 185; GSYNIGFANTGNNNIGVGLTGNGQIGIGSLNSGSNNIGLFNSGSGNIG 1998 ----ATLDSGGPEFGL -- PGTSNYG 452 Pred. No. --KVHYTRAGNFRF--64; 20.2%; Best Local Similarity 20.2 Matches 119; Conservative 100 TLED-1737 267 323 d ð 셤 g ð 셤 ò ò g ð ď 셤 ò δ 쉱 ठ d ਨੇ

Search completed: October 26, 2004, 09:05:38 Job time : 81 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- nucleic search, using frame_plus_p2n model

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Run on:

Total number of hits satisfying chosen parameters:

summaries

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

3413475 seqs, 2563800928 residues

Searched:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

BLOSUM62

Scoring table:

Title: Perfect score:

Sequence:

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Sequence 2, Appli
Sequence 11957, A
Sequence 16, Appl
Sequence 16, Appl
Sequence 2008, Appl
Sequence 17, Appli
Sequence 18, Appli
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APPLICANT: Rosey, Everett Lee
APPLICANT: Sinistaj, Meri
APPLICANT: Sinistaj, Meri
APPLICANT: Sinistaj, Meri
APPLICANT: Sinistaj, Meri
APPLICANT: Parsons, Ustlef
APPLICANT: Parsons, Usu
APPLICANT: Ankenbauer, Robert G.
TITLE OF INVENTION: LAMSONIA DERIVED GENE AND RELATED FLGE
TITLE OF INVENTION: POLYPEPTIDES, PEPTIDES AND PROTEINS AND THEIR USES; FILE REFERENCE: DAVI150.001APC
CURRENT APPLICATION NUMBER: US/10/009,823A
CURRENT APPLICATION NUMBER: PCT/AUGO/00437
PRIOR APPLICATION NUMBER: PCT/AUGO/00437
PRIOR APPLICATION NUMBER: US 60/133,973
PRIOR FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 60, Appl
Sequence 58, Appl
Sequence 18, Appl
Sequence 79, Appl
Description
                                                                                                                                                                                                  6 US-10-335-977-56
6 US-10-335-977-16
6 US-10-335-977-1
6 US-10-335-977-3
6 US-10-335-977-3
6 US-10-335-977-3
6 US-10-335-977-3
6 US-10-335-977-3
7 US-10-346-2
7 US-10-35-977-3
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6 US-10-280-122A-11957
5 US-10-127-032-16
6 US-10-282-122A-14579
6 US-10-335-977-58
16 US-10-398-221-10
16 US-10-398-221-2058
6 US-10-398-221-3855
US-10-398-221-3855
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-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2 1/USPTO_spool/US10009823/runat_26102004_100131_1718/app_guery.fasta_1.647
-O=/cgn2 1/USPTO_spool/US10009823/runat_EagEap -SUFFIX=rnpb-MINMATCH=0.1
-LOOPCL2 -LOOPERXT=0 -UNITS=bits -START=1 -END=-1 -MATRIXI-Blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MX=10
-TTRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MX=10
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1. (cgn2_6/ptodata/1/pubpna/PCT_RUM PUB.seq:*
2. (cgn2_6/ptodata/1/pubpna/PCT_RUM PUB.seq:*
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1 MMGSLFIGATGMKTHSTGLG......NSKSVTTADTMLQKALELKR
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SUMMARIES

	Db 901 GCACCATTAGTCAATGGTTTTCCACAAATTTTGTTGGTGCAGGAATACAG 960	Db 1021 TCCGCTGCTGCCATAGGTACAGAATTGCGAATTGCCATCATGATGCCAATACAAAAA 1080 Qy 361 SerSerGlyAsnSerThrAlaArgAsnGlySerSerThrArgArgTyrSerGlnAsp 380 Db 1081 TCCAGCGGTAATTCTACAGCAAAAAAGGATCTTCAACAAAAAAAA	381 GlyTyrProGlnGlyAspLeuValAspValThrIleThrSerGluGlyLysLeuGlnGly	Oy 401 LystySerAsserGlnValValAspPheTyrAsn11eProLeuAlaArgPheThrSer 420 1201 AAGTATAGTAATAGTCAGGTTGTTGATTTTTTATATATTTTAGTAGCGCTTTAGAAT 1260 OV 421 GluAsnGlvGlvGlvGlvGvarasanHistyrSeralaThrEenserGargivGlvGlvA	1261 GAGGATGGATTAAGACGAGAAAGGGAATAACCATTATTCCGCAACACTTGACTCAGGGGGGGG	441 ProGlubheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGlu 4	461 ThrSerAsnValAspNetSerArgGluMetValAsnMetIleIleIleGli 	481 GlnMetA 1441 CAGATGA	Oy 501 Lysarg 502 	RESULT 2) GENERAL INFORMATION: APPLICANT: Wang, Liangsu APPLICANT: Zamudio, Carlos APPLICANT: Malone, Cheryl	/ APPLICANT: Haselbeck, Robert // APPLICANT: Ohlsen, Kari // APPLICANT: Zyskind, Judith // APPLICANT: Wall, Daniel	; APFLICANT: Travick, John ; APPLICANT: Carr, Grant ; APPLICANT: Robert ; APPLICANT: Forsyth, R.	APPLICANT: XU, H. TITLE OF INTERNITOR: FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A	; CUKKENY FILING DAIE: 2003-02-20 ; PRIOR APPLICATION NUMBER: 60/191,078 ; PRIOR FILING DATE: 2000-03-21 ; PRIOR APPLICATION NUMBER: 60/206,848 ; PRIOR FILING DATE: 2000-05-23
; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 2 ; LENGTH: 1509 ; TYPE: DNA ; CRGANISM: Lawsonia intracellularis US-10-009-823A-2	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: D0.00\$ Mismatches: Cuery Match: 100.00\$ Mismatches: 0 Cuery Match: 100.00\$ Mismatches: 100.00\$	502) x US-10-009-823A-2 (1-1509) 31ySerLeuPhelleGlyAlaThrGlyWetLysThrHisSerThrGlyLeuGly	DB I ATGATGGGGGGTTTGTTTATTGGTGCAACGGTATGAAACCCATAGTACAGGGTTGGGT 60 Qy 21 ThrValSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValVal 40	41	Qy 61 GlnalaGlyMetGlyalaGlnValGlySerValargthrIlePheThrGlnGlyAlaPhe 80	Qy 81 GlubroGlyasnSerValThraspLeualaileGlyGlyLysGlyPhePheGlnValThr 100	Oy 101 LeugludspLysValHisTyrThrargAlaglyAsnPheArgPheThrGlndspGlyPhe 120	Qy 121 LeuAsnAspProSerGlyPheThrLeuMetGlySerArgileSerAsnAsnProAsnIle 140	Oy 141 LysLysGluThrLeuGluProIleGlnLeuAspPheAsnAspProThrValAlaLysSer 160	Oy 161 ProalalysThrSerThrAlaLeuAsnalaValValAsnLeuGlyAspSerThrAspLys 180 	Oy 181 ThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGluSerTrpLysGlyAsnGlyThr 200	Qy 201 ProProlleSerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGln 220	Qy 221 GlyasnSerHisaspileThrValTyrPheAspGlyalaProSerSerThrGlySerLys 240	Qy 241 ThrPheGluTyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThr 260	Qy 261 AspSerAlaGlyLeuLeuMetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys 280

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                                                                                                                                   IleThrValTyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeu 245
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                                                     -----TyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSerHisAsp
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; Publication No. US20030113742A1
; GENERAL INFORMATION:
; APPLICANT: Whiteley, Marvin
; APPLICANT: Lory, Stephen
; APPLICANT: Greenberg, Everett Peter
; TITLE OF INVENTION: BIOFILM FORMATION
; TITLE OF INVENTION: BIOFILM FORMATION
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|GGCTTGAGCGGATTGGCCGGTGCGTCGTCGATCTCGACGTCATCGGCAACAACATCGCG
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Matches:
Conservative:
Mismatches:
Indels:
                 PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR FILING DATE: 2010-02-09
PRIOR FILING DATE: 2010-02-16
PRIOR PLING DA
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ORGANISM: Burkholderia cepacia
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Best Local Similarity:
Query Match:
DB:
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    ----GlySerLysThrPheGluTyrLeuVal---AlaMetAsnProSerGluAsp
                                                                                                                    -----ATGAGCTTCAACGTCACCTTC
                                                                                  254 GlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPhe
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Yskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Presyth, R.
APPLICANT: Porsyth, R.
                                                                                                                        709 TCGAACAAGACGCCG--
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Matches:
Conservative:
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FILE REFERENCE: UIZ-070CP
CURRENT APPLICATION NUMBER: US/10/127,032
CURRENT APPLICATION NUMBER: US 00/285,190
PRIOR APPLICATION NUMBER: US 60/285,190
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-4
NUMBER OF SEQ ID NOS: 170
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1389
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; ORGANISM: Pseudomonas aeruginosa
US-10-127-032-16
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715 ACGGGCACGTCGACGCCC--------
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                                      LeuAsnAlaValAsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnPro
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FILE REPERENCE: ELITRA,034

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CURRENT APPLICATION NUMBER: 05/10/282,122A

CURRENT PILING DATE: 2003-02.0

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PRIOR APPLICATION NUMBER: 60/206,48

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PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PELICATION NUMBER: 60/230,335

PRIOR PILING DATE: 2000-09-09

PRIOR PELICATION NUMBER: 60/242,578

PRIOR PELICATION NUMBER: 60/242,578

PRIOR PILING DATE: 2000-10-23

PRIOR PELICATION NUMBER: 60/253,625

PRIOR PELICATION NUMBER: 60/253,625

PRIOR PELICATION NUMBER: 60/253,625

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-10-20

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136 TCGGTCGCA-----TCGGCCGTCAACAATCCGATCGGCATCGCACGATG 180
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Matches:
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ORGANISM: Burkholderia mallei
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US-10-282-122A-14579
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121 TTTGTGGATATGCTCTCTCAAGTCAAACTCATCGCTACGCCACCCCTATAAAAACGGGTTG 180
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241 TITICGCAAGGAATATCCAAAACACGGATGTCAAAACCGATCTAGCGATTCAAGGGGAT 300
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                                                                                                                                                                                                                                GTGAGAAACGGGAGCGATACCGGTAATAAAGGGAGCGATACGGACGCTTTAAAAGTGGAT 480
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                                                                                                                    75 PheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaileGlyGlyLys 94
                                                                    113 PheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMet-----
                                       ---GlnAlaGlyMetGlyAlaGlnValGlySerValArgThrile
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                                                                                                                                      NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTM-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...2157; SEQUENCE DESCRIPTION: SEQ ID NO: 58: US-10-335-977-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                               ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 021.09-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                   US-10-335-977-58
; Sequence 59, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ 1D NO: 58:
SEQUENCE CHARACTERISTICS:
LENGHY 2157 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: Massachusetts
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ORIGINAL SOURCE:
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Mismatches:
Indels:
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FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR PILING DATE: 2001-10-04
PRIOR PILING DATE: 2001-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
SEQ ID NOS: 4025
SOFTWARE: PatentIn version 3.0
LENGTH: 1163020
LENGTH: 1163020
TYPE: DNA
ORGANISM: Listeria innocua
                                                                                                                                                                                      nucleotide:
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Matches:
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NAME/KEY: misc_feature
LOCATION: (1)...(end)
OTHER INFORMATION: n can be any
US-10-398-221-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheGlnMetAsnSerLysSerValThrThrAlaAspThrMetLeuGlnLysAlaLeuGlu 499
                 ---IleLysSerGlnGln 332
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US-10-398-221-10
US-10-398-221-10
; Faquence 10, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: KLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
                                                                                                                                                                                                                                                                                                                                                                                      366 ThrAlaArgAsnGlySerSerSerThrArgArgTyrSer----
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2146 CTCAAGCAA 2154
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                 325 AspPheGly-
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639657 639777 640107 195 TrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyrAlaGlnProMet 214 114 40 26 16 20 115 PheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMetGlySerArglle 135 SerAsnAsnProAsnIleLysLysGluThrLeuGluProIleGlnLeuAspPheAsnAsp 155 ProThrValAlaLysSerProAlaLysThrSerThrAlaLeuAsnAlaValAsnLeu 175 GlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGluSer 1 MetMetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 639598 grgacarcaaaraararricccaargcgaacaccagggraraaaaaaaagggrccrr ThrvalSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValVal PheGlnAspLeuPheSerGlnAsp------LeuAlalleGlySerThrGlySer GlnGlyProAsnGlnAlaGlyMetGlyAlaGlnValGlySerValArgThrIlePheThr 97 PheGlnVal-----ThrLeuGluAspLysValHisTyrThrArgAlaGlyAsnPheArg

PRIOR APPLICATION NUMBER: FR 00/12 697 NUMBER OF SEQ ID NOS: 4025 SOFTWARE: 2000-10-04 SEQ ID NO 2058 LENGTH: 3011208 IENGTH: 3011208 TYPE: DIA ORGANISM: Listeria innocua US-10-398-221-2058 Alignment Scores: 1.09e-35 Length: 3011208 Score: 484-50 Matches: 137 Best Local Similarity: 27.024 Mismatches: 177 Best Local Similarity: 42.214 Conservative: 77 Best Local Similarity: 18.748 Indels: 105 US-10-009-623A-1 (1-502) x US-10-398-221-2058 (1-3011208)	Qy 1 MetMetGlySerLeuPheileGlyAlaThrGlyWetLysThrHisSerThrGlyLeuGly 20	Qy 41 PheGlnAspLeuPheSerGlnAspLeuAlaIleGlySeiThrGlySer 56	Qy 77 GlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLysGlyPhe 96	OY 115 PheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuWetGlySerArgile 134	OY 155 ProThrValAlalysSerProAlaLysThrSerThrAlaLeuAsnAlaValValAsnLeu 174 130283 GCAATTCCAGGCGAACAAAAAATGGTAAGCTTAAGGGGTAACATTCCACTTGATTGG 730342 OY 175 GlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGluSer 194 Db 730343 GGCAAAAAGATACGATTTCTTCCAGA	Oy 215 ArgValTyrAspGlnGlnGlyAsnSerThrSerAsnTyrSerTyrAlaGlnProMet 214 215 ArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPheAspGlyAla 233 215 ArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPheAspGlyAla 233 730373 TCTGTATACGATAATGCTGGAAAACATAAACTTCAAGTCAATATGAAAGCTGCGACA 730432 Oy 234 ProSerSerThrGlySerLysThrPheGluTyrIeuValAlaMetAsnProSerGluAsp 253 730433 CCAGATGCGAGTGCTATACCTATGAATATGAAATTCAAATGGAC 730480 Oy 254 GlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPhe 273
OY 215 ArgvalTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPheAspGlyAla 233	Qy 314 PheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsn 333 Db 640327	Qy 354 SerMetMetProIleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSerSer 373 :: :::::: Db 640366 AACTACGGTACCAACCAA 640383 Qy 374 ThrArgArgTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAspValThrIleThr 393 Db 640384 GTATTCTCACCAACTTCTGACGGAAAAGGCGCTGCAACTGTAAAAGACTACGCAGTTACC 640443	Qy 394 SerGluGlyLySLeuGlnGlyLySTyrSerAsnSerGlnValValAspPheTyrAsnIle 413 Db 640444 GATTCTGGTTATTGCAGTGAGTTACTCAGACGTACAGTTATCCCAGTTGCCCCAACTT 640503 Qy 414 ProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyrSer 433 Db 640504 GCGGTTGCTACTTCTCCAATGAAAAGGCGTTAGTCAAAATGGGGAATATGTT 640563	Qy 434 AlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGlyLys 453	Qy 474 IleIleIleGlnArgGlyPheGlnMetAenSerlysSerValThrThrAlaAspThrMet 493 1::	SULT 7 10-398-221-2058 Sequence 2058, Application US/1035 Sequence 2058, Application US/1035 Sepulcation No. US20040018514A1 SEPULCANT: KUNST, Frederik APPLICANT: GLASER, Philippe TITLE OF INVENTION: Listeria inno FILE REFERENCE: 344 702 - US CURRENT APPLICATION NUMBER: US/10 CURRENT FLING DATE: 2003-03-27 PRIOR FILING DATE: 2003-03-27 PRIOR FILING DATE: 2001-04

) NAME/KEY: misc_feature ; LOCATION: (1). (end) ; OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u US-10-398-221-3855	Alignment Scores: 5.46e-38 Length: 5998 Pred. No.: 469.50 Matches: 134 Score: Similarity: 41.62% Conservative: 77 Best Local Similarity: 26.43% Mismatches: 191 Query Match: 18.16% Indels: 105 DB: 10500000000000000000000000000000000000	MerMetGlySerLeuPhelleGlyAlaThrGlyMetLy	Oy 21 ThrvalSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTVrLysGlnGlnGlnValVal 40	Oy 41 PheGlnAspLeuPheSerGlnAspbeualaileGlySerThrGlySer 56	Oy 57 GINGIYPEOASHGINAlaGIYMEtGIYAlaGINVAlGIYSETVAlAKGTHrIlePheThr 76	Cy 77 GINGLYALaPheGluProGlyAsnSerValThrAspLeualalleGlyGlyLysGlyPhe 96	Oy 97 PheGlnValThrLeuGluAspLysValHisTyrThrArgAlaGlyAsnPheArg 114	Qy 115 PheThrGlnaspGlyPheLeuAenAspProSerGlyPheThrLeuMetGlySerArgIle 134	Oy 135 SerAsnAsnProAsnIleLysLysGluThrLeuGluProIleGInLeuAspPheAsnAsp 154	Qy 155 ProThrValAlalysSerProAlaLysThrSerThrAlaLeuAsnAaValValAsnLeu 174	Qy 175 GlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGluSer 194	Oy 195 TrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyrAlaGlnProMet 214	215 ArgValTyrAspGlnGlnGlyAsnSerHisAsplleThrValTyrPheAspGlyAla 233	Db 5337 TCTGTATATGTTGCTGGCGGAAAACATAAACTTCAAGTGAATATGAAAGCTGCTACA 5396	Qy 234 ProSerSerThrGlySerLysThrPheGluTyrLeuValAlaMetAsnProSerGluAsp 253	Oy 254 GlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPhe 273	Qy 274 SerSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySerAlaThrLys 293
Db 730481 GGAAAAGCGTTAACTCCTCCA	730523 ACGCGAAGCCAACTTACAACCCTGATGCA	9 6	Qy 354 SerMetMetProlleGlnThrSerSerClyAsnSerThrAlaArgAsnGlySerSer 373 ::::: Db 730631 AACTACGGTACCAACAA 730648	Qy 374 ThraxgargTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAspValThrIleThr 393	Oy 394 SerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValValAspPheTyrAsn11e 413	Oy 414 ProLeuhlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyrSer 433	Qy 434 AlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGlyLys 453 Db 730829 CCAGGATATCTTCTGGAGATGCAGTTTACGGCGTTGCTGGCCAAAACGGAGCTGGCGGA 730888	OY 454 LeuSerValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMetValAsnMet 473	Qy 474 IleIleGlnArgGlyPheGlnMetAsnSerLysSerValThrThrAlaAspThrMet 493 :::	Qy 494 LeuGlnLysAlaLeuGluLeu 500 	RESULT 8 US-10-398-221-3855 ; Sequence 3855, Application US/10398221	; Publication No. US20040018514A1 ; GENERAL INFORMATION: ; APPLICANT: KUNST, Frederik	; APFLICANT: GLASER, PALLIPPE ; TITLE OF INVENTION: Listeria innocua, genome and applications ; FILE REFERENCE: 344 702 - US	; CURRENT APPLICATION NUMBER: US/10/398,221 ; CURRENT FILING DATE: 2003-03-27	; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061 ; PRIOR FILING DATE: 2001-10-04 ; PRIOR APPLICATION NUMBER: FR 00/12 697 ; PRIOR FILING DATE: 2000-10-04	; NUMBER OF SEQ ID NOS: 4025 ; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 3855 : IENGTH: 5998	TYPE: DNA ORGANISM: Listeria monocytogenes 4b FEATURE:

Best Local Similarity: 25.73% Mismatches: 187 Query Match: 16.03% Indels: 121 DB: 9 Gaps: 13 US-10-009-823A-1 (1-502) x US-09-790-988-1 (1-640681)	Qy 4 SerLeuPheileGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGlyThrValSer 23	Oy 24 ASIASINILEALAASIANIAASITHIILEGIYTYILYSGINGINGINGINAIVAIPHEGINASP 43	Qy 44 LeuPheSerGlnAspLeuAlaileGlySerThrGlySerGlnGlyProAsnGlnAlaGly 63 ::	Oy 64 MetGlyAlaGlnValGlySerValArgThrIlePheThrGlnGlyAlaPheGluProGly 83	Qy 84 AsnSerValThrAspLeuAlaIleGlyGlyLysGlyPhePheGlnValThrLeuGlu 102	Qy 103 AspLysValHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsn 122	Qy 123 AspProSerGlyPheThrLeuMetGlySerArgIleSerAsn 136 :::	'Qy 137 AsnProAsnIleLysGluThrLeuGluProIleGlnLeuAspPheAsnAspProThr 156	Qy 157 ValalıysSerProAlaLysThrSerThrAlaLeuAsnAlaValValAsnLeuGly 175 ::	Oy 176ASPSerThrAspLysThrGlnSerGluAlaAsnProTyrPhe 189	Oy 190 AlaLeuLeuGluSerTrpLysGlyAsnGlyThrProProIleSerThrSerAsnTyrSer 209 372714 ACTTATATTAGC372725	Qy 210 TyralaGinProMetArgValTyrAspGinGinGiyAsnSerHisAspIleThrValTyr 229	Qy 230 PheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeuValAlaMetAsn 249	Qy 250 ProSerGluAspGlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGly 269	Qy 270 ThrWetThrPheSerSerAsnGlyGluLeuLyBAsnWetThrAlaPheThrFroThrGly 289 ::: :::::	290 SeralaThrLysAspLeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuProGln 309	Db 372912 AAAGATTCTAAAAAG
Db 5487 AATGCGCAGGGCGAATTAACAAACCCAGACGCA	Oy 314 PheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerClnGlnAsn 333 Db 5556AAACAAGTCAAT 5567	Qy 334 MetTrpAlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLySLeuPro 353	QY 354 SerMetMetProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSerSer 373 Db 5595 AACTACGGAACCAA 5612	Oy 374 ThrargargTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAspValThrIleThr 393 :::	QY 394 SerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValValAspPheTyrAsnIle 413	Oy 414 ProLeualaargPheThrSerGluAspGlyLeuargArgGluGlyAsnAsnHisTyrSer 433	Qy 434 AlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGlyLys 453 Db 5793 CCAGGATTATCTTCTGGCGATGCAGTATACGCGTTGCTGGCCAAAATGGCGCTGGCGG 5852	Qy 454 LeuSerValAsnGlnLeuGluThrSerAsnValAspWetSerArgGluMetValAsnWet 473 Db 5853 ATTAGGGGTTCTTCTAGAAGGTTCAAACGTACACTTGTCCCGGGAATTCGTTAACTTA 5912	Qy 474 IleIleGlnArgGlyPheGlnMetAsnSerLysSerValThrThrAlaAspThrMet 493 ::	Qy 494 LeuGlnLysAlaLeuGluLeu 500 Db 5973 ATGAATCAAACTGTGCACTTG 5993	RESULT 9 US-09-790-988-1 ; Sequence 1, Application US/09790988	563	RA KI DNA OF BACTER	PPLICATION NU ILING DATE: LICATION NUME ING DATE: 200	NUMBER OF SEQ ID NOS: 7 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1 LENGTH: 640681	; TYPE: DNA ; ORGANISM: Buchnera sp. 02-09-790-988-1	Alignment Scores: 2.4e-29 Length: 640681 Score: 414.50 Matches: 132 Percent Similarity: 39.96\$ Conservative: 73

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408 ValAspPheTyrAsnIleProleuAlaArgPheThrSerGluAspGlyLeuArgArgGlu 427
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                               428 GlyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGly
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                                                                                    292 ThrLysAspLeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuProGlnPheSer
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291 72 201 367 258

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241 TITICGCAAGGCAGCCCTAAAGAAACGGAGAATAATTTAGATATTTGCTATTACAGGTAAA 300
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121 TITAACGACTIGITITACCAAGCGATGCAATACGCCGGCACCAACACAAGCAACACGACT
                                  61 -------GlnAlaGlyMetGlyAlaGlnValGlySerValArgThr1le
                                                                                                      75 PheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLys
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               RESULT 11
US-10-335-977-1
US-10-335-977-1
; Sequence 1, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
    APPLICANT: DOUGLAS SMITH et al
    APPLICANT: DOUGLAS SMITH et al
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION ELIATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     789
107
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109
254
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                         COUNTRY: USA

ZIP: 02109-1875

COMPUTER: READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Windows NT 4.0

SOFTWARE: UNIX

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/335,977

FILING DATE: 30-Dec-2002

PRIOR APPLICATION NUMBER: 08/93,002

ATORNEY/AGENT INFORMATION:

NAME: MAINTED ATE: 17-DEC-1997

ATORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 36,207

REFERENCE/DOCKET NUMBER: 36,207

TELEPRONE: (617)1227-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-009-823A-1 (1-502) x US-10-335-977-1 (1-789)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...789
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-335-977-1
                                                                                                                                                                    NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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288.00
28.68%
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DB:
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414 ProleuhlaArgPheThrSerGluAspGlyLe 520 ACTTGGCLAATTTGCAATCGGCGGGGGGG[] 580 ATCACCACGCTGGGGGGTGCGATGGGGGGGGTGCGGGGGGGG	HargargGluGlyasnAsnHisTyrSer 433 TCATTCTATGGGGATAATTGTTTCC 579 YLeuProGlyThrSerAsnTyrGlyLy8 453 YLeuProGlyThrSerAsnTyrGlyLy8 453 CAACCGGATTCTCAAGGCTTAGGCAAG 639 LASPMetSerArgGluMetValAsnMet 473	rLysserValThrThrAlaAspThrMet 493	10335977 99A1 MITH et al MUCLEIC ACID SEQUENCES MUCLEIC ACID SEQUENCES MUCLEIC ACID AND AMINO ACID SEQUENCES MUCLEIC ACID AND THERAPEUTICS DIAGNOSTICS AND THERAPEUTICS SS: We cockribld Street Street Street M: Windows NT 4.0 DATA: DEATA: DATA: DEATA: EBR: US/10/335,977 TA: TA: TA: TA: TA: TA: 10335,977 TA: TA: TA: TA: TA: TA: TA: T	
O O O O O O O O O O O O O O O O O O O		474 Ileileiledinargdlyphedinmeta	-977-2 AL Application US/ tion No. US200400527 AL INFORMATION: RAPLICANT: DOUGLAS S IITLE OF INVENTION: TITLE OF INVENTION: CORRESPONDENCE ADDRESSEE: LAHI STREET: 28 Stat CITY: BOSTON STATE: Massachu CONPUTER: Massachu CONPUTER: EADABLE FO MEDIUM TYPE: CD COMPUTER: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING SYSTE SOFTWARE: IBM P OPERATING DATE: 30 PRIOR APPLICATION NUM APP	PILING DATE: 17-DEC-1997 ATTORNEY/AGENT INFORMATION: NAME: Mandagouras, Amy E. REGISTRATION NUMBER: 36,207 REFERENCE/DOCKET NUMBER: GTN-018 TELEPHONE: (617)227-7400 TELEPHONE: (617)742-4214 TELEPHONE: (617)742-4214 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 816 base pairs TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEN

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95 GlyPhePheGlnValThrLeuGluAsp---LysValHisTyrThrArgAlaGlyAsnPhe 113
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478 ATCGGT------483
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                                                                                                                                             1 MetMetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20
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              816
1107
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           Length:
Matches:
Conservative:
Mismatches:
Indels:
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            Pred. No.: 2.73e-20
Score: 288.00
Percent Similarity: 28.68%
Best Local Similarity: 21.02%
Query Match: 11.14%
Alignment Scores:
Pred. No.:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...837
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
               TELEPHONE: (6.7)227-7400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TELECOMMUNICATION INFORMATION:
                                                                                                                                           TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
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28.68%
21.02%
11.14%
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Best Local Similarity:
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       314 PheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsn 333
                                                                              334 MetTrpAlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLy8LeuPro 353
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NI 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTONNEY/AGENT INFORMATION:
NAME: MANDERS, 17-DEC-1997
NAME: MANDERSON NUMBER: 36, 207
REFERENCE/DOCKET NUMBER: GIN-018
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CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                    Sequence 3, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILLING DATE: 2000-10-06
PRIOR PRILING DATE: 2001-03-27
NUMBER OF FLEING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FEACESQ for Windows Version 4.0
SOFTWARE: PEACESQ for Mindows Version 5.50 ID NO 1888
LENGTH: 555
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-1888
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237.00
49.70%
34.91%
9.16%
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Best Local Similarity:
Query Match:
DB:
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US-09-974-300-1846
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                 214 MetArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPheAspGlyAla 233
                                            ---GTGGATGGCACG 519
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                                                                                                                          254 GlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPhe
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APPLICANT: Berka, Randy M.
APPLICANT: Clausen, DGroth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
TILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
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US-09-974-300-1888
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; Ratent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085,500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT APPLICATION NUMBER: 09/680,598
; PRIOR APPLICATION NUMBER: 00.0-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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GATACGATGGCGTTGCTTTTGCGAAAGAGTTTAATGCAGTCCATCAA-----AGCGGG 1038
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724 GGCATTGTGTCA-----ATAGAAGTCCTTGACGTAAACGGCCAGTCT-----CTGGGC
                             ValTyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeuValAla
                                                                                                                SerAlaGlyLeuLeuMetSer-----GlyThrMetThrPhe
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Publication No. US20040052799A1
GENERAL INFORMATION: GENERAL INFORMATION: MUTLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: BELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
                                                             772 AAGGITCITGÁCGGCCAAACTICACGÁCTGAAACT-
                                                                                             248 MetAsnProSerGluAsp------
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                          CTGGAAATCGCAAAAAGAGGCTTGTCCGCGCAGCAATCAGCTCTCAGGCGTGACAGCAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 PheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLysGlyPhePheGlnVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrLeuMet------GlySerArgIleSerAsnAsnProAsnIleLysLysGluThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 TyrPheAlaLeuLeuGluSerTrpLysGlyAsnGlyThrProProlleSerThrSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------AsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                           145 ACCCTTATCCGTCCGTATCAAGAGAC---TCTGTCGGACTTGCAGGC----
                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 Phe-----LeuAsnAsp-
      NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1846
LENGTH: 1524
                                                                                        Bacillus licheniformis
                                                                                                                                                   2.46e-12
215.50 .
37.21%
22.93%
8.33%
                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                     US-09-974-300-1846
                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                       TYPE: DNA ORGANISM:
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Sequence 2, Application US/10449462
; Sequence 2, Application US/10449462
; bublication No. US20030202983A1
; GENERAL INFORMATION:
    APPLICANT: Pizer Products, Inc.
    TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS AND RELATED METHODS AND
    TITLE OF INVENTION: MATERIALS
    FILE REFRENCE: 3153.01017/PC10589A
    CURRENT APPLICATION NUMBER: US/10/449,462
    CURRENT FILING DATE: 2003-05-29
    FRIOR APPLICATION NUMBER: US/20/689,065
    PRIOR FILING DATE: 1999-10-12
    PRIOR FILING DATE: 1999-10-22
    PRIOR FILING DATE: 1999-11-05
    NUMBER OF SEQ ID NOS: 112
    SEQ ID NO 2
    LENGTH: 5445

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 AACGTAGACATGAGCAGAGAAATGGTTAATATGATTATTATTCAACGTGGTTTTCAGATG
                                                                                                                                                                                                                                                                                                             APPLICATION PEIZER Products Inc.

TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS, AND RELATED
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
FILE REFERENCE: PC10589A
CURRENT APPLICATION NUMBER: US/02/689,065
PRIOR PILING DATE: 2002-08-01
PRIOR PILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 5445
                                                                                             487 ValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeuLysArg
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Conservative:
Mismatches:
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US-10-449-462-2
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; ORGANISM: Lawsonia intracellularis
US-10-210-296-2
                                                                                                                                                                                                                              Sequence 2, Application US/10210296 Publication No. US20030021802A1 GENERAL INFORMATION:
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100.00%
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            398 LeuGlnGlyLysTyrSerAsnSerGlnValValAspPheTyrAsnIleProLeuAlaArg 417
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TICACTAACGATCAAGGCTTAAGGAAAATCGGCGGTAACCTCTATGAAATGCAAGAAGGC 228
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                                                                                                STATE: Massac....-
COUNTRY: USA
ZIP: 02109-1875
ZIP: 02109-1875
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RCM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURREY APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
FILING DATE: 31-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPAX: (6.77)742-4214
INFORMATION POR SEQ ID NO: 78:
SEQUENCE CATACATERISTICS:
TELEPAX: (6.77)742-4214
INFORMATION POR SEQ ID NO: 78:
SEQUENCE CHASTICS:
TELEPAX: (6.77)742-4214
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Mismatches:
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LOCATION: (B) LÖCATION 1...459
; SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-10-335-977-78
                       ADDRESSEE: LAHIVE & COCKFIELD
STREET: 18 State Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Helicobacter pylori
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201.50
53.68%
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Best Local Similarity:
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Pred. No.:
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Query Match: 7.33* Indels: 35 DB: 16 Gaps: 6 US-10-009-823A-1 (1-502) x US-10-335-977-82 (1-1395) QY 1 MetMetGlySerLeuPheIleGlyAlaThrGlyMetLySThrHisSerThrGlyLeuGly 20 Db 1 ArGAACGACACACTTATAAACGCTTATAGCGGGATCAAGACCAACCA	Db 121 iTThisiaccritititities and the contributes are controlled by the contributes and the contributes are controlled by the controlled b	; TYPE: DNA ; ORGANISM: Burkholderia fungorum US-10-369-493-28400
Score: Percent Similarity: 193.00 Matches: 40	UND 19 ORDIGATION NO. US20040052799A1 DDICATION NO. US20040052799A1 GENERAL INFORMATION: DIAMONSTICA ACID AND AMINO ACID SEQUENCES PAPLICANT: ORDIGAS SMITH et al TITLE OF INVENTION: NUCLECT ACID AMINO ACID SEQUENCES CORRESPONDENCE ADDRESS: ADDRESSED: LAHIVE & COCKFIELD CITY: BOSCON CONTRIBUTION: CONTRIBUTION: MARSACHUSET & COUNTRY: USA COMPUTER READALE FORM: WEDILW TYPE: CD/ROM ISO9660 COMPUTER: LIB PC COMPALIA CONFUTER: LIB PC COMPALIA CONFUTER: LIB PC COMPALIA CONFUTER: LIB PC COMPALIA APPLICATION NUMBER: 08/993,002 PRIOR APPLICATION NUMBER: 08/993,002 PRIOR APPLICATION NUMBER: 08/993,002 PRIOR APPLICATION NUMBER: 08/993,002 ATORNEY APPLICATION NUMBER: 08/993,002 RIB REPERVEZ/GOCKET NUMBER: 35,277 ATORNEY/AGENT: 1P-DEC-197 ATORNEY/AGENT: NIPORMATION: REFERENCE/OCCKET NUMBER: 35,277 ATORNEY/AGENT: NIPORMATION: TELEPHONE: (617)227-740 TELEPHONE: (617)227-740 TREEPHONE: (617)227-740 TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONESS: double TREEPHONE CHARACTERISTICS: TELESTERIA SOURCE: DRIGATION: (8) LOCATION: 1.1395 DOUGST: COURTION: SEQ ID NO: 82: DOUGST: COURTION: SEQ ID NO: 82: DOUGST: COURTION: SEQ ID NO: 82: DOUGST: COURTION: SEQ ID NO: 82:	Pred. No.: 1.12e-09 Length: 1395 Scoret Similarity: 43.14* Conservative: 29 Percent Similarity: 28.92* Mismatches: 81

7 6 4			-
Alignment scores Pred. No.:	1.59e-08 Length:	ò	246ValA
Percent .	34.25% Conservative:	ପ୍ର	900 CGGCGCGATCG
Best Loc Query Mai	Best Local Similarity: 20.81% Mismatches: 224 Query Match: 6.98% Indels: 233	È	259
DB:	15 Gaps:	원	960 GCTCGCCGGC
US-10-00	A-1 (1-502) X US-10-369-493-28400 (1-1965)	Š	260T
දී ද්	1 MetMetGlySerLeuPheIleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20	đ	1020 CACACAGAACA
g ;		Š	269GlyThrM
Š É	ACAP CICAGO CARA CATCAGO A ACACTAGO A CACCAGO A CACCAGO A CACAGO A	쇰	
3 8		Š	284 aPheThrProT
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3 8	V. [Succession of the Control of the	Š	304 lAsnGlyLeuP
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3 8	29	à	324 uAspPheGly- ::::
Š	FIGNSHOLIMIA :::::::::::::::::::::::::::::::::::	q Q	1215 GAACGCCĠĠĊG
ga	ווניאפריופיונים ביינים	<i>λ</i> ο	344 laileGlyThr
<i>हे</i> :		අු	1274 CCGCCACCACC
DP	II CACCAGCIAI I I CACCGGCI I GCAGAACGI C	ò	359 lnThrSerSer
Õ	GlyAsnSerValThrAspLeuAlaIleGlyGlyLysGlyPhe	q	1334 CGAGCAACAC
셤		ò	372SerSerThr
ò		qa	1394 CGAACTCGACC
අ	415ACGCTGGTGAACCAGATCAACGCCGCGGGTCAGCAATACGACGCGCTGCGC 465	ò	386 spleuvalAsp
ð.		g	 1454 CGACGGTGACC
ය දු	466 CAGAGCGTCAACACGCAACTCACCATTTCGCAGATTAACAGCTACTCGCAGCAG 525	ò	391
Š	136 nAsnProAsnIleLysLysGluThrLeuGluProIleGlnLeuAspPheAsnAspProTh 156	-	1514 TGGTGCCGTAI
qa	526 ATCGCGCAACTGAACGGACAGATCGCCCAGGCCAGCACGC 565	ò	401 vsTvrSerAsn
ò	156 rValAlaLysSerProAlaLysThrSerThrAlaLeuAsnAlaValValAs 173	; <u>8</u>	
q	566AAGGGCAGCCGCCGAACCAGTTGCTGGACCAGCGCGATCTC-GCCGTGTCCAA 617	1 . è	419 hrSer
ò	173 nLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGl 193	2 6	
QC	618 CCTGTCGCAGTTGATCGGCGTGAACGTCGTCAACAGCAACGGCAGCTACAGTGTGTTCAT 677	3 8	
ò	193 userTrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyrAlaGlnPr 213	G 6	
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ą:		gg .	1/51 AUGICAACAA
ò	233 aProSerSerThrGlySerLysThrPheGluTyrLeu 245	Š 1	
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246	ValalaMetAsnProSerGluAspGlySerAlaAlaAserGly 259
006	CGGCGCGATCGCCGTGAGCTTCTCCGCGCAGGTCAACGCGCAGAACGGGCTTCGGTATCAC 959
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096	GCTCGCCGGCGCCAAGGCGGCGCGCGCTGTTCTCGGTGGGCGGCCCGACCGTCTACGCGAA 1019.
260	ThrAspSerAlaGlyLeuLeuMetSer
1020	CACACAGAACACGGGAACGCGTGGTGGTGGTTCGCGGGACGCCACGCAGGCGAC 1079
269	GlyThrMetThrPheSerSerAsnGlyGluLeuLysAsnMetThrAl 284
1080	 ccggcgactacacgcctacacgcgaccctacacgctgacgaca
284	aProLeuV
1140	GGGCACCGTGGTGGGCAACTAACCTGAGCCAGCCGAT 1181
304	oGlnPheSer
1182	SILLILIIII CAACGGCCTGAATTTCTCGACCACCGGCACGAT 1214
324	uAspPheGly-IleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAlaSerAlaAlaA 344
1215	GAACGCCGCGGGATTCGTTCACAGTCGAGCCGACG-CGCGGCGCGCTGAACAGTTTCGCGA 1273
344	lalleGlyThrAspIleGlyLysLeuProSerMetMetProlleG 359
1274	
359	lnThrSerSerGlyAsnSerThrAlaArgAsnGlySer371
1334	CGAGCAACCGGCACCGCCACGATTACGCAGGCACGGTGACGGCCGGC
372	SerSerThrArgArgTyrSerGlnAspGlyTyrProGlnGlyA 386
1394	ದಿರದಿದ
386	spleuValAspVal 390
1454	 GGCCGGTAC
391	ThrileThrSerGluGlyLysLeuGlnGlyL 401
1514	TGGTGCCGTAITCGTCGGCGCGCGCGCGCGCGCGCGATCAACAACAACGACGCGGGCC 1573
401	ysTyrSerAsnSerGlnValValAspPheTyrAsnIleProLeuAlaArgPheT 419
1574	-00 -00
419	1
1631	ACGCGCTGGCATTGTCGAATT 16
432	yrseralaThrLeuAspSerGlyGlyProGluPheGlyLeuProGly
1691	TGTCCACCGCGAAAGCGATGTCGGGCGGGACGGTCACGCTGACGGGCGTATGCGAACT 1750
448	ThrSerAsnTyrGlybysLeuSerValAsnGlnLeuGluThrSerAsn 463
1751	ACGICAACAATAICGGCAACCAGACCAACAGATCCAGACCTCGAGGACGGCGCAGA 1807
464	ValAspMetSerA 468
1808	GITCGCIGGIGACGCAGATCACCGCGCGCAGCAGICGGITTCGGGCGTGAACATCAACG 1867
468	rgGluMetValAsnMetIleIleIleGlnArgGlyPheGlnMetAsnSerLysSerValT 488
1868	AAGAAGCAACCAACCTGCTTCAGTATCAGCAACTGTATCAGGCGAACAGCAAGGCTCATCC 1927

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618 CCTGTCGCAGTTGATCGCCGTGAACGTCGTCAACAGCAACGGCAGCTACAGTGTGTTCAT 677
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                                                                                                    156 rValAlaLysSerProAlaLysThrSer-----ThrAlaLeuAsnAlaValAs
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                                                             526 ATCGCGCAACTGAACGGACAGATCGCCCAGGCCAGCACGC--
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                                                                                                         Sequence 31160, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: APPLICANT: Octomer C.

APPLICANT: APPLICANT: Slatery S.

APPLICANT: APPLICANT: Octomer C.

APPLICANT: APPLICANT: Octomer C.

APPLICANT: APPLICANT: AN UNBER: US 10 (5.052)B

FILE REFERENCE: 38-10 (5.052)B

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 31160

LENGTH. 1066
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12. TATGCGGAAAGCGGCCAGTACACGGGTTCGGGCTATCTGCCGCAAGGGGTCTCGACC 180
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Matches:
Conservative:
Mismatches:
Indels:
                        AGACCGCAGACCCTGTTCCAGACGATACTC 1959
488 hrThrAlaAspThrMetLeuGlnLysAlaLeu 498
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US-10-369-493-31160
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	કે ક	89 LeualaileGlyGlyLysGlyPhePheGlnValThrLeuGluAspLysValHisTyrThr 108
	8 8	ArgalaglyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr
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	\ \dots \text{d}	AsnAlavalvalAsn AACGCAACCACTGGT
468 rgGluMetValAsnWetllellelleGlnArgGlyPheGlnMetAsnSerLysSerValT 1868 AGAAGCAACCTCAACTATATCAGAACTGTATAGGGAAGGAA	장 음	189 PheAlaLeuLeuGluSerTrpLysGlyAsnGlyThr
488	<i>ර්</i> සි	204 SerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSer 223 ::
RESULT 22 US-10-193-764-64 : Sequence 64. Application US/10193764	ò a	224 HisaspileThrValTyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGlu 243 2278 GTTACTGTTACTGCAAATAGCGGTGCATTAACCACTTTGGCAGGCTCTACAATTAAA 2334
Publication No. US20030133943A1 GENERAL INFORMATION: APPLICANT: LOOSMORE, Sheena M. APPLICANT: Yang, Yan-Ping	λο α <u>α</u>	244 TyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAla 263 2335 GGAACCGAGAGTGTAACCACTCAAGTCAATCAGGGGGATATCGGGTACGATTTCTGGT 2394
APPLICANT: Klein, Michel H. TITLE OF INVENTION: PROFECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH TITLE OF INVENTION: MOLECULAR WEIGHT PROFEINS FILE PREPERVER: 1014-1749MIS	දුරු පුර	264 GlyLeuLeuMetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys 280
CURRENT APPLICATION NUMBER: US/10/193,764 CURRENT FILING DATE: 2002-07-12 PRIOR APPLICATION NUMBER: 09/167,568 DATOS FILING DATE: 1998-10-07	දු දු	281 AsnMetThrAlaPheThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnPro 300
NUMBER OF SEQ ID NOS: 91 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 64 TENGRY 2.26	දු සි	301 AlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGln 320
	ઠે ક	321 ProLeuThrLeuAspPheGlylleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAla 340
1.78e-07 Length: 173.50 Matches: 37.30% Conservative:	G & G	Seralaalaalaalaalaalaalaaseeseeseeseeseeseeseeseeseeseeseeseese
Best Local Similarity: 22.18% Mismatches: 210 Query Match: 6.71% Indels: 101 DB: 24	& &	
US-10-009-823A-1 (1-502) x US-10-193-764-64 (1-3285) Ov 30 AsnThrIleGlvTvrivsGlnGlnGlnValValPheGlnAsDLeuPheSerGlnAspLeu 49	8 8	GlyTyrProGlnGlyAspLeuValAspValThrIleThrSerGluGlyLysLeu
	음 &	2689 GGTAGCGTTGCAGGAAGTATTAATGCCGCCAATGTGACACTAAATACTACAGCACTTTA 2/48
GlnAlaGlyMetGlyAlaGlnVal	7 A	
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129 LeuMetGlySerArgIleSerAsnAsnProAsnIleLysLysGluThrLeuGluProIle 148 :::	149 GlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThrAlaLeu 168		169 ASRALAVALVALASRILEUGLYASDSErThrASPLYSTHrGINSErGluAlaASRProTyr 188 3816 AACGCAACCACTGGTAACGTGGAGATAACCGCTCAAACAGGTAGTATC 3863		3864 CTAGGTGGAATTGAGTCCAGCTCTGGCTCTGTAACACTTACTGCAACCGAGGGGGCGCTCTT 3923	GCTGTAAGCAATATTTTCGGGCAACACC	224 HisAspileThrValTyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGlu 243	GTTACTGTTÄCTGCAAATAGCGGTGCATTAACCACTTTGGCAGGCTCTÄCÄATTAAA	244 TyrLeuvalAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAla 263 4008 GGAACCGAGAGTGTAACCACTTCAAGTCAATCAGGGGATATCGGGGGATACGATTTCTGGT 4067	264 GlyLeuLeuMetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys 280	4068 GGCACAGTAGAGGTTAAAGGCAACCGAAAGTTTAACCACTCAAATCCAAATTCAAAAATTAAA 4127	AsnMetThrAlaPheThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnPro		301 AlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGln 320 4188 GGTAATACGGTAAATA		4221 GATTTAACAGTTGGGAGAATGGCGCAGAAATTAATGCGACAGAA 4262	341 SeralaalaalalleGlyThrAspIleGlyLysLeuProSerMetMetProIleGlnThr 360		361 SerSerGlyAsnSerThrAlaArgAsnGlySerSerThrArgArgTyrSerGlnAsp 380		381 OLYTYTETOGINGLYASDIGG	GlnGlvivsTvrSerAsnSerGln	ACTACCGTGAAGGGTTCAAACATTAATGCAACCAGGGGTACCTTGGTTATTAACGCAAAA		GACGCTGAGCTAAATGGCGAGCAGTGGGTAACCACACAGTGGTAAATGCAACCAAC	427 GluGlyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuPro 446	::: 4542 AATGGCTCCGGCAGCGTAATCGCGACAACCTCAAGCAGAGTGAACATCACT 4592	uThr	4593 GGGATTTAATCACAATAAATGGATTAAATATCATT 4628
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Carr, Grant
Yamamoto, Robert
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone; Cheryl
APPLICANT: Haselbeck, Robert
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Zyskind, Judith
Wall, Daniel
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APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS OF NON-TYPEABLE
TITLE OF INVENTION: HAEMOPHILUS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/092,880
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 09/155,614
PRIOR PLING DATE: 1996-04-01
PRIOR APPLICATION NUMBER: 08/617,697
PRIOR FILING DATE: 1996-04-01
PRIOR FILING DATE: 1995-04-01
PRIOR FILING DATE: 1995-04-01
SOFTWARE: PARELICATION NUMBER: PCT/US97/04707
PRIOR FILING DATE: 1997-04-01
SOFTWARE: PARELICATION NUMBER: PCT/US97/04707
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4372 ACTACCGTGAAGGGITCAAACAITAAIGCAACCAGCGGIACCITGGITAITAACGCAAAA 4431
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                                              3958 GGAACCGAGAGTGTAACCACTTCAAGTCAATCAGGCGATATCGGCGGTACGATTTCTGGT
                                                                                                                                                  4018 GGCACAGTAGAGGTTAAAGCAACCGAAAGTTTAACCACTCAATCCAATTCAAAATTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1312 GGTAGCGTTGCAGGAAGTATTAATGCCGCCAATGTGACACTTAAATACTACAGGCACTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyLeuLeu------MetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 SeralaalaalaIleGlyThrAspIleGlyLysLeuProSerMetMetProIleGlnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 SerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGlnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 GlyTyrProGlnGlyAspLeu----ValAspValThrIleThrSerGluGlyLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407 ValValAspPheTyrAsnIleProLeuAlaArgPheThrSerGluAspGlyLeuArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427 GluGlyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    447 GlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487 ValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeuLysArg 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GlnGlyLys-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 41760, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               1138 GGTAATACGĠTÁÁÁT-----
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1171 -------ACGGTGGGGGGGGTGACCAATACCGGTAACGTTG 7209 7270 ACCGATGGATCTGGAGAATGGGGGGGCTTCTAGCATTAGCGGCGGCGTTA-- 7326 ------Accesacceracceraccidabi 7347 |||| :::|||||| ||| GGGGAATGGGCCATTCGGCCAGACGTCATTACTGAATATCGCC 7134 7135 AGTGGG-----GCCAGTGCGAATATTAATGGCTATCGCCAG-------7170 83 GlyAsnSerValThrAspLeuAlaIleGlyGlyLysGlyPhePheGlnValThrLeuGlu 102 103 AsplysValHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsn 122 43 AspleuPheSerGlnAspleuAlaIleGlySerThrGlySerGlnGlyProAsnGlnAla 62 GlyMetGlyAlaGlnValGlySerValArgThrIlePheThrGlnGlyAlaPheGluPro 82 SerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValValPheGln 42 3 GlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGlyThrVal 22 Identification of Essential Genes in Microorganisms - See File Wrapper or PALM US-10-009-823A-1 (1-502) x US-10-282-122A-41760 (1-11118) Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: PRINTE OF INVENTION Identification of Essential CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR PILING DATE: 2000-05-22 PRIOR PELING DATE: 2000-05-22 PRIOR PELING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR PILING DATE: 2000-05-26 PRIOR PILING DATE: 2000-09-06 PRIOR PILING DATE: 2000-09-06 PRIOR PILING DATE: 2000-09-09 PRIOR PILING DATE: 2000-09-09 PRIOR PILING DATE: 2000-10-23 PRIOR PILING DATE: 2000-10-23 PRIOR PELING DATE: 2000-11-27 PRIOR APPLICATION NUMBER: 60/257,931 PRIOR PILING DATE: 2000-11-22 PRIOR PILING DATE: 2000-11-22 PRIOR PILING DATE: 2000-11-22 PRIOR APPLICATION NUMBER: 60/257,931 PRIOR APPLICATION NUMBER: 60/257,931 PRIOR PILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/257,931 PRIOR APPLICATION NUMBER: 60/257,931 PRIOR APPLICATION NUMBER: 60/257,931 PRIOR APPLICATION NUMBER: 60/267,636 PRIOR APPLICATION NUMBER: 60/267,636 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PRIOR PILING DATE: 2001-02-09 PRIOR Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614
SEQ ID NO 41760
LENGTH: 11118 172.50 32.30% 21.72% 6.67% ; ORGANISM: Yersinia pestis US-10-282-122A-41760 Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: 7075 7210 63 23 .. 8 8 8 셤 셤 8 원· 첫 원 ò 8 A ð

7386	7.386	
162	AlaLysThrSerThrAlaLeuAsnAlaValValAsnLeuGlyAspSerThrAspLysThr 181	
00	lnSerGluAlaAsnProTy	
7432	- 1	•
202	ProlleSerThrSerAsnTyrSerTyralaGlnProMetArgValTyrAspGlnGlnGly 221	
222	IleThrValTyrPheAspGlyAlaProSerSerTh	
7468	TIGGGCAGCATT 7482	01
242	PheGluTyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSer 258 :::	~ *
259	GlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPheSer 274	
7	283	
7603	16	O1
284	AlaPheThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnProAlaProLeu 303	_
304	ValasnGlyLeuProGlnPheSerAlaasnPheValGlyAlaGlyIleGlnProLeuThr 323 ::: ::: :::	~
324	LeuAsp 325	
7768	ATTATCGGCGGAGCAG	_
326		_
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337	4GC 79	10
357	ProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArg 376	
7936	rregram	OI.
-	yrSerGlnAspGlyTyrProGlnGlyAspLeuValAspValThrIleThrSerGluGly 396	
7993	GATGATGCCGAAGTCACCCTGACCAGCAAC 80	^
397	LysLeuGlnGlyLysTyrSerAsnSerGlnValValValPheTyrAsnIleProLeu 415 :::	œ
416	AlaArgPheThrSerGluAspGlyLeuArgArgGluGly 428	
8074	CIGGACGATATTGCTCTTTAATCATGCGTTGACCGGTAACGGCTTGCTGAATGTGCCG 8133	m
429	AsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGly 447	~
J 4	ThrserasnTvrGivLvsLeuSerValAsnGluThrSerAsnValAspMetSer 467	
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123 AspProSerGly---PheThrLeuMetGlySerArgIleSerAsnAsnAsnIleLys 141

7327

7348 ATCAAGGGTGGCGATTTCACCATC-----AGCATCGATAACAAT-

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142 LysGluThrLeuGluProIleGlnLeuAspPheAsnAspProThrValAlaLysSerPro 161

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,		Oy 480 PhedlnMetAsnSerLysSer 486 ::: ::	APPLICANT: O'Toole, George A. APPLICANT: Main-Fah TILLE OF INVENTION: METHOR TO STUDY AND MECHANISMS OF TILLE OF INVENTION: BIOFILM-SPECIFIC ANTIBIOTIC RESISTANCE FILE REFERENCE: 14537-002.001 CURRENT APPLICANTION NUMBER: US/10/246,330 CURRENT FILING DATE: 2002-09-18 PRIOR APPLICATION NUMBER: US 60/323,241 PRIOR APPLICATION DATE: 2002-09-18	WOMERS TO SEL ID NOS: 34 NOMERS FOR THE NOS: 34 SEQ ID NO 3 SEQ ID NO 3 LENGTH: 7407 TYPE: DNA PSeudomonas aeruginosa FATURE: NAME/KEY: CDS LOCATION: (1)(7404)	Alignment Scores: 3.46e-06 Length: 7407 Pred. No.: 166.00 Matches: 113 Score: 15.00 Mismatches: 64 Best Local Similarity: 22.42\$ Mismatches: 189 Query Match: 15 US-10-009-823A-1 (1-502) x US-10-246-330-3 (1-7407)	Qy 20 GlyThrValSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnVal 39 Db 3892 GGCACGGTCGACGCCGTGGCC	Qy 59	Qy 92 GlyGlyLysGlyPhePheGlnValThrLeuGluAspLysValHisTyrThrArgAlaGly 111
AAC Metvalasnmet AACACCACA AlaAspThrMet	:::	GENERAL INCREMINION: APPLICANT: DOUGLAS SMITH et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES TITLE OF INVENTION: NUCLEIC ACID AND THEAPEUTICS DAGNOSTICS AND THERAPEUTICS NUMBER OF SEQUENCES: 10031 CORRESPONDENCE ADDRESS: STREET: 28 STATE STATE STATE STATE CITY: BOSTON CITY: BOSTON	STATE: Massachusetts COUNTRY: USA ZIP: 02109-1875 COMPUTER READABLE FORM: MEDIUM TYPE: CD/ROM ISO9660 COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0 SOFTWARE: UNIX CURRENT APPLICATION DATA:	APPLICATION NUMBER: US/10/335,977 FILING DATE: 30-Dec-2002 FILING PAPLICATION DATA: APPLICATION NUMBER: 08/993,002 FILING DATE: 17-DEC-1997 ATTORNEY/AGENT INFORMATION: MAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207 FILING REFERENCE/DOCKET NUMBER: GTN-018 TELECOMMUNICATION INFORMATION:	TELEPHONE: (617)227-7400 TELEFAX: (617)224-14 INFORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS: TYPE: nucleic acid TYPE: nucleic acid STRANDEDNESS: double MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO) ANTI-SENSE: NO) ORIGINAL'SOURCE:) FRATURE: PEATURE: NAME/KEY: misc feature LOCATION: (B) LŌCATION 1273 SEQUENCE DESCRIPTION: SEQ ID NO: 55: US-10-335-977-55	Alignment Scores: 3.07e-08 Length: 273 Pred. No.: 166.00 Matches: 35 Score: 64.37% Conservative: 21 Best Local Similarity: 64.23% Mismatches: 31 Query Match: 6.42% Indels: 0 DB: 16	US-10-009-823A-1 (1-502) x US-10-335-977-55 (1-273) Qy 400 GlyLysTyrSerAsnSerGlnValValAepPheTyrAsnIleProLeuAlaArgPheThr 419

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laAsnThrileGlyTyrLysGlnGlnGlnVal 39
ssential Genes in Microorganisms
                                                                                                                                                                                                                                                                                       ed - See File Wrapper or PALM.
                                                                                                                                                                                                                                                                                                                                                                                                       arches: 113
onservative: 64
ismarches: 189
ndels: 24
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	Oy 386 AspLeuValAspValThrIleThrSerGluGlyLysLeuGlnGlyLysTyrSerAsnSer 405	5155GCCGGCAACACCGGGCCCGGTCAGCACGACGC-GGTGGCCCC 444 GlyLeuProGly 447 5205 GGCCACCCGGT 5216 SULT 30 -10-335-977-77	GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: DOUGLAS SMITH et al IITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS	NUMBER OF SEQUENCES: 1 10031 CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD STREET: 28 State Street CITY: BOSTON STATE: Massachusetts COUNTRY: 193A	COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER: LDM ISO9660 COMPUTER: LBM PC Compatible COMPUTER: LDM Windows NT 4.0 SOFTWARE: UNIX CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/335,977	FILING DATE: 30-Dec-2002 FILING APPLICATION DATE: 06/993,002 FILING DATE: 17-DEC-1997 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 36,207 REFERENCE/DOCKET NUMBER: GTN-018	TELECHMANDALCATION INFORMATION: TELEPRAK: (617)227-7400 TELEPRAK: (617)742-4214 INFORMATION FOR SEQ ID NO: 77: SEQUENCE CHARACTERISTICS: LENGTH: 372 base pairs TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid TOPOLOGY: circular MOLECULE TYPE: DNA (Genomic)
	92 GlyGlyLysGlyPhePheGlnValThrLeuGluAspLysValHisTyrThrArgAlaGly 111	132 SerArgIleSerAsnAsnProAsnIleLysLysGluThrLeuGluProlleGInLeudsp 151	AGGTC 43 YrSer 20	210 TyraladinProMetargValTyrAspGinGinGlyAansErHisAspIleThrvalTyr 229 4190 GTGGTCAACGTGGCGCGCAGCCAAGCAATGTCGACAGTGCGCCGGGGTGATCACT 4449 230 PheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeuValAlaMet 248 4150 GTGGATGGCGTGGCCCGGCGGGCGCG	249 ASNProSerGluAspGlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMet 267 ::: ::: ::: ::: ::	272 ThrPheSerSerAsnGlyGluLeuLysAsnMetThrAlaPheThr 286 ::	301 AlabroLeuValAsn

us-10-009-823a-1.rnpb

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13159 ------Accarcacaccaccaccaccaccaccaccaccaccacca 13188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13189 CTCAACGGTCACAACTACAGGGCCACCGACGCATCGGGCAACTGGACCTTAACCGTG 13248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13309 -----AGTGCAGCAGCAACACCGCCAGCAGCCAATTTACTGGTCGAC--- 13356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 LeuGluProIleGlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThr 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 SerThralaLeuAsnalaValValValasn-----LeuGlYAspSerThrAspLysThr 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 ServalThrAspLeuAlaIleGlyGlyLysGlyPhePheGlnValThrLeuGluAspLys 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 ValHisTyrThrArgAjaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||------AGCGGCCTGCCGGACGTCACCATCAACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnvalvalPheGlnAspLeuPheSerGlnAspLeuAlaile-----GlySerThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 -------AsnAsnileAlaAsnAhalaAsnThrileGlyTyrLysGlnGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 SerGlyPheThrLeuMetGlySerArglleSerAsnAsnProAsnIleLysLysGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 ThrGlnGly-------AlaPheGluProGlyAsn-------
                                                                                                                                                                                                                                                                                                                                                                                                     25165
145
71
189
236
35
PILING DATE: 01-Apr-2002
CLIASSIFICATION & Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTONNEY/ACENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 960296.95017
TELECRANDINCATION INFORMATION:
TELECRANDINCATION INFORMATION:
TELECRANDINCATION INFORMATION:
TELECRANDINCATION INFORMATION:
TELECRANDINCATION INFORMATION:
TELECRANDINCATION 15000
TELEFAX: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECTLE TYPE: DNA (genomic); SEQUENCE DESCRIPTION: SEQ ID NO: US-10-114-170-39
                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                        2.53e-05
165.00
33.70%
22.62%
6.38%
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Query Match:
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Pred. No.:
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Perna, Nicole T.
Plunkett, Guy
Walch, Rod
TITLE OF INVENTION.
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS.
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnMetAsnSerIysSerValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeu 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrSerAsnValAspMetSerArgGluMetValAsnMetIleIleIleGlnArgGlyPhe 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431
                                                                                                                                                                                                                                                                                                                                                                                                          CGCATCGGTATITWAGCTTTCACTAACGATCAAGGCTTAAGGAAAATCGGCGGTAACCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                           Tyr----SerAlaThrLeuAsp------SerGlyGlyProGlu 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 Pheclyleu-----ProclyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGlu 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246
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                                                                                                                                                                                                                                                                                                                                  412 AsnijeProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.44Mb storage
                                                                                                                                                                  372
392
488
111
                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.4
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
                                                                                                                                                                                                                                                                                  US-10-009-823A-1 (1-502) x US-10-335-977-77 (1-372)
                                                        NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...372; SEQUENCE DESCRIPTION: SEQ ID NO: 77:US-10-335-977-77
                        ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39, Application US/10114170 Publication No. US20030023075A1 GENERAL INFORMATION:
                                                                                                                                                                  5.39e-08
165.50
51.64%
31.97%
6.40%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAA 372
          ANTI-SENSE: NO
                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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US-10-114-170-39
                                                                                                                                                        Alignment Scores:
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DB:
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Oy 284 aPheThrProThrGlySerAlaThrLy Db 951 GTTCGCTAACTTTTAGACGGCGATAA RESULT 33 US-10-147-2998-3	; Sequence 3, Application US/10147299A ; Publication No. US20040058323A1 ; GENERAL INFORMATION: ; APPLICANT: HAAKE, DAIVD A. ; APPLICANT: HAAKE, DAIVD A. ; APPLICANT: REIS, MITERMAYER GALVAO	; APPLICANT: MATSUNAGA, JAWES ; APPLICANT: CRODA, ULLIO HENRIQUE ROSA ; APPLICANT: SIQUEIRA, ISADORA CRISTINA ; APPLICANT: RILEY, LEE W.	; APPLICANT: BAROCCHI, MICHELE ; APPLICANT: YOUNG, TRACY ANN ; TITLE OF INVENTION: PROTEINS WITH REPE ; TITLE OF INVENTION: DOMAINS PRESENT I	CURRENT APPLICATION NUMBER: US/10/147, CURRENT APPLICATION NUMBER: US/10/147, NUMBER OF SEQ ID NOS: 33	SUCTIONALS: FACENCIN VEI. 2.1 SEQ ID NO. LENGTH: 5863 TYPE: DNA	om: Leptospiia Aiscimeii 299A-3 Scores:	Score: 162.00 Massing State Of Massing State Of Massing State Of Massing State Of Of Of Of Of Of Of Of Of Of Of Of Of	.Ò-147-29	Qy 7 IleGlyAlaThrGlyWetLysThrHis ::: ::: Db 1229 GTTGGTAGTACGATATCACGCCGCC	Oy 26 Ilealaasnala	Qy 30 AsnThrIleGlyTyrLysGlnGlnGlnGlr	Oy 49D 1409 AGTGATCAAGTTGCCTGGAACAGCTCT	Qy 50 AlaileGlySerThrGlySerGlnGly	Qy 70 SerValargThrilePheThrGlnGl) Db 1517ACAGCAAGGATCACCGCA	Qy 90 AlaileGlyGlyLysGlyPhePheGlr:::::: Db 1568 TCGGTCAATGCAGCAACTTTAGTTTCT	Qy 110 AlaGlyAsnPheArgPheThrGlr::
Pred. No.: 3.31e-07 Length: 1029 Score: 164.00 Matches: 84 Percent Similarity: 39.58* Conservative: 49 Best Local Similarity: 25.00* Mismatches: 130 Query Match: 6.34* Indels: 74 DB: Gabs: 14	23A-1 (1-502) x US-10-335-97 32 IleGlyTyrLysGlnGlnGlnValV 7 CTGGGCTTTAAGTATTCTAAGGGCTT 7 CTGGGGCTTT	52 GlyserThrGlyserGlnGlyProAsnGlnAlaGlyMetGly	66 AlaGlnValGlyS : 127 GTAGGCGTGGATG	Oy 86 ValThraspLeualaileGlyGlyLysGlyPhePheGlnValThrLeuGluAspLysVal 105	Oy 106HisTyrThrArgAla-GlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAs 123 247 ACGCGCAATTCACCAGAGCATGGGGAGTTTCTTTGGACTCGCAAGGGAGTTTGGTTAC 306	Qy 123 pProSerGlyPheThrLeuMetGlySer	Qy 134 eSerasnAsnProAsnIleLysLysGluThrLeuGluProIleGlnLeuAspPheAsnAs 154	Oy 154 pproThrValalaLysSerProAlaLysThrSerThrAlaLeuAsnAlaValVa 172	Oy 172 lasnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLe 192 Db 483 AAACGCTGGAAAGCATGCGGATCAGACAGCGGCGGTATTCGCTTTAGA 530	Qy 192 uGluSerTrpLysGlyAsnGlyThrProProIleSerThrSerAsnTyrSerTy 210	Qy 210 ralaginProMetargValTyraspgingingiyasn 222 	Qy 223 SerHisAspIleThrValTyrPheAspGlyAla	Oy 234 -ProSer 235 Db 711 CCCTTCTGCAGAAACAGCACGCTTGAGTTGAATGGGGTTAAGATTTCTTTC	Oy 236 -SerThrGlySerLyeThrPheGluTyrLeuValAlaMetAsnProSerGluAspGlySe 255	Oy 255 ralaalaSerGlyThraspSeralaGlyLeuLeuMetSerGlyThrMe 271	Oy 271 tThrPheSerSerAsnGlyGluLeuLysAsnMetThr

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CTAATTCTTCAATATTACAAATATCTAATTTAAAT 1468
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||||::
|CATCGGTGGAGTAGATATTACGGTTTCTTTAAAT 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCAAGTGGTTTCCGATTCCCATTCGATAGCTCGA 1348
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IN LEPTOSPIRA SPECIES
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Matches:
Conservative:
Mismatches:
Indels:
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Db 2684		FRIOR FILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-09-06 PRIOR FILING DATE: 2000-09-06 PRIOR FILING DATE: 2000-09-09 PRIOR FILING DATE: 2000-10-23 PRIOR FILING DATE: 2000-10-23 PRIOR FILING DATE: 2000-10-23 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-11-27 PRIOR FILING DATE: 2000-12-22 PRIOR FILING DATE: 2000-12-22 PRIOR PRIOR PRIOR NUMBER: 60/257, 931 PRIOR PRIOR PRIOR ON THE ENGLISH ON THE ENGLISH OF ENGLISH ON THE ENGL
LeumetGlySerArglleSerAsnAsnProAsnIleLysLysGluThrLeu	225	3393 GCCGAICTTACAGTAATCGCTCCAGTTTAACCAGCATTCAAATCGATCCTACACATCCG 2452 302 ProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyLleGlnPro 321 :::

Qy 295 LeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPhe 314	315 2344 335 2365	Qy 355 MetMetProIleGlnThrSerSerGly	Db 2443Ahridgohdcharranahdcharrantarrangancccaachancan 2496 Qy 386 AspleuValAspValThrIleThrSerGluGlyLysbeuGlnGlyLysTyrSerAsnSer 405 :::	2557 423 2611	Qy 439 GlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerVal 456	0 0		RESULT 35 US-09-881-752A-149 VS-09-881-752A-149 VS-09-881-752A VS-09-881-752A-149 VS-09-881-752A VS-09-881-752A-149 VS-09-881-752A VS-09-881-752A-149 VS-09-881-752A-149 VS-09-881-752A-149-149-149-149-149-149-149-149-149-149		TITLE OF INVENTION: GENOME ; FILE REFERENCE: 06132/041002 ; CURRENT APPLICATION NUMBER: US/09/881,752A ; CURRENT FILING DATE: 2001-06-15 ; DEFINE PRILING DATE: 2001-06-15	FRIOR FILING DATE: 1997-04-01 NUMBER OF SEQ ID NOS: 370 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 149 LENGTH: 3793 TYPE: DNA	; TYPE: DNA ; ORGANISM: Helicobacter pylori
; TYPE: DNA ; ORGANISM: Helicobacter pylori US-10-282-122A-22709	Alignment Scores: 5.4e-06 Length: 3693 Pred. No.: 160.00 Marches: 115 Score: 160.00 Marches: 115 Percent Similarity: 21.86 Mismatches: 179 Query Match: 16 Gaps: 26	-10-009-823A-1 (1-502) x US-10-282-122A-22709 (1-3693) 20 GlyThrValSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyTrLysG	Oy 40 ValPhedinaspecurasserinaspecularies/yer	Oy 77 GlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLysGlyPhe 96 1789	Db 1804 TTCCAACAAAGCATT 1818 Qy 117 GlnaspGlyPheLeusnaspProSerGlyPheThrLeuMetGlySerArg1leSerAsn 136 [117 GlnaspGlyPheLeusnaspProSerGlyPheThrLeuMetGlySerArg1leSerAsn 136 [117	Qy 137 AsnProAsnileLysLysGluThrLeuGluPro	Db 1939 TIGAGGGCGAATTTTTACCAGCTCATCAATACCATAACCAGCAAGTGCCTACAGACATG 1598 Qy 169 AsnalaValValAsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyr 188 Ch	189 PhealaLeuLeuGluSerTrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyr	SerTyrAlacInProMetArgValTyrAspGlnGlnGlyAsnSerHiaAspIleTnrVal TGCTATCAGCAATGGTCCGATTCTAAGGCT TyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeuValAlaMet	Db 2131 TATTACAGGGGTTGCAAAGGGCTTTAGGGTATCAAACG	Oy 269 GlyThrMetThrPheSerSerAsnGlyGluLeuLys	2278 AAGAGCGTTAATGGAGG

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2328	Db 2388 ATCAAC 2393 Qy 315 ValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsnMet 334 Db 2394ACAGCCTACCAGATGCTCACA	Db 2415 GACGCCAGGGAAGGAAATTAGGGACT2441 Qy 355 MetMetProlleGlnThrSerSerGlyAsnSerThr 366	Qy 367 AlaArgAsnGlySerSerThrArgArgTyrSerGlnAspGlyTyrProGlnGly 385	386	Qy 406 GlnValValAspPheTyrAsnIleProLeuAlaArgPheThrSerGluAsp 422	Oy 423 GlyLeuArgArgGluGlyAsnAsnHisTyrSerAlaThrLeuAspSer 438	Qy 439 GlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGlyLySLeuSerVal 456	Qy 457 AsnGlnLeuGluThrSerAsnValAspMetSerArgGluMetValAsnMetIle 474	Oy 475IleIleGlnArgGlyPheGlnMetAsnSerLysSerValThrThrAlaAspThr 492	Qy 493 MetLeuGlnLysAlaLeu 498 1:: ::: Db 2901 AGCGCTTTTCAAGCCATT 2918	RESULT 36 US-10-282-122A-12963 ; Sequence 12963, Application US/10282122A ; Publication No. US20040029129A1	; GENERAL INFORMATION: ; APPLICANT: Aming, Liangsu ; APPLICANT: Zamudio, Carlos ; APPLICANT: Malone, Cheryl	; APPLICANT: Haselbeck, Robert ; APPLICANT: Oblsen, Kari ; APPLICANT: Syskind, Undith ; APPLICANT: Wall, Daniel	; APPLICANT: Trawick, John ; APPLICANT: Carr, Grant ; APPLICANT: Yamamoto, Robert ; APPLICANT: Porsyth, R.	; APPLICANT: Xu, H. ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms ; FILE REFERENCE: ELITRA.0344 ; CURRENT APPLICATION NUMBER: US/10/282.122A	
; FEATURE: NAMS/KEY: CDS ; LOCATION: (51)(3740) US-09-881-752A-149	Alignment Scores: Pred. No.: Score: Score: Accept Similarity: Dest Local Similarity: Ouery Match: Glob: Gaps: Alignment Scores: 160.00 Matches: 179 Mismatches: 179 Gaps: 26	19 (1-3793) AbsnThrleGlyTyrLygGlnGlnGlnVal	15/4		Qy 77 GlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLysGlyPhe 96 :::! :::::: Db 1839	Oy 97 PheGlnValThrLeuGluAspLysValHisTyrThrArgAlaGlyAsnPheArgPheThr 116 ::::::	GlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMetGlySerArgileSerAsn 136	AsnProAsnIleLysLysGluThrLeuGluBro			OY 189 PheAlaLeuLeuGluSerTrpLysGlyAsnGlyThrProProIleSerThrSerAsnTyr 208	Oy 209 SerTyralaGlnProMetArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrVal 228 Db 2151 TGCTATCAGCAA	OY 229 TyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeuValAlaMet 248	249 AsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSer 268 ::: ::: :: ::::: :: :: ::: ::: ::: ::: ::: ::: ::::	QY 269 GlyThrMetThrPheSerSerAsnGlyGluLeuLys	

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rThralaLeuAsnalaValAsnLeuGlyAspSerThrAspLysThrGlnSer---Gl 184
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Matches:
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Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
              PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PELING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-09
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APPLICATION NUMBER: 60,200, FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
APPLICATION NUMBER: 2000-05-26
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ORGANISM: Burkholderia fungorum
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526 CAAATTCAAGCGGGCGCGTTGGCTTTAGTGAGTTTTAGCGAACCTAAAAAAA 585
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                                                                       183 SerGluAlaAsnProTyrPheAlaLeuLeuGluSerTrpLysGlyAsnGlyThrProPro 202
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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SOFTWARE: Patentin version 3.1
SEQ ID NO 28180
LENGTH: 6615
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Matches:
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/293,47
PRIOR APPLICATION NUMBER: 60/293,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-28180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ._awlck, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                            586 ATAGGGCAAAACCTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
                                                                                                                                                                          203 IleSerThrSer 206
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531 GTCTCTGACTCT 642
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Best Local Similarity:
Query Match:
DB:
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US-10-282-122A-28180
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253 AGGAGTCTT-----GCGCGCTTTGAAGGACGAATAAACCCCCTAGATTTTGCCCTA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 TTAAGGCTTTACCAAGAATACCGAGAGCAACTGCCCTTAGAAGATCAAACCAAAGCGAGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 GCGAAGTATCTCAACCGCAACCTCAATCGTGCCTATTCTATCAGAAATCTATACGGAT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 GlyGlyLysGly---PhePheGlnValThrLeuGluAspLysValHisTyrThrArgAla 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 ACAAGCCCTAACCTCTATTTTGCGATACAGACTAATGAGGCGGTCGCTTATACCAGAGAC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 GlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMet 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424 ---TCACGCTCCGGTTTGAACGAAAAAAGGAGGATCATGCTCATGCCTAACGCTGAAATT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 GluThrLeuGluProIleGlnLeuAspPheAsnAspProThrValAlaLysSerProAla 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 GAÁGTGGATCAAAATGGTGGAATCACTTTTAGGGAT-------AATGAAGCC 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 LysThrSerThrAlaLeuAsnAlaValValAsnLeuGlyAspSerThrAspLysThrGln 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnileAlaAsnAlaAsnThrileGlyTyrLysGlnGlnGlnValValPheGlnAsp--- 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---LeuPheSerGlnAspLeuAlaIle 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 GlySerThrGlySerGlnGlyProAsnGlnAlaGlyMetGlyAlaGlnValGlySerVal 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 ArgThrilePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIle 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::
13 TATTATGCGGCCACAGGGCAATGCCTACACAATTTAACCGCTTGGATTTAACCTCTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PhelleGlyAlaThrGly---MetLysThrHisSerThrGlyLeuGlyThrValSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 GGGCATTTCAGCGTTGATAAAGACGGCTTTTTGGTAACCCTTAATGGTTTTAAGGTGCTT
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338
340
847
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Matches:
Conservative:
Mismatches:
Indels:
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                     FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LÕCATION 1...810
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
  APPLICATION NUMBER: 08/993,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Helicobacter pylori
                                                                                                                                                                          TELEPHONE: (617)227-7400
TELEFRA: (617)42-4214
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: circular
MOLECTLE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                         LENGTH: 810 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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151.50
43.30$
25.89$
5.86$
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-10-335-977-17
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Search completed: October 31, 2004, 03:22:14 Job time : 2291 secs

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version 5.1	(c) 1993 - 2004 Compug	
Gencore		
	Copyright	

OM protein - nucleic search, using frame_plus_p2n model

October 31, 2004, 03:11:41 ; Search time 4223 Seconds (without alignments) 5621.461 Million cell updates/sec Run on:

US-10-009-823A-1 2586 1 MMGSLFIGATGMKTHSTGLG......NSKSVTTADTMLQKALELKR 502

score: Title: Perfect so Sequence:

Scoring table:

0.5 BLOSUM62 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

4526729 segs, 23644849745 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
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-DB=CenEmbl -QFWT=fastap -SUFFIX=rege -MINMATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS=bits -GTART=1 -RND=-1 -MATRIX=blosum62 -TRANS=human4-0.cdi -LIST=45
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-NO MAAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMBOUT=120 -WARN TIMBOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DBLEXT=7

GenEmbl:* Database :

gb_pat:*
gb_ph:*
gb_pr:*
gb_ro:*
gb_ro:*
gb_sts:*
gb_y:*
gb_vi:* gb_ba:* gb_htg:* gb_in:* gb_om:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			dР				,
Result No.	υ. ω	Score	Query Match	Query Match Length DB ID	DB	QI.	Description
		1235	47.8	300343		1 1235 47.8 300343 1 AE017310	
υ	1 (1	196	37.2	37.2 300029	-	AE017314	AE017314 Desulfovi
	3	693.5	26.8	26.8 110000	н	AE017180 04	Continuation (5 of
	7	595.5	23.0	23.0 9612	rH	AF122909	AF122909 Treponema

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)		67		251	-	1461	19 Trepon
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C	0	57.	:	1255	Н	1385	3853
י כ	10,		:	9015	н	713	17132 Yers
)	11	57.	. :	505	н	5	414150 Yersinia
C	12	55		1002	Н	15	1450
)	13	ໍ່ເດ	:	059	Н	729	291
	1 4	34	_	523	~	TPU28219	₽ •
O	15	534.5	_	26536	Н	2	112
	16	53	:	5	-	BX321857	1857
U	17	28	.:	2	-4	AE013102	3102
	₽		_:	2	Н	AE004539	939
Ü	19	50	Ψ.	듔	-1	BBU43739	σ
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	21	0	ς.	5	Н	BORFLGE	o,
	22	0	ς.	2	Н	AL646078	_
	23	ത	Ξ.	132	н	STFLGE	7
	24	on	ά.	75	н	AE008751	AE008751 Salmonell
	25	ത	~	5405	H	AL627269	AL627269 Salmonell
U	56	ຸດາ	Α.	0198	н	AE016840	AE016840 Salmonell
,	2.5	ເດ	_	32	н	AE016759	AE016759 Escherich
	8	·on	_	922	Н	AE005317	AE005317 Escherich
	0 0	ເຫ	_	2260	Н	AP002555	AP002555 Escherich
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C	. E	4	<u>_</u>	1954	н	AE001509	AE001509 Helicobac
)	3.0	485	m	2	7	AC095028	AC095028 Leishmani
	6	4	m.	5005	-	AL591976	926
	3.4	84.	m	5	Н	AL596166	Listeri
	м С	84	'n	9024	-	AE017324	7324 Listeri
	36	4	ď	4998	9	AX417038	117038 Sequenc
	3.7	4	ď	499E	9	AX417039	417039 Sequenc
	80	84	'n	4996	9	AX417042	117042 Sequenc
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	4	83	e.	1337	н	ın	15135 Shigell
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	43	w	ω,	8	Н	8	ntinuation (20
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ט ט	4.5	481	18.6	851	н	12	R
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ALIGNMENTS

J00343 bp DNA linear BCT 27-APR-2004 Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough, section 2 of 12 of the complete genome. AE017310 AE017285 Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough
Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaceae; Desulfovibrio.

1 (bases 1 to 300343)
Heidelberg,J.F., Seshadri,R., Haveman,S.A., Hemme,C.L.,
Paulsen,J.T., Kolonay,J.F., Eisen,J.A., Ward,N., Methe,B.,
Brinkac,L.M., Daugherty,S.C., DeBoy,R.T., Dodson,R.J., Durkin,A.S.,
Madupu,R., Nelson,W.C., Sullivan,S.A., Fouts,D.E., Haft,D.H.,
Selengut,J., Peterson,J.D., Davidsen,T.M., Zafar,N., Zafar,N., Zou,L.,
Radune,D., Dimitrov,G., Hance,M., Tran,K., Khouri,H.M., Gill,J.,
Utterback,T.R., Feldblyum,T.V., Wall,J.D., Voordouw,G. and The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough Nat. Biotechnol. (2004) In press Fraser, C.M. ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AE017310 LOCUS DEFINITION JOURNAL PUBMED REFERENCE AUTHORS REFERENCE AUTHORS TITLE

2 (bases 1 to 300343)
Heidelberg, J.F., Seshadri, R., Haveman, S.A., Hemme, C.L.,
Paulsen, I.T., Kolonay, J.F., Eisen, J.A., Ward, N., Methe, B.,

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GVAFVDVNEQNPRALAFYRHXGFEVVGRSERDGMGMPYPLLHMALRHEHDQK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRDS FEDTRHLTGRLRKAVLDILYYAKKRDLWEVVVAERFATETAEL IEGKAVNRGV
GFQLETAAESGTFEADAGALSAALVVILLENAVEACAAERSRPEHSVTFSVGGDANHVE
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                                                                                                                                                                                             Direct Submission
Direct Submission
Submitted (18-MAR-2004) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
On Apr 27, 2004 this sequence version replaced gi:46448084.

Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Desulfovibrio vulgaris subsp. vulgaris str.
Hildenborough"
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JOURNAL
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complement (4019. .4420)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerTrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyrAlaGlnPro
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                                                                                                                                                                   YMESKHSLNSIMHWYTPRATLGWRENPAMTVATFAFHISIVLLALFAPGHATMMDYAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 LeuGluAspLysValHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPhe 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 LysLysGluThrLeuGluProlleGlnLeuAspPheAsnAspProThrValAlaLysSer 160
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74
163
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Matches:
Conservative:
Mismatches:
Indels:
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49.61%
47.76%
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Best Local Similarity:
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Pred. No.:
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Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough
Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough
Bacteria; Porteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaceae; Desulfovibrio.

[bases 1 to 300029]
Heidelberg, J.F., Seshadri, R., Haveman, S.A., Hemme, C.L.,
Bellsen, J.A., Ward, N., Methe, B.,
Brinkac, L.M., Daugherty, J.F., Eisen, J.A., Ward, N., Methe, B.,
Brinkac, L.M., Daugherty, J.F., Eisen, J.A., Fouts, D.E., Haft, D.H.,
Selengut, J., Peterson, J. D., Davidsen, T.M., Zafar, N., Zhou, L.,
Sadune, D., Dimitrov, G., Hance, M., Tran, K., Khouri, H.M., Gill, J.,
Utterback, T.R., Feldblyum, T.V., Wall, J.D., Voordouw, G. and
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Heidelberg,J.F., Seehadri,R., Haveman,S.A., Hemme,C.L.,
Paulsen,I.T., Kolonay,J.F., Eisen,J.A., Ward,N., Methe,B.,
Brinkac,L.M., Daugherty,S.C., DeBoy,R.T., Dodson,R.J., Durkin,A.S.,
Madupu,R., Nelson,W.C., Sullivan,S.A., Fouts,D.E., Haft,D.H.,
Redune,D., Dimitrov,G., Hance,M., Tran,K., Khouri,H.M., Zhou,L.,
Utterback,T.R., Feldblyum,T.V., Wall,J.D., Voordouw,G. and
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NAHVLRVRELAASRGADVVKICAKIEEELQGLSDEBQAEMLGSYGIDESGLVSIIRTG
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Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough, section 6 of 12 of the complete genome.
AE017314 AE017285
AE017314.1 G1:46449255
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match to protein family HWM PF05193"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough Nat. Biotechnol. (2004) In press 15077118
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Submitted (18-MAR-2004) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
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'transī_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
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17426 CAGAACATCACGCTCAATGTCAACTCCGACTCCAATCCGGGTAACGACAAGAGCAGCAGC 17367
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223
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                               LysValHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 ThrSerThrAlaLeuAsnAlaValValAsnLeuGlyAspSerThrAspLysThrGlnSer
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                                                                                                                                                                                                                                                                                                                                                               64 MetGlyAlaGlnValGlySerValArgThrIlePheThrGlnGlyAlaPheGluProGly
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Matches:
Conservative:
Mismatches:
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Continuation 75 of
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                                                                        ThrArgArgTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAspValThr1leThr
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                                                 16709 GGTCTGACCTCTTCGCAGCGCCAGCCCAGTGCAACGACAAGCTACGCCGGTTCGTCATCG
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| ACACAGTTCCAGAAGCAGGACGGCTACGTTCGGCTTCTTGCAGAACATCACTGTCGAC
                                                                                                                           394 SerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValAspPheTyrAsnIle
                                                                                                                                                                                                                            434 AlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsn-----
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                                                                                                                                                                            ProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyrSer
                       SerMetMetProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSerSer
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1soolsgaarpteellggynpkeroglgmyasidtiftgallottetggyndlalogsge
1lookldaratsvyraarbeellbegtuvarvogmarefarytsgotedlui
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1karpodytlgylenfilogsgiligyysingybogiggilagyskyttygsbest
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KONFAETRVPKQQLGKDDFLQLLIAQLTHQDPTSPMEDTQFIGQMAQFSSLEQMTNNN
KNPAALNELMTGSSAVNAVGKKVDLDLGSSQVSGYISAATRGINPEVMVNGNWYNWGA
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LNSKEAYLKEPKONLLKKPKTETOKPNSEHSQAGKSQKNDLELNLKI LNEDFKEEIKDF
LPODVKEDETI SLLSDEALKKLDKSEKKKAQSFDDEKTEQAGKLGLLSKADKKDLSKK
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NGFBFAEFNLNWSGFSGQEGFAESFESFSDFVYKNQEQDLRQLEKTADNLSTYSYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                protein id="AAD20615.1"
db_xref="G1:4426941"
'tränslation="MQALDVRAQALPVKEPEREDSGDIKRADAEPVRNGDSFLAMIKK
  Carolina
Submitted (22-JAN-1999) Epidemiology, University of North Carolir at Chapel Hill, CB#7400 2107 McGavran-Greenberg, Chapel Hill, NC 27599, USA
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protein_id="AAD20617.1"
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                                                                                      1. .9612
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1646. .2155
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Treponema denticola Tapl (tapl), flagellar hook assembly scaffolding protein FlgD (flag), flagellar hook protein FlgE (flgE), flagellar motor protein Morb (motb), flagellar motor protein Morb (motb), flagellar motor protein Morb (motb), flii (flii), flagellar switch protein Flim (flii), flagellar switch protein Flim (flii), flagellar switch protein Flim AF122909
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Stamm,L.V. and Bergen,H.L.
Stamm,L.V. and Bergen,H.L.
spirochete Treponema denticola ATCC 35405
FEMS Microbiol. Lett. 179 (1), 31-36 (1999)
      AlaPheThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnProAlaProLeu 303
                                                                                                                                                                   ProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAla 340
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema
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                                                                                      ValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIle-----Gln
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Stamm,L.V. and Bergen,H.L.
Direct Submission
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Matches:
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DYNBYSGLSGFLQKLFGRK"
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SHKDNCKFIRAISSKRSK"
8859. .8984
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167
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205
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Matches:
Conservative:
Mismatches:
Indels:
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transl_table=11
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595.50
46.15$
32.12$
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Best Local Similarity:
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Pred. No.:
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DB:
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PF04542; match to protein family HMM PF04545"
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gene

GOS

gene

gene

SOS

CDS

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7.1"
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transl_table=11
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|transl_table=11
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gene
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TQTLKRAQGGDVILLAGKGHEDYQIIGTQKFPFSDVKVAEEALQGR"

3617. - 4297
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                                                                                             locus_tag="Bd3204"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::: |||::: |||::: |||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||||
181076 GACCGCGAATGGGAATTCAAAGGTTTGGTT------GACGGTAAAGAG 181035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181415 GGTTCCGACGGTGACTCCTACACTCCTTCCACTTCCACGTGAAGGCTAC 181356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||||
181355 CTGGTAACAACGAC---------AATCAACGCGTACAGGGCTTCTT 181317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181316 ACAGATGAGAAGGGCAATATCGTCAACAAATGACCGATATCAAATTCCCTCGC---GCT 181260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 GlyThrProProlleSerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAsp 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 GlnGlnGlyAsnSerHisAsplleThrValTyrPheAspGlyAlaProSerSerThrGly 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerLysThrPhegluTyr-----LeuValAlaMetAsnProSerGluAspGlySerAla 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 LeuGluaspLysValHisTyrThrargAlaGlyAsnPheArgPheThrGlnAspGlyPhe 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 Leu-----AsnAspProSerGlyPheThrLeuMetGlySerArgIleSerAsnAsnPro 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 AsnilelysiysGluThrLeuGluProlleGlnLeuAspPheAsnAspProThrValAla 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 LysSerProAlaLysThrSerThrAlaLeuAsnAlaValValAsnLeuGlyAspSerThr 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 AsplysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGluSerTrpLysGlyAsn 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 AlaserGlyThrAspSerAlaGlyLeu-----LeuMetSerGlyThrMetThrPheSer 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GinalaGlyMetGlyAlaGlnValGlySerValArgThrIlePheThrGlnGlyAlaPhe 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetMetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 PheGlnAspLeuPheSerGlnAspLeuAlaIleGlySerThrGlySerGlnGlyProAsn
                                                                                                                                                                                                                                                                                                                                        349965
160
73
171
119
                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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579.50
44.55%
30.59%
22.41%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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181014 ATCACTGGGGGGGAAGAAGGCGAAAACAGGGGCAAACAGGGGCTGGCT
125 SerAmnijyoluiceliyaAandacchaAandriccaccaccaccaccaccaccaccaccaccaccaccacca

513

75

92

126

753

166 849 186 909

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985 CAGATGGTTTTCTCAAGGGTCCCCGGTACAAACAAC-------CAGTGGCTCGCA 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            514 GGTGTTAACCCGAAAGAAGTAGGCTCGGTGTTATGGTCGCAAGCATTGATACGGTACAC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 PheThrLeuMetGlySerArgileSerAsnAsnProAsnIleLysLysLysGluThrLeuGlu 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 AsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSerHisAspIle 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 AlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeu 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 MetSerGlyThr-------MetThrPheSerSerAsnGlyGluLeuLysAsn 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 MetThralaPheThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnProAla 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProTyrPheAlaLeuLeuGluSerTrpLysGlyAsnGlyThrProProIleSerThrSer 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGlnPro 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 SerGlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGlnAspGly 381
                                     394 GITATCGGAAATAACGICGCAAACGIGAATACCACAGGITITAAGCGCGCGCAGAGITAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                    21 ThrvalSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValval
                                                                                                                   SerGlnGlyProAsnGlnAlaGlyMetGlyAlaGlnValGlySerValArgThrIlePhe
                                                                                                                                                                                                                                                                                                                              PhePheGlnValThrLeuGluAspLysValHisTyrThrArgAlaGlyAsnPheArgPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 AlaLeuAsnAlaValValAsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  850 GATGTTGCCTATGCGTGCAACCTTGATAAACGTTTACCCGAATTGCCCGAAGGTGCAAAT
                                                                                                                                                                                                                                                  ThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLysGly
                                                                                                                                                                                                                                                                                     574 ACACAAGGAGCCTTGCAAACTACCGGAATCAATACTGATATTGCGATACAAGGAAACGGA
                                                                                                                                                                                                                                                                                                                                                                 Treithattitaaaagaeggagaaaagaettieracacacagcagigeariteggigt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGACATTGAGGGCAGCAAATAATCAATACATCCGATCCGAAGACCTTAATTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 ProlleGlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----caaaaattgatgcaaagctacaacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 ThrValTyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeuVal
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                                                                                             PheGlnAspLeuPheSerGlnAspLeuAlalleGlySer-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 ATGATGAGATCATTATTTTCCGGCGTTTCCCGGAAATGCAAAATCACCAGACAAGAATGGAT 393
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Limberger,R.J.
Direct Submission
Submitted (20-DEC-1993) Ronald J. Limberger, Microbiology,
Wadsworth Center for Labs and Research, David Axelrod Institute,
New York State Dept. of Health, 120 New Scotland Ave, Albany, NY
12201, USA
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Matches:
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Query Match:
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Best Local Similari
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246

1257

361

us-10-009-823a-1.rge

Alignment Scores: 2.21e-25 Length: 110000 Pred. No.: 563.00 Matches: 173 Score: 563.00 Matches: 173 Percent Similarity: 39.87 Conservative: 75 Best Local Similarity: 27.81 Mismatches: 190 Query Match: 1.77 Gaps: 184 DB: 10-009-823A-1 (1-502) x CR522870_30 (1-110000)	Qy 4 SerLeuDhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGlyThrValSer 23 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	Qy 24 AsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValValPheGlnAsp 43 Db 27912 AACAACCTCGCCAACACTATTGCCTATAAGGGATCTCGTACAAGTTTTCAGAT 27971	Qy 44 LeuPheSerGlnAspLeuAlaIleGlySerThrGlySerGlnGlyProAsnGlnAlaGly 63 Db 27972, CTCTTATCCTCCAGGGTCACTGGTTCGGGTGGCACCTCTCAAGTAGGC 28019	Qy 64 MetGlyAlaGlnValGlySerValArgThrIlePheThrGlnGlyAlaPheGluProGly 83	Qy 84 AsnSerValThrAspLeuAlaIleGlyGlyLysGlyPhePheGlnValThrLeu 101 :::	Oy 102 GluAspLysValHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeu 121	Db 28200 GTAAACCCGGCGGCCTACGGGTATAGCCTACGGCGCAGACGTGAACTTGCA 28259 Qy 131 131	Db 28260 GGTGGCGATCCTAGTGATATTTTTTTTGATGGCGCTGGCATGAAAGGTGCCGCCACC 28319	Qy 132 SerArgileSerAsnAsnProAsnIleLysLysGluThrLeuGluProIleGlnLeu 150	Oy 151 AspPheAsnAsp 154 ::::: Db 28380 GATGCCAGCAATACCATCCTATAATTTTCCGAGGAGCTCACGGGACCCGCG 28439	154154	160	Db 28500 AAAACCGCAGAGAAACAGCTGGGAGTGCTACTACACGCGAAAAGAAACCATGGCAACGGT 28559	28560 ACACTGCCACTTCACGCTCCATCAAGGCGGGAGAGGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGATGCCGCA 28	Oy 172 ValaenLeuGlyAepSerThrAspLysThrGlnSerGlualaAsnProTyrPheala 190	Qy 191 LeuLeuGluSerTrpLysGlyAsnGlyThrProProlleSerThrSer 206	Oy 206
Db 1300 CGCAATACGATTACACAGTTTGCCGAAAGAGCACTACAAAAGCATATCAGCAGGACGGT 1359 Cy 382 TyrProGlnGlyAspleuValAspValThrlleThrSerGluGlyLySLeuGlnGlyLys 401 Db 1360 TACGCAATGGCTATCTTGAGATTTCAAATTGACCAAAGTGGTATTATCACCGGCGTA 1419 Cy 402 TyrSerAsnSerGlnValValValPaspPheTyrAsnIleProLeuAlaArgPheThrSerGlu 421 Cy 1420 TATTCAAACGGTGCAAAGCCGTGAAATGGGGGGGCGTTTTGGCAAGCTAGCT	Oy 422 AspGlyLeuArgArgGluGlyAsnAsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyPro 441	Oy 442 GluPheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThr 461 :::	Qy 462 SerasnValaspMetSerargGluMetValasnMetIleIleGlnargGlyPheGln 481	Qy 482 MetAsnSerLysSerValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeuLys 501 :::	Cy 502 Arg 502 Db 1720 CGG 1722	io split into 36 fragments ent Name Begin Er	870_00 870_01 100001 21 870_02 200001 31 870_03 300001 41	1870_04 400001 51 1870_05 500001 61 1870_06 600001 71	870_07 700001 81 870_08 800001 91 870_09 900001 101	CK522870_11 1100001 1110000 CR522870_11 1100001 1310000 CR522870_13 1300001 1410000	1870_14 1400001 151 1870_15 1500001 161 1870_16 160001 171	870_18 1800001 191 870_19 1900001 201 870_20 200001 211	1870_21 2100001 221 1870_22 2200001 231 1870_3 2300001 241	1870_24 2400001 251 1870_25 2500001 251 1870_25 2500001 261	870_27 270001 281 870_28 280001 291 870_29 290001 301	1100001 311 1100001 311 1100001 321 1100001 331 1100001 341	870_34 3400001 35100 870_35 350001 35233 on (31 of 36) of CR522870 fr

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DDENISKQAINPGINFGAVCTSKAALLSLYRQYALEQGOGIRVNAVNADRIRSGLL
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VAAMIR:
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FVTLAENFI ESRRAIYSPPVI TPPAKPMNLADMAHIAPYLRAAFARSSAISEKKHMI F
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(AP003011) probable oxidoreductase [Mesorhizobium loti]"
Yersinia pestis KIM
Yershina pestis KIM
Bacteria; Proteobatteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Wisconsin, 445
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                                                                                 Lasses 1 to 12559)
Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G.F.
Liss, P., Perna, N.T., Rose, D.J., Mau, B., Zhou, S., Schwartz, D.
Straley, S.C., McDonough, K.L.E., Brubaker, R.R., Plana, G.V.,
Blattner, F.R. and Perry, R.D.
                                                                                                                                                                                                               Genome Sequence of Yersinia pestis KIM J. Bacteriol. 184 (16), 4601-4611 (2002) 12142430
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Yersinia pestis KIM section 253 of 415 of the complete genome.
AE013853.1 GI:21959364
  28740 GGAAGCCCGTCGTCGACTAGACAAGAGCCTGCGGGAAAACAAAAGCATCTGCACCTTT 28799
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                                                                                                                                    GlyAsnSerHisAspIleThrValTyrPheAspGlyAlaProSerSerThrGlySerLys 240
                                                                                                                                                                                                                                                                                                                    AspSerAlaGlyLeuLeuMetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 SerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGlnAsp 380
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                                                                        GACTACAAGGATCCCAAGACCTTCACCTATTCCGCCTCGGTACAAATTTTTGACAGTCTT
                                             --------AsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGln
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QQDGDAYNVSFAGGISIVQGPNAYKVBAIFSSADATRLTLGYKRGNGEATEVDESRIT
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Complement (6912. .7856)

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complement (6912. .7856)

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/function="mutative structure; surface structures"
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residues 7 to 314 of 314 are 81.29 pct identical to
residues 7 to 314 of 314 are 61.29 pct identical to
residues 8 to 316 of 316 from GenPept : >gb|AAL20112.1|
(ABG08751) flagellar biosynthesis (Salmonella typhimurium
LT2]"
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Conservative:
Mismatches:
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557.50
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Query Match:
DB:
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                                                                                                                                                                                                                                                           Yersinia pestis biovar Medievalis str. 91001 section 6 of 16 of the Complete genome.
AE017132 AE017042
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Song, Y., Tong, Z., Wang, L., Han, Y., Zhang, J., Pei, D., Wang, J.,
Zhou, D., Han, Y., Pang, X., Zhai, J., Chen, F., Qin, H., Wang, J., Li, S.,
Guo, Z., Ye, C., Du, Z., Lin, W., Wang, J., Yu, J., Yang, H., Wang, J.,
Huang, P. and Yang, R.
Direct Submission
Submitted (24-AFR-2003) The Institute of Microbiology and
Epidemiology, Academy of Military Medical Sciences, No. 20,
Dongdajie Street, Fengtai District, Beijing 100071, People's
Republic of China
Location/Qualifiers
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Versinia pestis biovar Medievalis str. 91001
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="YP1324"
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Yorsinia pestis KIM rplY. Contains Ribosomal protein L25
(Interpro|IPR001021, (GO:0008097))"
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                                                                                                             ValAspMetSerArgGluMetValAsnMetIleIleIleGlnArgGlyPheGlnMetAsn
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/insertion seq="IS1541"
complement (535. 1044)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="tnp_17"
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complement(535...1044)
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112. .396
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locus_tag="YP1325"
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'gene="rplY"
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 11835 AATGTCTTTTATGTTAAACGTGTGAAGATGCGACCGATGGGAATACTTGGGACGTCTAC 11776
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                                                        90 AlaileGlyGlyLysGlyPhePheGlnValThrLeuGluAspLys-----ValHis 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 ValAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAlaGlyLeu 265
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Score: 557.50 Matches: 145 Percent Similarity: 43.98* Conservative: 74 Best Local Similarity: 29.12* Mismatches: 196 Query Match: 1.56* Gaps: 11	US-10-009-823A-1 (1-502) x AE017132 (1-290155) QY	30 AsnThrIleGlyTyrLysGlnGlnGlnValValValPheGlnAspLeuPheSerGlnAs 	Cy 50 AlaileGlySerThrGlySerGlnGlyProAsnGlnAlaGlyMetGlyAlaGlnValGly 69 Db 289917GGTTCTCAGACCGGCATGGCCTAAAGGTCGCG 289885	Qy 70 SerValArgThrIlePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeu 89	90	Oy 107 TYTThratgalaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGly 126	127 PheThrleuMetGlySerArglleSerAsnAsnProAsnlleLysLysGluThrLeuGlu 146	147 ProlledlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThr 166	Qy 167 AlaLeuAsnAlaValValAsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsn 186 :::	Qy 187 ProTyrPheAlaLeuLeuGluSerTrpLysGlyAsnGlyThrProProlleSerThrSer 206 Db 289539 CCTTTT	207 AsntyrSertyrAlaGlnProMetArgValtyrAspGlnGlnGlyAsnSerHisAsp 	Oy 227 ThrValTyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeu 245	Oy 246 ValalaMetAsnProSerGluAspGlySerAlaalaSerGlyThrAspSerAlaGlyLeu 265 ::::::::::::::::::::::::::::::::::::	Qy 266 LeumetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLysAsnMetThrAlaPhe 285	Qy 286 ThrProThrGlySerAlaThrLySASpLeuAsnAlaTrpGlnProAlaProLeuValAsn 305	Qy 306 GlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGlnProLeuThr 323 Db 289218 GGTGCGCCCGCACAAGTTTCGCACTGAATGTTGCGGGCAGT	<pre>Qy 324 LeuAspPheGlyIleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAlaSerAlaAla 343</pre>

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gene

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GOA: 08ZFK5"
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MTGNISAGRHLLNSSTGEYLLYQIYQNSPRTLIWGDGSNGGATQVIATDGTLQCVILX
AQLFASNTQPTAGVYLDTLLVTVTY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Joce="Similar to Pseudomonas aeruginosa PA01 probable pili assembly chaperone TR:AAG08038 (EMBL.AE004879) (262 abl fasta scores: E(): 0, 43.2% id in 243 aa, and to Escherichia coli chaperone protein CssC precursor SW:CSC1_ECOLI (P53518) (232 aa) fasta scores: E(): 0.0013,
                                                                                                  E()
                    aa)
protein AfaC precursor SW:AFAC_ECOLI (P53517) (859 fasta scores: E(): 1.4e-13, 22.7% id in 631 aa and Pseudomonas aeruginosa hypothetical protein Pa4652 TR:AAG08039 (EMBL:AE004879) (790 aa) fasta scores: /codon start=1 /trans1_table=11
                                                                                                                                                                                                                protein"
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/gene="YPO1697"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SW:CSC1_ECOL1_(P53518
21.9% id_in_242_aa"
/codon_start=1
/trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="YP01697"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="YPO1698"
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transl_table=:
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VTLPPNSSFNVNTLTESGSGTIAMLCTGTGVSLLASFVLNATVASTTNTLKLKNSAGD
VIPYITYSDAGYNNALAIGNVINYAGNSSLLIVTLFQISANLPYTRTGSNNAINVNV
SAGTYTDVINLNMYNYDLCAISLFSLCGGRESGTATSTVTVKLTVSNDCVINSAPNVN
FGSYALITOFRAVNONISATCTKNAFFTYTITNGNNFYARPWRMKTLTGSTDYLQYQLY
QGAGVIPWNVTNKRTSTATGTQQLIPYNAVINPQQAQKTVGTYQDNVSVVLEY"

complement (1663. . .1728)
                                                                                                                                                                                   /noce="Similar to Streptomyces coelicolor hypothetical
protein SC6G4.19C TR:O86782 (EMBL:AL031317) (190 aa) fasta
scores: E(): 6.5e-10, 41.3# id in 104 aa, and to Bacillus
halodurans BHG089 protein TR:O9KEF4 (EMBL:AP001510) (134
aa) fasta scores: E(): 0.034, 30.5* id in 95 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1093. .2082)

dgene="YPOL4695"

/note="Similar to Pseudomonas aeruginosa hypothetical
protein TR.AAG08040 (EMBL:AE004879) (315 aa) fasta scores:
B(): 0, 41.5% id in 299 aa. and to Pseudomonas fluorescens
hypothetical 23.5 kba protein TR:Q9KIM7 (EMBL:AR228767)

(231 aa) fasta scores: E(): 1.2e-13, 29.9% id in 231 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="TrembL:08ZFLO"
/translation="MaTLPOXXEDVERWARGDTEQVADELLALVLNGTKTATCAALDD
EGYPQAGDIFVVVNRNQPACAVELTEVELKTFDQVDEAHALAEGEGDSTLAYWRKTQ
ORFFEEYDMFS.PDMLICMKFXVLETF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tränslation="MGKSIVKIRQFEVDDAELSSQTKGEHTLSIPCKSDPDLCMQLDG
WDENTSIPALLDGKDTLLYKQHYDQHQDAWVMKVT"
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/gene="YPO1695"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (646. .885)
/gene="YPO1.694"
/note="Similar to Escherichia coli hypothetical protein
Yebv SW:YEBV ECOLI (P76274) (78 aa) fasta scores: E():
4.1e-19, 57.9* id in 76 aa"
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/note="Similar to Escherichia coli outer membrane usher
                                                                                                                                                                                                                                                                                                                                                                    /product="conserved hypothetical protein"
/protein_id="CARO90513.1"
/db_xref="GI:15979724"
/db_xref="TrEMBL:Q8ZFL0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //Lambal_addie=ivalue=ival pypothetical protein"
/product="conserved hypothetical protein"
/protein id="CARC90514.1"
/db_xref="GI:15979725"
/db_xref="TIEMBL:Q92FK9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="putative membrane protein"
/protein_id="CAC90515.1"
/db_xref="GI:15979726"
                          db_xref="taxon:214092"
/note="biovar: Orientalis"
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for YPO1695 by TMHMM2.0"
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/gene="YPO1694"
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/transl_table=11
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                                                                                 147. .536
/gene="YPO1693"
                                                                                                                                                                  /gene="YP01693"
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/transl_table=
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                                                   115700 AATGTCTTTAAAGGTGCTGAAGATGCGACCGATGGGAATACTTGGGACGTCTAC 115759
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Leptospira interrogans serovar Lai str. 56601
Bacteria; Spirochaetes; Spirochaetes; Leptospiraceae; Leptospira. 1 (Dases 1 to 10029)
Ren, S.X., Fu,G., Jiang, X.G., Zeng,R., Miao, Y.G., Xu,H., Zhang, Y.X., Xiong,H., Lu,G., Lu,L.F., Jiang,H.Q., Jia,J., Tu,Y.F., Jiang,J.X., Cu, Kai, Z., Sheng,H.H., Yin,H.F., Zhang,Y.V., Zhang,Y.Q., Cai, Z., Sheng,H.H., Wan,H., Huang,H.L., Olan,Z., Wang,S.Y., Zhang,Y., Shen,Y., Qiang,B.Q., Xia,Q.C., Guo,X.K., Danchin,A., Saint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343
                                                                                                                                                                                                                                                                                                                          Thr ProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnProAlaProLeuValAsn 305
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                                                                                                                                                                                                                                                  227 ThrVal --- TyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeu
                                                                                                                                                        364 AsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGlnAspGlyTyrPro
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                                                                                                          246 ValalaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAlaGlyLeu
                                                                                                                                                                                                                  LeuMetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLysAsnMetThrAlaPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 AsnSerGlnValValAspPheTyrAsnIleProLeuAlaArgPheThrSerGluAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444 GlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsn
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AE011450.1 GI:24196692
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AGCGGTATGAACGCAGCATCCAGTAATCTAGATGTGATCGTAACAATATCGCCAACTCG 115186
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                                                                          /translation="MKNHTLVVFSLSLVCGLLLFQAYPVNAVSKTANITVTATLLPTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaileGlyGlyLysGlyPhePheGlnValThrLeuGluAspLys------ValHis 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 AsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSerHisAspIle 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnThrileGlyTyrLysGlnGlnGlnValValPheGlnAspLeuPheSerGlnAspLeu [1] [1] [1] [1] [1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATGCCCGTAACGGCCAGTTAAGCTGGATGAAAACCGTAATATCGTCAATATGCAAGGT
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145
74
196
83
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557.50
43.98%
29.12%
21.56%
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Best Local Similarity:
Query Match:
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JOURNAL PUBMED REFERENCE AUTHORS

FEATURES

COMMENT

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PNANLLPWELVSETKTURSYDPETESVILDELQSETIKTNSTETLARPESISTSELIE
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Submitted (12-WAR-2002) Chinese National Human Genome Center at Submitted (12-WAR-2002) Chinese National John Shanghai 201203, China Shanghai 250 Bi Bo Road, Shanghai 201203, China Updated information will be available at our World Wide Web site (http://www.chgc.sh.cn/lep/). Comments to the authors are
Girons, I., Somerville, R.L., Wen, Y.M., Shi, M.H., Chen, Z., Xu, J.G. and Zhao, G.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Strain 56601 is maintained by the Institute Epidemiology and Microbiology, Chinese Academy of Preventive Medicine"
                                             Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing Nature 422 (6934), 888-893 (2003)
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                                                              916
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                                                                                                                                                                                                                        MetAsnProserGluAspGlySerAlaAlaSerGlyThrAspSerAla-----
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Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.

1 (Dases 1 to 300594)
Nacimento, A.L., Martins, E.A., Monteiro-Vitorello, C.B., Ho, P.L., Harke, D.A., Verjovski-Almeida, S., Hartskeerl, R.A., Marques, M.V., Oliveira, M.C., Menck, C.F., Leite, L.C., Carrer, H., Ferro, E.S., Perro, M.I., Furlan, L.R., Gamberini, M., Giglioti, B.A., Gose, Neto, A., Goldman, G.H., Goldman, M.H., Harakava, R., Jernomo, S.M., Junqueira-De-Azevedo, I.L., Kimura, E.T., Kixanmee, E.B., Lemos, E.G., Lemos, M.V., Marino, C.L., Nunes, L.R., De Oliveira, R.C., Perriard, G.G., Reis, M.S., Schriefer, A., Siqueira, W.J., Sommer, P., Tgai, S.M., Simpson, A.J., Ferro, J.A., Camargol, L.B., Kitajima, J.P., Setubal, J.C. and Van Sluys, M.A., Comparative Genomics of Two Leptospira interrogans Serovars Reveals Novel Insights into Physiology and Pathogenesis
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Piocnuz L1-130"
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Nascimento, A.L., Ko, A.I., Martins, E.A., Monteiro-Vitorello, C.B., Hoselber, L. Haake, D.A., Verjovski-Almeida, S., Hartskeerl, R.A., Marques, M.V., Oliveira, M.C., Menck, C.F., Leite, L.C., Carrer, H., Coutinho, L.L., Degrave, W.M., Dellagostin, O.A., El-Dorry, H., Ferro, R.S., Ferro, M.I., Furlan, L.K., Gamberini, M., Giglioti, E.A., Genser, S.A., Goldman, M.H., Harakava, R., Junqueira-De-Azevedo, I.L., Kimura, E.T., Lemos, E.G., Lemos, M.V., Martino, C.L., Nunes, L.R., De Siqueira, R.C., Pereira, G.G., Reis, M.S., Schriefer, A., Sommer, P., Taai, S.M., Simpson, A.J., Ferro, J.A., Camargo, L.E., Kitajima, J.P., Setubal, J.C. and Van Sluys, M.A.
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AE017291 AE016823
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TITLE JOURNAL

FEATURES

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REFERENCE AUTHORS

JOURNAL PUBMED

TITLE

AUTHORS REFERENCE

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transl table=
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I SRSEEA I RLSRIL VDQATELAER I ERKATTDKI AGRDTKTEGNKNTKNQSTTEGKNS
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8766. .8954
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84 199 102 12 Length:
Matches:
Conservative:
Mismatches:
Indels: US-10-009-823A-1 (1-502) x AE017291 (1-300594) Gaps: 5.09e-24 550.00 43.63% 27.90% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: Score:

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MetMetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20

251203

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PheGlnAspLeuPheSerGlnAspLeuAlaIleGlySer------ThrGly

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251382 251739 252129 252130 GCGATTCAAAATTTTGATCTTAAGAGAA---GCAGGAAATGGTAAACGGAATCACT 252186 251442 251502 251562 251622 251796 251829 251949 252009 252204 252204 152 172 290 328 348 368 115 275 388 187 227 247 308 95 251950 ACTCAACTTTCCGTTGATGTTTCTGGAACCGGCGGACAAAACACTCCAACTTCCAGGTAAC AsnGlySerSerSerThrArgArgTyrSerGlnAspGlyTyrProGlnGlyAspLeuVal GGTGTGAATCCTCAACAAGTTGGTTTGGGTTTTTGATCGTGCGATTGATAAATCATG trititarcercaaggacggreacaartriatacaaggeceeergritiaaccrc ||||::: ::: |||| 251623 AGACTGGATGATAAAGGAAATAAATACATCAATTCGGCAGCTTCGATTGAA---GATATT AsnleuGlyAspSerThr------AspLysThrGlnSerGluAlaAsnPro 251797 -----ĠĊĠATGATTAACGAT----------------------CĊAGATCCTAAGATGAGA ::: ||| 251890 ATGGAATTTTACAAGGTTCGTGATAACACTTGGAAGGCTAGATTGAGTATGACGATTCA LysSerGlnGlnAsnMetTrpAlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAsp ||||||||::: |||||||:::||| TTTCAGGATATGATTCTCAGGAGCTCAGAGGCGCTTCCGAGCCTAAAGAGAATATTGGA PhePheGlnValThrLeuGluAspLysValHisTyrThrArgAlaGlyAsnPheArgPhe ArgileSerAsnAsnProAsnIleLysLysGluThrLeuGluProIleGlnLeuAspPhe AsnAspProThrValAlaLysSerProAlaLysThrSerThrAlaLeuAsnAlaValVal 251740 AATTTGAATTCTTCTGCTCCGGCGGTTCCGCCTGACGCAACCAAGAAGAATCACT---251830 AGGGGACATGTTACCACGATTAATACATTTGACGATCAAGGGATTCAAAGAGAATTTAAA ValTyrpheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeuValAla 252010 ACTGAATTAGAATTTGGTTTTACTCCGGATGGAAAACTAGTATACGTTTCTGACGGTGTG -----AsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySer-------AlaThrLysAspLeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuPro GInPheSeralaAsnPheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIle 349 IleGlyLysLeuProSerMetMetProlleGlnThrSerSerGlyAsnSerThrAlaArg SerGlnGlyProAsnGlnAlaGlyMetGlyAlaGlnValGlySerValArgThrilePhe 188 TyrPheAlaLeuLeuGluSerTrpLysGlyAsnGlyThrProProlleSerThrSerAsn TyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSerHisAspIleThr ------GlyLeuLeuMetSerGlyThrMetThrPheSerSer-----ThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLysGly 116 ThrGlnAspGly---PheLeuAsnAspProSerGlyPheThrLeuMetGly-----Ser 248 MetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAla-----CAATTCTCCTCTGACTTT---1 1 1 1 1 1 1 1 1 1 1 309 252187 329 252204 252204

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1460. 1668

1471. 1668

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1771. 1668

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                                                                                                                                                                                                                                                                                 .::||| ::: ||| ::: ||| 252253 TCTTTTTCGATCATACAGATTACGAGTGTGTTTTCGAACGGAGTGCGTCAG 252312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treponema pallidum flagellar hook (flgE), (orf4), flagellar motor protein (motA), flagellar motor protein (motA), flagellar motor protein (motB), (fliL), and flagellar switch protein (fliM) genes, complete cds, and (fliX) U28219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
1 (Dases 1 to 5230)
Limberger, R.J., Slivienski, L.L., El-Afandi, M.C. and Dantuono, L.A.
Organization, transcription, and expression of the 5' region of the
fla operon of Treponema phagedenis and Treponema pallidum
J. Bacteriol. 178 (15), 4628-4634 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (01-JUN-1995) Ronald J. Limberger, Wadsworth Center, NY
State Dept. of Health, 120 New Scotland Ave., P.O. Box 22002,
Albany, NY 12201, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             469 GluMetValAsnMetIleIleIleIleGlnArgGlyPheGlnMetAsnSerLysSerValThr ::::||||||||||||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThralaaspThrMetLeuGlnLysAlaLeuGluLeuLysArg 502
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Limberger, R.J.
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DEFINITION
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TPU28219
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VERSION
KEYWORDS
SOURCE
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TITLE
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PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
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us-10-009-823a-1.rge

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CDS	gen RBS CDS	ORIGIN Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	\$ 6 & 6 & 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

AE001244/c

RESULT 15

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REFERENCE AUTHORS

MEDLINE PUBMED REFERENCE AUTHORS

JOURNAL

TITLE

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FEATURES

gene

CDS

tRNA gene

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S Fraser. C.M., Worris, S.J., Weinstock, G.M., White, O., Sutton, G.G., Bodson, R., Gwinn, M., Hickey, E.K., Clayton, R., Ketchum, K.A., Sodespren, B., Hardham, J.M., McLeod, M.P., Salzberg, S., Peterson, J., Sodespren, B., Hardham, D., Howell, J.K., Chidambaram, M., Utterback, T., McDonald, L., Artiach, P., Bowman, C., Cotton, M.D., Fuji, C., Garland, S., Hatch, B., Horst, K., Roberts, K., Watthey, L., Weidman, J., Saith, H.O. and Venter, J.C.

L. Submitted (06-MAR-1998) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
Location/Qualifiers
Location/Qualifiers
Location/Qualifiers
Location Weidman pallidum subsp. pallidum str.
                                                                                                                                                                                                  Treponema pallidum subsp. pallidum str. Nichols section 60 of 87 of the complete genome.
AE001244 AE000520
AE001244.1 GI:3323005
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Treponema pallidum subsp. pallidum str. Nichols
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
1 (Dases I to 26536)
Fraser, C.M., Norris, S.J., Weinstock, G.M., White, O., Sutton; G.G., Bodson, R., Gwinn, M., Hickey, E.K., Clayton, R., Ketchum, K.A., Sodergren, E., Hardham, J.M., McLeod, M.P., Salzberg, S., Peterson, J., Khalak, H., Richardson, D., Howell, J.K., Chidambaram, M. Utterback, T., McDonald, L., Artiach, P., Bowman, C., Cotton, M.D., Fujil, C., Garland, S., Hatch, B., Hurst, K., Roberts, K., Sandusky, M., Weidman, J., Smith, H.O. and Venter, J.C.
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                                                                                                                                                 1387 GATACGGTGTŤĠAGTŤŤĠĀĠĊĠĊ 1410
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US-10-009-823A-1 (1-502) x AE001244 (1-26536)

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ОÞ	ACTTT
ò	ThrGly
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gene	gene CDS	misc_feature gene CDS	gene		misc_feature gene CDS
25574	Oy 395 GludlyLysLeudlnGlyLysFyrSerAanSerGlnValValAspPheTyrAsnIlePro 414		RESULT 16 BX321857 LOUS LOUS LOUS LOUS LOUS LOUS LOUS LOUS	AUTHORS Chain, P., Lamerdin, J., Larimer, F., Regala, W., Land, M., Hauser, L., AUTHORS Chain, P., Lamerdin, J., Larimer, F., Regala, W., Land, M., Hauser, L., Hooper, A., Klotz, M., Norton, J., Sayavedra-Soto, L., Arciero, D., Hommes, N., Whitzeker, M. and Arp, D. TILLE Complete genome sequence of the ammonia-oxidizing bacterium and JOURNAL J. Bacteriol. 185 (9), 2759-2773 (2003) MEDLINE 22586410 PUBMED 12700255 REFERENCE 2 (bases 1 to 313050) AUTHORS Larimer, F. TITLE Direct Submission	JOURNAL SUBMITTEE OF LIZ-NOV2 SUBMITTEE ON DEADS IN NITEDSMONDED SUBMITTEE OF DEADSMONDED SUBMIT

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Mismatches:
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Matches:
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Thermoanaerobac I Thermoanaerobac Bacteria; Firmi Thermoanaerobac I (bases I to Bac, O., Tian, Y. Chen, Y., Xue, Y. Tan, H., Chen, R. A Complete Sequence Res. 12 21992816			Tian,Y., Direct Su Submitted of Scienc	<pre>source 110303 /organism.="Thermoanaerobacter tengcongensis MB4" /mol_type="genomic DNA" / # frain="MB4" /db_xref="taxon:273068" gene</pre>	/gene="fight" Journal	spirochete gi[1165267]gb AAA8506.11 (043739) rige [Borrelia burgdorferi] gi[268183]gb AAG6665.1] (ABO01137) fiagellar hook protein (figs) [Borrelia burgdorferi], score 278, E-value 1.00E-73" /codon start=1 /transl_table=11 /product="Flagellar basal body and hook proteins" /protein_id="RAM24655.1"	/ db xref="61:20516445" / db xref="61:20516445" / translation="MLRSMYSALSGLQAHQARLDVIGNNIANVNTVGYKASRWTFKEI / translation="MLRSMYSALSGLGAYALASIDTLFTRGGAQRTDNPTDLSIDGNGFF	misc_feature complement(11671259) /gene="F1983" /locus tag="TTT1433" /note="Pfam match to entry f1g_bb_rod, Flagella basal body	rod protein, score 58.3, E-Value 1.30E-13" RBS complement (12801284)
SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED PUBMED	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	KEFEKENCE AUTHORS TITLE JOURNAL FEATURES						
204 SerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGln 220 31592 AATGTAGCTAATCCCATTCTACTTCGGGAGAAATTTTGACGTTTT 31651 221 GlyAsnSerHisAspIleThrValTyrPheAspGlyAlaProSerSerThrGlySer 239 31652 GGTAATTCCATATTATATTTCAGAAAACAGCTGCATCCACTTGGGGCTA 31711 240 LySThrPheGluTyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGly 259 31712 TANACAGCCGTGGARGGTACATAGTGATCCTACTGGATATCTGCT 31762	ThraspSerAlaGlyLeuLeuMetSerGlyThrMetThrPheSerSerAsnGlyACGGATAGCTTTAATCCATCGGGGTAGCTTTAATCCATTAATCATTGAGCTTTAATCATTCAGGGTAGGGTAATAGAGGTAGAGATAGAGAAAAAAAA	Problemontarion of the control of th	320 GINProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsnMetTrpAlaGlyAlaPro 339		380 ASPG1yTyrProGlnGlyAspLeuValAspValThrIleThrSerGluGlyLysLeuGln 399		460 GluthrSerAsnvalAspMetSerArgGluMetValAsnMetIleIleIleGlnArgGly 479 32183 GAAGAATCCAATGTTGATCTGACGACCGAGCTGATCCTGATCATGACGCGGGTC 32242 480 PhcGlnMetAsnSerLySerValThrThralaAspThrMetLeuGlnLysAlaLeuGlu 499 ::: ::: :::: :::: :::: 32243 TATCAGGCCAATGCCAATGCAGCACCATCATGAAT	500 Leu 500 ::: 32303 Arc 32305	RESULT 17 AE013102 AE013102 LOCUS AE013102 AE013102 AE013102 DEFINITION Thermoanaerobacter tengcongensis MB4, section 129 of 244 of the complete genome. ACCESSION AE013102 AE018691 VERSION AE013102.1 GI:20516444

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TAGELLAR HOOK PROTEIN FLGE gi|7463172|pir||Cr0135

pirochete gi|165267|gb|AAA85606.1| (143739) FlgE
Borrelia burgdorferi] gi|2688183|gb|AAC66665.1|

ARBOULLST) Flagellar hook protein (flgE) [Borrelia codon state=1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 ThrvalSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValVal
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107
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Matches:
Conservative:
Mismatches:
Indels:
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528.50
43.95%
28.91%
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Query Match:
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flagellar hook assembly protein [Borrelia burgdorferi]
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assembly protein (flgD) [Borrelia burgdorferi], score
85.1, E-value 3.00E-16"
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25022 bp DNA linear BCT 19-FEB-2003 PAO1, section 100 of 529 of the complete Pseudomonas aeruginosa PAO1 Pseudomonas aeruginosa genome. AE004539 AE004091 AE004539.1 GI:9946985 LOCUS DEFINITION

ISM Pseudomonadaceae FACT

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

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I (bases 1 to 25022)

Stover.C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Indrey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Indrey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Hostbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z. and Paulisen, I.T.

Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogan

IN Nature 406 (6799), 959-964 (2000)

(bases 1 to 25022)

Stover, C.K., Phan. X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagroud, M., Galber, R.L., Gollery, L., Tolentino, E., Westbrock, Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K., E., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E., W., Lory, S. and Olson, M.V.
Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University of Washington, 3 (bases 1 to 25022)

Pseudomonas aeruginosa Community Annotation Project (PseudoCAP) Direct Submission Submitted (04-FEB-2003) Department of Molecular Biology and Biochemistry, Simon Fraser University, 8888 University Dr., Burnaby, British Columbia VSA 1S6, Canada

This represents the February 3, 2003 version of the continually updated, reviewed, Pseudomas aeruginosa PAO1 genome annotation, from PseudoCAP (see http://www.pseudomonas.com for latest updates and links to alternate annotations). PseudoCAP is coordinated by Fond S.L. Brinkman (Simon Fraser University, Canada) and Robert E.W. Hancock (University of British Columbia. Canada). We welcome submission through www.pseudomonas.com of any proposed changes.

of the protein name. Function experimentally demonstrated in P. aeruginosa. Function of highly similar gene experimentally confidence, is used to rate our confidence of the Protein name accuracy c Class 1: F Class 2: F

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3: Function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity to an experimentally studied gene.

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Borrelia burgdorferi fesmid clone 31, complete seguence.
U43739
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Borrelia burgdorferi
Bacteria, Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
Borrelia burgdorferi group.
1 (bases 1 to 34817)
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Submitted (21-DEC-1995) John J. Dunn, Biology Department,
Brookhaven National Laboratory, PO Box 5000, Upton, NY 11973-5000,
                             305 AsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGlnProLeuThrLeu
                                                           8846 ACTĠĠĊAATĊĊĠĊĊĠACTCCC-----ĠĠĊACĊĠĠĊTĠGATTĊĊĠGCĠGCCTCĠ
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8795 CCGGGCTTCAGCATCGACGGACCACCAACGTGATCCAGTTCAGTCCGGCC------
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8705 TCGAACAAGACGCCG-------------AIGAGCTICAACGTCACCTTC 8740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 GlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPhe 273
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Conservative:
Mismatches:
Indels:
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45.84%
29.21%
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ILLI VUYSKRSELDE FORTHELD VITTE GELVALS STREET LIKKSIN FEGET TO VITTE STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET ST
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'transī table=
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EAKRINLQNELENTKI EGKVSVENI ACSGVKLYI KNAFYELSKDYNNVTFI EDDNY I K
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/codon start=1
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                                                                                                                                                                                                                                                                      'note="orf37; Method: conceptual translation supplied by
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/note="orf36; Method: conceptual translation supplied by
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14560 AATTTTGTAGAAACAAGCAATTCAGGTCAAGTTAGAATAGGCGAAACTGGACTTGCTGGA 14501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 IleGlnThrSerSerGly------350 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 SerSerSerThrArgArgTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAspVal 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 ThrileThrSerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValValAspPhe 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLysLeuProSerMetPro 357
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                                               191 LeuLeuGluSerTrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyr 210
                                                                                                                                                                                                                                                      251 SerGluAspGlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThr 270
                                                                                                                                                                                                                                                                                                                      271 MetThrPheSerSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySer 290
                                                                                                                                                                                                                                                                                                                                                                                         291 AlaThriysAspLeuAsnAla-----TrpGlnProAlaProLeuValAsnGlyLeu 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 TyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMet 470
                                                                                                                                                                                   231 AspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeuValAlaMetAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 ProGlnPheSerAlaAsnPheValGlyAlaGlyIleGlnProLeuThrLeuAspPhe---
                                                                                                                AlaGlnProMetArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14860 ATTCCTATAACATTTAATGTTTTGGGTGCAAATGTAGGTGAAGTTGGTGAGCAGCAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   471 ValAsnMetIleIleIleGlnArgGlyPheGlnMetAsnSerLysSerValThrThAla
                                                                                                                                                                                                                                                                                                                                                          15010 GTTGTAAAAGATTTAAATACGCCTAATTTATGGAATGCAACAGTATTAATAAATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14380 GATCAATTATTACAAGAACTTGTAAGATTGAAA 14348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15550 TITICAAGATATGATATCGCAATCTATTTCTGGAGCTTCTCGCCCTACTGATGCTCGTGGT 15491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15370 TTTTTTTAAAAGAAGGTAAAATTTGTTTTATACAAGAGCCGGTGCTTTTGACGTG 15311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15310 GACTCTGATCGACATCTTGTAAATCCTGCAAAT-------GGAATGCGAATTCAA 15263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mankfrlpivplsppnpppynnsobovnsastdlenesslpifbe
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AKKUSFQSIFKKMILKKEEIISSGNDYVKLEEKIEASLKDKQDRLKKF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 ThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMetGlySerArgileSer 135
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                                                                                   note="flagellar protein required for flagella formation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 ThrvalSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValVal 40
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 MIMLPPVMISLPFKLILFVMVDGWTLITSGLIKSFM"
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                        note="flagellar switch protein"
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                                                  complement (9847. .10473)
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Best Local Similarity:
Query Match:
DB:
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putative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                             YSTGNHLHFTI FKNGKTENPMKYLR"
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                                                                                                                                                                                                                                                                                                                             Bacteria, Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia burgdorferi group.

I (bases I to 4430).

Inthigra, R., Casjens, S., Huang, W.M., Sutton, G.G., Clayton, R., Lathigra, R., White, O., Ketchum, K.A., Dodson, R., Hickey, E.K., Owine, M., Owigherty, B., Tomb, J.F., Pleischmann, R.D., Richardson, D., Hanson, W., van Vugt, R., Palmer, N., Adams, M.D., Gocayne, J., Weidman, Y., Utterback, T., Warthey, L., McDonald, L., Artiach, P., Hatch, B., Smith, H.O. and Venter, J.C. Cotton, M.D., Horst, K., Roberts, K., Hatch, B., Smith, H.O. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Clayton, R.A., Lathigra, R., White, O., Ketchum, K.A., Dodson, R., Hatkey, B.K., Gwinn, M., Dougherty, B., Tomb, J., F., Fleischmann, R. D., Richardson, D., Peterson, J., Kerlavage, A.R., Quackenbush, J., Salzberg, S., Hanson, W. van-Vug, R., Palmer, N., Adams, M.D., Artiach, P., Bowman, C., Utterback, T., Watchey, L., McDonald, L., Artiach, P., Bowman, C., Garland, S., Fujii, C., Cotton, M.D., Horst, K., Roberts, K., Hatch, B., Smith, H.O. and Venter, J.C. Submission.
Submitted (12-DEC-1997) The Institute for Genomic Research, 9712
AE001137 44380 bp DNA linear BCT 17-MAR-2003 AE001137 AE000783 (section 23 of 70) of the complete genome. AE001137.1 GI:2688160
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134. .1516
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20700 GACTCTGATCGACATCTTGTAAATCCTGCAAAT-------GGAATGCGAATTCAA 20653
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                                                                                                                                                                                                                      ACTCAAGGAGCTTTTCAAAGCACTCAAAAAGCATCTGATCTTGGAGTTAGTGGCAACGGA 20761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20401
                                                                                                                  251 SerGluAspGlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThr 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProGlnPheSerAlaAsnPheValGlyAlaGlyIleGlnProLeuThrLeuAspPhe--- 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 AlaGlnProMetArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPhe 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 MetThrPheSerSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySer 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 AlaThriysAspLeuAsnAla-----TrpGlnProAlaProLeuValAsnGlyLeu 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 Asp------ProThrValAlaLysSerProAlaLysThrSerThrAlaLeuAsnAla 170
  55
                                                                                          75
                                                                                                                                                                                   95
                                                                                                                                                                                                                                                                                                   20760 TITITITATITIAAAAGAAGGTAAAATITGTITIATACAAGAGCCGGTGCTITIGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 Asn-----AsnProAsnIleLysLysGluThrLeuGluProIleGlnLeuAspPheAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20940 TTTCAAGATATGATATCGCAATCTATTTCTGGAGCTTCTCGCCCTACTGATGCTCGTGGT
                                                                                                                                                                           ThrighnglyalapheglubroglyasnSerValThraspLeuAlalleGlyGlyLysGly
                                                                                                                                                                                                                                                                      Phe Phe GlnValThrLeuGluAspLysValHisTyrThrArgAlaGlyAsnPheArgPhe
                                                                                                                                                                                                                                                                                                                                                              ThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMetGlySerArgIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 ValValAsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20532 GCTTGTAATCTTGATAAGAGATTGCCCTTAATTCAAGAAGGTGCGAATCCTGCAGATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 LeuLeuGluSerTrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 AspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeuValAlaMetAsnPro
                                                                                          SerGlnGlyProAsnGlnAlaGlyMetGlyAlaGlnValGlySerValArgThrIlePhe
--ThrGly
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LSSDDVVIYTPERPTSITDAYGIIKVLSYRMENIKNLRLIVNRVANVSEAKGVAKKVI
                                                                                                                                                                                                                                                                                                                   SDGEPFIRKSSKGVFIKVISFKGGGIPIKYQDVIFKLELHSNIENFNKDIVKGIVENA
SGYYEKIADPESDPSENVTWMVQISENSMSVTIEFTAPGINGAEIFAQDIFNILKKYG
VIDIAILKDKVAKFVDYPVYGEPVELARGLEPVKGKDSYIDFIVDENNRFGEYEVSSI
                                                                                                                                                                                                                                                                                                                                                                                    GPRNYIEGEELARI I PPGKGYDGYTVFGKYLKSESGQDIDFILGENTFRDGYKTRAKC
NGYMSYSDGYI SYHNI YLVKGDVGPATGDI VNNGMYLVQGNYLDGYNI MAKSGIEVKG
IVORCNLKTDGSI I FHGSYNGKGDSKI YARGNYRAKFLENTLAKGGSTBTURGGTYNS
SIVSKRYLLCI GKASKI VGSNYCAKEVRAYSI GSDRS CETCI DVGYDP BI KDLLTRF
TSHLEK EKRLEVLYKDI VALKKNI VLI TIDKARKSLKI DSYNBFYNBSKI LRMEI KMI
BAKRI INLONELENTKI BGKVS VENI ACSGVKLY I KNA FYELSKDYNNYTFI EDDNY I K
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complement (8080. .8967)
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                                                                                   /note="similar to PID:1165252 GB:AE000783 percent identity: 100.00; identified by sequence similarity; mutative"
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| db_xref="GI:2688199"
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protein id="AAC66679.1"
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20191 ::: 20190 GTAAATTIGAAATIGGGAACAGTIGGAAGTTACACTGATTCAAITACTCAGTTIGCTGAI 20131 ------GlyIleLysSerGlnGlnAsnMetTrpAlaGly 337 358 IleGlnThrSerSerGly------350 371 SerSerThrArgArgTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAspVal 390 ::: :::::|||||| 20343 ---GAGCAAAATTCAAATTTT--------ACACTIGGGTTTGAC 338 AlaproAlaSerAlaAlaAlaIleGlyThrAspIleGlyLysLeuProSerMetMetPro 327 a 셤 ò .∂ ò

PIGDKEGAKSTKNITF LRVVKDLMTPULMAT MATTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOT	VLGANVGEVGEQL VY NGVLVGIYSNGIRRDE DIRGGVLEWANVDLAR ORIGIN	••	Percent Similarity: 41.62% Best Local Similarity: 28.06% Query Match: 19.45% DB: 1	US-10-009-823A-1 (1-502) x BORFLGE (1	Qy 1 MetMetGlySerLeuPheIleGl	Db 115 ATGATGAGGTCTTTATATTCTGG	Oy 21 ThrValSerAsnAsnIleAlaAs:	175	Qy 41 PheGlnAspLeuPheSerGlnAs;	Db 235 TTTCAAGATATGATATCGCAATC	Qy 56 SerGlnGlyProAsnGlnAlaGl	Db 295 GGGACTAATCCCAAGCAAGTTGG	Qy 76 ThrGlnGlyAlaPheGluProGl	Db 355 ACTCAAGGAGCTTTTCAAAGCAC	Qy 96 PhePheGlnValThrLeuGluAs	Db 415 TTTTTATTTTAAAGAAGGTAA	Oy 116 ThrGlnAspGlyPheLeuAsnAs	Db 475 GACTCTGATCGACATCTTGTAAA	Qy 136 AsnAsnProAsnIleLy:	Db 523 GGTTGGATGGCAAGAGATTTAGA	Qy 154 AspProThrValAl	 	Oy 171 ValValAsnLeuGlyAspSerTh	Db 643 GCTTGTAATCTTGATAAGAGATT	Qy 191 LeuLeuGluSerTrpLysGlyAsi	Db 703 GCACGCGGAACTTGGGTTGTCAA	Cy 211 AlaGinProMetArgValTyrAs	Db 733TTGTAIGA	Qy 231 AspGlyAlaProSerSerThrGly	Db 765	Qy 251 SerGluAspGlySerAlaAlaSe	Db 765
	OY 391 ThrileThrSerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValValAspPhe 410	Oy 411 TyrAsnIleProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsn 430 20010 GGCAAGATTGCTTCTTTTATGAATCCCGGAGGACTTGCAAAATCAGGCGATACT 19951	Qy 431 HisTyrSeralaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsn 450::::	Qy 451 TyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMet 470	Db 19890 CTIGGTGATATTAGATCTGGTGTTTTAGAAATGGCCAATGTTGATCTTGCAGAGCAATTT 19831	Oy 471 ValAsnMetIleIleIleGlnArgGlyPheGlnMetAsnSerLysSerValThrThrala 490	Db 19830 ACAGATATGATGGACCCAAAGGGATTTCAGGCAAATGCCAAAACCATTACCACTTTTT 19771	491 AspThrMetLeuGlnLysAlaLeuGluLeuLys 501	Db 19770 GATCAATTATACAAGAACTTGTAAGATTGAAA 19738	RESULT 21 BORFIGE	ĝ	bottedina buiguotifai itageilai 1100% proceil (1198) gelle, Collyfor 168.	ACCESSION 143849. VERSION 143849.1 GI:1184295	ALIWOKUS Ilageliai nook piotein; ilgs gene. SOURCE Borrelia burgdorferi (Lyme disease spirochete) ODGENICM Borrelia burgdorferi		REFERENCE 1 to 1499)			OUGGAAL MICZOBIOLOGY 140 (FC 11), 2531-2540 (1594) MEDIUNE 95111614 PTHMED 7812434		Unpublished (1996)	COMMENT On Feb 11, 1996 this sequence version replaced g::903/02. Original source text: Borrelia burgdorferi (individual isolate	FEATURES DATE CLone: pALLES CLone LIBIARY: HB19 COSMID) DNA: FEATURES	/oring="Borrelia burgdorferi"	/ NOT LYPE= 9enouic Days: / isoTate=#HB19	/dD xrel="raxol:139" /clone="babli28" /clone="babli28"	gene 115. 1443	/gene="IJgE" 11514943 /14043	/gene=.rugs= /codon start=1	/transldole=11 /product="flagellar hook protein" /protein:4-manager:1:	/ December 1 - April 1 - April 1 - April 1 - April 1 - April 2 - A	/ LIMINALM LOIS-TWINSLESSYSOLDEN VIGNIALMY VIA LISTAVAN LAGO ISOSISGASETIDARGGTUN ROVOLGMUN VASIDTI HTQQARQSTQKASDLGYGGNGFF ILKEGKNLFYTRAGAFYVDSDRHLVN PANGMRIQGMMARDLEGEKVINTASDIEDLII

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FPACNLDKRLPLIQEGASPADIARGTWVVNKSLYDSFGNVSVLE
TIVLINGEQNSNFTLGFDNEGALAS.INGOPGOKGDILOIPITFN
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DIGKILALASFNNFGGLAKSGDTNFVETSONSGOVRIGETGLAGLG
AEQFTDMIVTQRGFQANAKTIITSDQLLQELVRLKN"
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271 MetThrPheSerSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySer 290 766	1045 1105 1105 1105 1105 1225 1225 1228 1288 1289 1289 1345 1405	AL646078 AL646078 Ralstonia solanacearum GMI1000 megaplasmid, complete sequence; segmence; segment 3/11. AL646078 AL646053 AL646078.1 GI:17430778 Ralstonia solanacearum Ralstonia solanacearum Bacteria; proteobacteria; Betaproteobacteria; Burkholderiales; Salanoubat, M., Genin, S., Artiguenave, F., Camus, J.C., Cattolico, L., Chandler, M., Sulasma, M., Malen, M., Walana, W., Schiex, T., Siguier, P., Thebault, P., Whalen, W., Wincker, P., Levy, M., Weissenbach, J. and Boucher, C.A. Genome sequence of the plant pathogen Ralstonia solanacearum Nature 415 (6871), 497-502 (2002)
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/gene="RSp0315"
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PROTEIN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="mexC"
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complement (2966. .6115)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (6136. .7293)
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                                                                                                                                                                                                                                                                                                                                                                                                                         "gene="mexb"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45280 TCGTACACCCGCAACGGCCAGTTCCAGACCGACAAGAACGGCTACATCTCCGCCACC 45339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45340 GGCCAGAACCTGACGGCTACGGCGTGGATGCGACCGCCAAGATCAACACCGCCGTGCTG 45399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 HisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 GlyAlaThrGlyMetLysThrHisSerThrGlyLeuGlyThrValSerAsnAsnIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 AsnalaasnThrIleGlyTyrLysGlnGlnGlnValValPheGlnAspLeuPheSerGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45055 AATGCCAACACGCTCGCTACAAGAAGTCGACGGCCGAGTTCGGCGACGTGTATGCGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 AspieuAlaIleGlySerThrGlySerGlnGlyProAsnGlnAlaGlyMetGlyAlaGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyPheThrLeuMetGlySerArgIleSerAsnAsnAsnProAsnIleLysLysGluThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 valGlyServalArgThrIlePheThrGlnGlyAlaPheGluProGlyAsnSerValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 AspLeuAlaileGlyGlyLysGlyPhePheGlnVal-----ThrLeuGluAspLysVal
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Gene name confidence : hypothetical
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Matches:
Conservative:
Mismatches:
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Gaps:
                                                                                                                                                                                         predicted by Codon usage
predicted by Homology
predicted by FrameD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDPVPSKTPFSVSDADSYNKKGTVTVYDSQGNAHDMVVFVKTKDNEWAVYTHDSSDP
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                                                            STFLGE 1320 bp DNA linear BCT 08-MAR-2000 Salmonella typhimurium flgE gene for flagellar hook protein.
                                                                                                                                                                                                                                                                                                                                                  Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 1320)

Homma, W., DeRoseler, D.J. and Macnab, R.M.

Flagellar hook and hook-associated proteins of Salmonella typhimurium and their relationship to other axial components of
                                                                                                                                                                                                           flagellar hook protein; flagellar protein; flgD gene; flgB gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (16-FEB-1990) Macnab R.M., Yale University, Dept of
Submitted (16-FEB-1990) Macnab R.M., Yale University, Dept of
Molecular Biophysics and Biochemistry, Box 6666, 260 Whitney
Avenue, New Haven CT 06511, U S A
See <XS.094> for flgF gene.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1320
144
76
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Salmonella translation" /mol type="genomic DNA" /db_xref="taxon:602" /map="23min"
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Salmonella typhimurium
Salmonella typhimurium
Sacteria; Protechacteria; Gamma
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.96e-23
498.00
43.91%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             flagellum
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RESULT 23
STFLGE
LOCUS.
DEFINITION
ACCESSION
VERSION
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MEDLINE
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REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                        ORGANISM
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FEATURES
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                                                                                                                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                                          -----ACCACGCCGTTCTCG 45510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GCGGCATGAGCATC 45750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45823 TACGCCACCGCCTGGCCAGCTACTCGGTCGGGACCGATGGCACCATCACGGGCCGC 45882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45883 TACTICCAACGCCGCACGTCGACGCTGGGCCAGATCGCCATGACCAACTTCAAGGCGCCG 45942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46003 CAGATGÁGCACGCCGGCATGGGCTCGTTCGCCTGCTCGTCGTCGTCGCGGTGGTGGAGCAG 46062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15400 ACCAACCTGCAGATCCCGGTGAACGAT------CTGGCGCCCGCTGGCGACCACC 45447
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                                                                                                                                                                                                                                                                                                                        204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 ThrSerAsn-----TyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGly 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 SerAlaGlyLeuLeuMetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLysAsn 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 MetThrAlaPheThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnProAla 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 ProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGlnPro 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342 AlaAlaAlaIleGlyThrAspIleGlyLysLeuProSerMetMetProIleGlnThrSer 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrProGlnGlyAspLeuValAspValThrIleThrSerGluGlyLysLeuGlnGlyLys 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrserAsnSerGlnValValAspPheTyrAsnIleProLeuAlaArgPheThrSerGlu 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 AspGlyLeuArgArgGluGlyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyPro 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluPheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThr 461
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                                                                                                                                                                                                                                                                                                                        185 AlaAsnProTyrPheAlaLeuLeuGluSerTrpLysGlyAsnGlyThrProProlleSer
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Qy 341 SeralaalaalaileGlyThrAspIleGlyLysLeuProSerMetMetProIleGlnThr 360 Db 871ACC 873 Qy 361 SerSerGlyAsnSerThrAlaArgAsnGlySerSerSerSerThrArgArgTyrSerGlnAsp 380 ::	Qy 441 ProGluPheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGlu 460 Db 1087 GCGCTGCTGGGGACTGCCGGTACTTCGGTAAGCTGACGACGCGCGCG		REFERENCE 1 (Dases 1 to 20753) AUTHORS McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W., Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M., Du, F., Hou, S., Layman, D., Leonard, S., Nquyen, C., Socti, K., Holmes, A., Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Stoneking, T., Nhan, M., Waterston, R. and Wilson, R.K. TITLE Complete genome sequence of Salmonella enterica serovar Typhimurium LTZ COURNAL Nature 413 (6858), 852-856 (2001) REDIBERIORE 2 (bases 1 to 20753)	AUTHORY AUTHORY AUTHORY CONSERVA CONSERVA TITLE Direct Submission JOURNAL Submitted (25-MAR-201) Genome Sequencing Project Genetics, Washington University School of Medicine, 4444 Forest Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, NO 63108, USA COMMENT COMMENT Supported by NIH grant 5U 01 AI43283 Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER, http://www.tigr.org/sofflab/glimmer/glimmer.html and Genemark; http://opal.biology.gatech.edu/GeneMark/
st Local Similarity: 28.74\$ Mismatches: 167 ery Match: 19.26\$ Indels: 114 :	hrleugluaspiysvalhis' hrleugluaspiysvalhis' heleuasnaspirosergly' actis' as is seed action as is seed and a seed action as is seed at a seed action as is seed action as is seed action as is seed action as is seed action as is seed at a seed action as is seed action as is seed action as is seed action as is seed action as is seed action as is seed as is seed action as is	Db 466 CCGATCACCATTCCGAACACGCTGATGGCGGCGAAATCGACCACCACCGCG 516 Qy 169 AsnalaValValAsnLeuGlyAspSerThrAspLysThrGlnSerGlualaAsnPrcTyr 188 11.	222 6 4 2 2 4 2 6 4 2 6 8 4 6 6 8 4 6 6 8 4 6 7 3 9 6 8 7 3 9 6 8 7 3 9 6 8 7 3 9 9 6 8 7 3 9 9 6 8 7 3 9 9 6 8 7 3 9 9 6 8 7 3 9 9 8 9 8 9 8 9 8 9 8 9 8 9 8 9 8 9 8	Qy 281 AsnMetThrAlaPheThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnPro 300 Db 793 AACATCACCACCGGTACGATTAATGGGGGGACAGCG

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Location/Qualifiers
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basal body P-ring formation protein FLGA precursor.
(SW:FLGA_SALTY)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="belived to be export chaperone for FlgK and FlgL; flagella synthesis protein FLGN. (SW:FLGN_SALTY)" /codon_start=1 /transl_table=11
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                                                                                                                                                                                                                                 http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 20753

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Salmonella enterica serovar Typhi (Salmonella typhi) strain CT18, complete chromosome; segment 5/20. AL627269 AL513382
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3785 GATTCGIATAACAAAAAGGCACCGTCACCGTTTATGACAGCCAGGGTAATGCCCATGAC 3844
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                                                                                                        265
                                                                                                                                                                                                                                            AsnMetThralaPheThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnPro 300
                                                                                                                                                                                                                                                                                                                 301 AlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGln 320
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Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                      246 ValAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAlaGlyLeu
                                                                                                                            3887 GIGIACACCCATGACAGCAGCGATCCTGCACACCACACAACAACGGGG------
                                                                                                                                                                                                                                                                                                                                       321 ProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAla
                                                                                                                                                                                                                                                                                                                                                                                                                     -------ATGCAGCAGAAC--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 GlyryrProGlnGlyAspleuValAspValThrileThrSerGluGlyLysLeuGlnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 IleThrValTyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeu
                                                                    ---GTGAAAACCAAAGATAATGAATGGGCC
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                                                                                                                                                                             LeuMetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys------
                                                                                                                                                                                                                                                                                 3992 AACATCACCACCGGTACGATTAATGGCGCGACAGCG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4073 GGGGCTAATAACATCGTCGCCACCAAT-
                                                                      3845 ATGAACGICTATTT--
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3281 AGCGGCCTGAACGCTGGGGCCACCTTGATGTTATCGGTAATAACATCGCCAACTCC 3340
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TCAATGCAGATCAACCTG---AACTCAACGGACCCTGTACCGTCTAAAACG---- 3763
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-------GGTTCC-----AAAGTGGGGCTGGGCGTAAAAGTGCG 3424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 GlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThrAlaLeu 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 AlaileGlyGlyLysGlyPhePheGln---ValThrLeuGluAspLysValHisTyrThr 108
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144
76
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Matches:
Conservative:
Mismatches:
Indels:
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PTAINQWISGPESEDVOLCWVGPQITRRVKKHINAVPLGFADGYPYLINBASINDLOO
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GEMWTPGTGDAASVWLSDTAEQVNLLVVEPGENAALCLLAQPGVVIAGRTMQLGDAIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVYAYAGYTAINISSPNTPGIRTLOYGDALDDLITAIKNKONDLOYIHHKYVPYAVKI
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EIIRRLSLELKGQLPIIGVGGIDSVIAAREKIAAGATLVQIYSGFIFKGPPLIKEIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Orthologue of E. coli YCBW ECOLI; Fasta hit to YCBW ECOLI (192 aa), 90% identity in 180 aa overlap. Note discrepency in position of translational start site."
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                                       9001. .4011
//gene="STY1079"
//fore="Orthologue of E. coli pyrD (PYRD_ECOLI); Fasta hit
co PYRD_ECOLI (336 aa), 95% identity in 336 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (4716. .5825)
/gene="STY1081"
/note="Orthologue of E. coli P75863; Fasta hit to P75863
(369 aa), 86$ identity in 367 aa overlap"
/codon startal
/transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="psocond" hydroorotate dehydrogenase signature 2" 4174. 4719 /gene="STY1080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="STY1079"
/note="Pfam match to entry PF01180 DHOdehase,
Dihydroorotate dehydrogenase, score 563.50, E-value
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/transl_table=11
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/gene="STY1080"
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Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D.,
Nain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G.,
Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T.,
Connetton, P., Croninh, A., Davis, B.K., Davis, R.M., Dowd, L., White, N.,
Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P.,
Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J.,
Stevens, K., Whitehead, S. and Barrell, B.G.
Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18
Nature 413 (6858), 848-852 (2001)
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family M1, score 245.10, E-value 1.9e-84"
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AQDGSGYQFLVEMLTDLNSRNPQVASRLIEPLIRLKRYDDKRQEKMRAALEQLKGLEN
LSGDLYEKITKALA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, UK
E-mail: parkhill@sanger.ac.uk
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Location/Qualifiers
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181. .2793
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       Salmonella.
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GGGATTAGCCAGAAGGTTTTTCCGCCTGGTAGACAGCAACGGTTCCTGTTTTATAGG ArgAlaGlyAenPhekrgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr ArgAlaGlyAenPhekrgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr GGCAACGGCCAGTTCAAACTGGACGACGAACCTGGTCAATATGCAGGGATGCAG LeuWetGlySerArglleSerAsnAsnProAsnIleLysLysGluThrLeuGluProIle	AsnalavalvalAsnLeuGlyAspSerThrAspLysThrGineserGlublaAsnProTyr TCAATGCGACTCACCGGACCCTGTACCGTCTAACGGACCTGTACGGACCTGTACGGACCTGTACGGACCTGTACGGACCTGTACGGACCTTAACGGACCTGTACGGACTCAACGGACCTGTACGACGGACTGAACGGACTGAACGGACTGAACGGACTGATGGAGTGATGCGAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSerHisAspAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSerHisAspIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	117668 ATGAACGTCTATTT	117815 AACATCACCACCGGACGACAGCG	361 SerSerdlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGlnAsp 380 :::
	3 4 5 6 5 6 5 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	8 8 8 8 8 8	6 6 6 6 6 6 6 6 6
/gene="STY1082" 5924. :8032 /gene="STY1082" /note="STY1082" /n	/translation="MNSLPASTARGLEELLKTELERGANGCOWYOGGTRED YQSLMWGRLAGRI ILDWGGEKVYSDLDLYFGVQAINWTEIFWFGATFAWHFSGLNDTI YQSLMWGRLAGRI ILDWGCEKVYSDLDLYFGVQAINWTEIFWFGATFAWHFSGLNDTI RNSQYGAMKVXDAIVDAFTRKNLPERWUDRESPDLRINWHLXGFTASIALDLSGGGLH IRGYRDRTGLAPIKEILAAAIVMRSGWQFGTPLLDPWGGSGTLLIEAAWATDRAPGL HRGHWFSGWAGDIBAAIWQUSVAABQTRAKGLABEYSSHYYGSDSDARVIARASNUAR RAGIGELITFEYWDVAQLSNFLPRGEYGTVISNPFYGERLDSDPALIAHSLLGRTWK NQFGGNLSIFSASPDLLGSLQLRADKQFKAKNGPLDCVQKNYHIAETTADSKPATVA BDYARRIAKNIKTAEKWAROGGSIEGYRLYDADLPFSTWAYONFYGYDAPPKTVV DAQKARQKLFDIIAATLSVLGIPPKTKYLKTRERQKGKNQYQKNSEKGFFLEYSEYNA RLWVNLTDYLDTGLFLDHRIARRMLGEMSKGNDFLNEINSTRANGGGARNTTT VDMSRTYLEMARRANLALLARGGTIRFSNNKGCTHIFSTTGSASVHAGLGGARNTTT VDMSRTYLEMARRANLALLARGGTIRFSNNKRGFRNDLGGLAELGITAQEITQKT LSPDFRANNRQHHNCWLIRAA" misc_feature 5927. 7060	/gene="STY1082" /note="Ffam match to entry PF01170 UPF0020, Uncharacterized protein family UPF0020, E-value 3.7e-231" E-value 3.7e-231" misc_feature 65066541 /gene="FTY1082" /note="PS01261 Uncharacterized protein family UPF0020 signature 80459952 /gene="STY1083" CDS /gene="STY1083"	/note="Fasta hit to YBIT_ECOLI (530 aa), 32* identity in 526 aa overlap Fasta hit to YJJK_ECOLI (554 aa), 34* identity in 524 aa overlap Pred. No.: Alignment Scores: 9.97e-21 Length: 254050 Matches: 144 Conservative: 76 Matches: 167 Conservative: 76 Conservative: 76 Conservative: 167 Conservative: 167 Conservative: 167 Conservative: 167 Conservative: 167 Conservative: 167 Conservative: 167 Conservative: 167 Conservative: 167 Conservative: 167 Conservative: 167 Conservative: 167 Conservative: 114 Conservative:	US-10-009-823A-1 (1-502) x AL627269 (1-254050) QY 10 ThrGlyWetLysThrHisSerThrGlyLeuGlyThrValSerAsnAsnIleAlaAsnAla 29 117104 AGCGGCTGAACGCTGCCGCACCAACCTTGATGTTGCGTAATAACATCGCCAACTCC 117163 QY 30 AsnThrIleGlyTyrLysGlnGlnGlnValValPheGlnAspLeuPheSerGlnAspLeu 49 Db 117164 GCCACCTATGGCTTTAAGTCCGGTACGGCATCATTGCCGATATGTCGCTAATAGTTGCCAATTGCCCAATTGCCCAATTGCCCAATTGCCCAATTGCCCATTGCCCATTGCCCATTGCCGATTGCCCATTGCCATTGCCCATTGCTCTTTTCCATTGCTCATTGCTCTTTTTCCATTGCTCTTTTTTCCATTGCTTTTTTACCGATTGCTCTTTTTACCTTTTTTTT

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Salmonella typhi CT18"
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                                                            118169 GCCTCTAACGTGGATTTGAGTAAGAGCTGGTGAATATGATCGTCGCGCAGCGTAACTAC 118228
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                                                                                                                                                                                                                                                                                                       /trānslation="MGDEKSLAHTRWNCKYHIVFAPKYRRQAFYGEKRRAVGSILRKL
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REFWCRGYYVDTVGKNTAKIQDYIKHQLEEDKMGEQLSIPYPGSPFTGRK"
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Deng, W., Liou, S.R., Plunkett III, G., Mayhew, G.F., Rose, D.J.,
Deng, W., Kodoyianni, V., Schwartz, D.C. and Blattner, F.R.
Comparative Genomics of Salmonella enterica Serovar Typhi Strains
Ty2 and CT18
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enterica subsp. enterica serovar Typhi Ty2
Salmonella enterica subsp. enterica serovar Typhi Ty2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.

    301983
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Typhi Ty2"

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                                                                                                                         481 GinMetAsnSerLysSerValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deng, W., Liou, S.-R., Plunkett, G. III, Mayhew, G.F., Rose, D.J., Burland, V., Kodoyianni, V., Schwartz, D.C. and Blattner, F.R. Direct Submission Submitted (25-SEP-2002) Laboratory of Genetics, University of Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="transposase for insertion sequence element
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Salmonella typhi CT18"
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complement(844. .1797)
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complement(164. .622)
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Score: Percent Best L	DB:	03 - 20 03 - 20	Q	δ	q	ර් ස්	8 8	7 d	È	qq	Š	q	δ,	С	ò	DP	È	qq	ò	Сp	ò	qq	ò	g G	È i	අු	දි සි	i è	දි සි	Š	; a	ò	
RALNALGATPMDLMSILQSWQSAGCLRAKLEI!" complement (55976295) /gene="£1gH".	/ JOCUS _ Edg="L140" complement (55976295) /gene="f1gH"	/iocus_rage=rin40" /note=rcorresponds to STY1219 from Accession AL513382: Salmonella typhi CT18"	/codon start=1 /rrans_table=11 //rrans_table=11	/product="ladgelat L-zing process precusor= /protein id="AA059564.1" /db.xref="G1:29137803"	/translation="mokyalhaypvmalmvatltgcamipakplvqgattaqpipgpv pvangsipqsaqpinygyqplfedrrprnigdtltivlqenvsasksssanasrdgkt	SFGFDTVPRYLQGLFGNSRADMEASGGNSFNGKGGANASNTFSGTLTVTVDQVLANGN LHVOGEKQIALINQCTBFIRFSGVNNPRTISGSNSVPSTQVADARIEYVGNGYINEAQN	MGMIQRFFINLSPM" complement (6350. ,7132)	/gatte="11ge" /locus_tag= complement (6350, 7132)		<pre>/note="distal rod protein; corresponds to STY1218 Irom Accession AL513382: Salmonella typhi CT18"</pre>	/codon_start=1 /transl_table=11	<pre>/product="flagellar basal-body rod protein FlgG" /protein_id="AAO69365.1"</pre>	/db_xref="G1:29137804" / reanslation="MISSIWIAKTGIDAQOTNMDVIANNLANVSTNGFKRQRAVFEDL	LYQTIRQEGAQSSEQTTLESGLQ1015VRPATERLHSQGNLSQTNNSKUVATKGQGF PQVMLPDGTSAYTRGGSFQVDQNGQLVTAGGFQVQDATTIPANALSITIGRGVVSVT	OOCGAAPVONGOLLITTEMNITGLESIGENITIETOSSGARRESIFGLNGAGLLITGEN VETSNVNVABELIVMIQVRAYEINSKAVSTTDOMLGKLTQL" Commilging 1986 79001	Complement (/140 /201/	/ JOCUS	/gente="fight" /locus _rtg=#11742" /note=_frortservings to grv1217 from Accession A1513382::	Salmonella typhi CT18" /codon start=1	/transl_table=11 /transl_table=11 /wrodinf_="mitative flace]lar hasal-hody rod protein FloF"	/protein_family	/translation="MDHAIYTAMGAASQTLNQQAVTASNLANASTBGFRAQLNALRAV vtranslation="MDHAIYTAMGAADASQTLNQQAVTASNLANASTBGFRAQLNALRAV	GNI QVGPTCQLTI QCHPVI CEGGPT TVPEGSETITI AADGTI SALNCOPPWIYAPVCR LKLVKAECKEVORSDDGLFRLI TABAQAERGAVLAADPSI RIMSGVI EGSNVKPVBAMT	DMIANARRFEMQMKVITSVDENEGRANQLISMS" complement (79229133)	/gene="flgE" /locus_tag="t1743"	complement (79229133)	/locus_tag="t1743" /note="corresponds to STY1216 from Accession AL513382:	/code state 1	/rransl table=11 /product=Hilagellar hook protein FlgE" /protein id=Mano6947 1"	MCATA	SVFYSRN	s: 1.22e-20 Length: 301983	
gene	CDS						gene	SES							i i	a B B	CDS							dene)	CDS						Alignment Scores: Pred. No.:	

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complement (9302. .9667)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 AsnThrIleGlyTyrLysGlnGlnGlnValValPheGlnAspLeuPheSerGlnAspLeu 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73748 CTGACGGGGTACCCGGCAACCGGTACGCCGCCGACTATTCAGCAAGGGGGCGAATCCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 GlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThrAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerValArgThr1lePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::
73568 GGTATCACTCAGGACTTTACCGATGGCACGACCACCAACACCGGGCGTGGTCTGGACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         derarcadeceagaacodrivirioscererodragaeacageaacogerecodrareracade
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 ArgalaglyasnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PhealaLeuLeuGluSerTrpLysGlyAsnGlyThrProProIleSerThrSerAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306358
143
74
171
110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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complement (9302. .9667)
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498.00
43.57%
28.71%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                   complement(6596.)
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8577. 8553
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spp (25734 | T200_SALTY Transposase for insertion sequence
element 1S200"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (8832. .9290)
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product="tRNA-Arg"
function="RNA; tRNA"
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7651. .8013
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                                                                                                                                                                                                                                                                                                 complement (6578.
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                                                                                                              codon start=1
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Fosfal, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R. Genome sequence of enterohaemorrhagic Escherichia coli O157:H7 Nature 409 (6819), 529-533 (2001)	11206551 (bases 1 to 9224) Perna,N.T., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D., Rese,D.J., Maybew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A., Posfai,G., Hackett,J., Klink,S., Boutin,A., Shao,Y., Miller,L., Grotbeck,B.J., Davis,N.W., Lim,A., Dimalanta,E., Poteamousis,K.,	Appeaded, J., Amaillatanear, J.S., Elli, J., Elli, S., Schwalz, J., J., Welch, R.A. and Blattner, F.R Direct Submission Direct Submission Submitted (22-OCT-2000) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA	Location/Qualifiers 19224 /organism="Escherichia coli O157:H7 EDL933" /mol_type="genomic DNA" /strain="EDL933" /serctype="0157:H7"	/note="enterohemorrhagic" 134 718 /gane="rimu" /note="synonym: Z1703"	134718 /gene="rimJ" /gene="rimJ" /function="enzyme; Macromolecule synthesis, modification: /function="enzyme; Macromolecule synthesis, modification: /function== maturation and modification" /note="Residues 1 to 194 of 194 are 100.00 pct identical to residues 1 to 194 of 194 from Escherichia coli K-12 Strain Moli65: Blo66"	<pre>/codon start=1 /transtable=11 /product="acetylation of N-terminal alanine of 30S ribosomal subunit protein S5" /protein_id="AAG55812.1"</pre>	<pre>/ db xref="G1:12514664" / translation="MFGYRSUYVKVELTTDRLVVRLVHDRDAWRLADYYAENRHFLKP / translation="MFGYRSUVVKVELTTDRLVVRLVHDRDAWRLADYYAENRHFLKP WEPVRDESHCYPSGWQARLGMINBEHKQGSAFYFGLFDPDEKRIIGVANFSNVVRGSF HACYLGYSIGQKWQCKGLMFEALTAAIRYMQRTQHIHRIMANYMPHNKRSGDLLARLG FEKEGYAKDYLLIDGQWRDHVLTALTTPDWTPGR"</pre>	7291376 /gene="yceH" /note="gyNonym: Z1704" 7291376 /gene="yceH" /function="orf; Unknown function" /note="Residues I to 215 of 215 are 99.06 pct identical to	residues 1 to 215 of 215 from Escherichia coli K-12 Strain MG1655: B1067" /codon start=1 /trail_table=11 /product=1orf hypothetical protein"	/ protein id="AAGSB13." / db.xcf="G1:12514663" / db.xcf="G1:12514663" / translation="MKYQLTALEANIGCLIEKQVTTPEQYPLSVNGVTACNQKTNR / translation="MKYQLTALEANIGCLIEKQVTTPEQYPLSVNGVVTACNQKTNR ZPVNNLSESEVOEQU-DNIVRHYILRTVSGFGNRVTKYEQRFCNSEFGDLKLSAAEVAL ITTLILRGAQTPGELRSRAARMYEFSDMAEVELTLEQLANREDGPFVVRLAREPGKRE SRYMHLFSGFVUDOPAVTDMSNAVDGDLQARVEALEIEVAELKQRLDSLLAHLGD" 1378. 2301	<pre>/gene="mviM" /note="gynonym: Z1705" 11782301 /gene="mviM" /function="putative factor; Not classified" /note="Residues 1 to 307 of 307 are 99.02 pct identical to</pre>
AUTHORS TITLE JOURNAL MEDLINE	PUBMED REFERENCE AUTHORS	TITLE JOURNAL	FEATURES SOURCE	gene	CDS			gene CDS		eu e b	CDS
- Albert			 		-				· · · · · · · · · · · · · · · · · · ·	 .	
209 SerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrval 228 :::		289 GlySerAlaThrLysAspLeuAsnAlaTrpGlnProAlaProLeu 303	304 ValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGlnProLeuThr 323 74168	44 AlaileGlyThrAspileGlyLysLeuProSerMetMetProileGlnThrSerSerGly 	364 AsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGlnAspGlyTyrPro 383	74252 CCGGGGGATCTGGTGAGTTATCAAATCAATGATGAGGGTAGGGTTGTGGCACTATTCC 74311 404 ASNSerGlnValValAspPheTYzAsnIleProLeuAlaargPheThrSerGluAspGly 423 74312 ASCGAACAAACAACTGGTGGGGGAGTTGTACTGGCGAACTTTGCCAACAACGAAGGT 74371	LeuargargGluGlyAsnAsnHisTyrSeralaThrLeuaspSerGlyGlyProGluPhe	444 GlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGuThrSerAsn 463	484 SerLysSerValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeuLys 501 ::::::::::	RESULT 28 ABOD5317 LOCUS DOCUS DEFINITION Escherichia coli 0157:H7 EDL933 genome, contig 1 of 3, section 141 ACCESSION AE005177 AE005174 ACCESSION AE005317.1 GI:12514603	KEYWORDS SOURCE Escherichia coli O157:H7 EDL933 ORGANISM Escherichia coli O157:H7 EDL933 Bacteria; Proteobacteria; Gammaprotecbacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
			•							AEO0531 LOCUS DEFINIT ACCESSI	KEYWORDS SOURCE ORGANI REFERENCI

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/note="Residues 1 to 219 of 219 are 95.89 pct identical to residues 1 to 219 of 219 from Escherichia coli K-12 Strain MG1655: B1072"
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Japane="figgs"

/note="synonym: 21711"

/syne="figgs"

/gene="figgs"

/function="structural component; Cell exterior

constituents: Surface structures"

/note="sesidues 1 to 138 of 138 are 99.27 pct identical to

residues 1 to 138 of 138 from Escherichia coli K-12 Strain

MG1655: B1073"
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Drertofadnsloygmslsalsgqikgmmvilosgn"
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basal-body rod"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 AsnīhrileGiyTyrLysGlnGlnGlnValValPheGlnAspLeuPheSerGlnAspLeu 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
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                                                                                                                                                                                                                                                                                                               /codon_start=1
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Mismatches:
Indels:
                                                                                                                               /gene="flgA"
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Surface structures"
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Matches:
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complement (4776. .5435)
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/note="synonym: Z1712"
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      Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVLGVALGTILLPSISKSPASGNHDBYNRLMUMGIRLCFLLLLDPSAVALGILSCPLTV
SLPOYGKFTAFDALMTQRALIAYSVGLIGLIVVKVLAPGFYSRQDIKTPVKIAIVTLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAG55817.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVLVMSGVLLGMLHIMPEWSLGTMPWRLLRLMAVVLAGIAAYFAALAVLGFKVKEFAR
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/note="Residues 1 to 511 of 511 are 100.00 pct identical
to residues 1 to 511 of 511 from Escherichia coli K-12
Strain MG165: B1069"
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/function="factor; Cell exterior constituents: Surface
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/product="anti-FliA (anti-sigma) factor; also known
RflB protein"
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the prophage VT1-Sakai carrying the rohemorrhagic Escherichia coli Sakai outbreak nargglyPheglimetAsnSerLysSerVal 487 DNA linear BCT 20-MAR-2004 complete genome, section 6/20. the prophage VT2-Sakai carrying the chemorrhagic Escherichia coli 0157:H7 1,K., Kuhara,S., Hattori,M., proteobacteria; Enterobacteriales; Y., Watanabe,M., Kimura,S.,
i,K., Hattori,M., Abe,H., Iida,T.,
iga,T., Honda,T., Sasakawa,C. and ole set of rRNA operons between an ocidi 0157:H7 Sakai strain and an 31655 324 (2000) ra Hattori, Kitasato Institute for sity; Kitasato 1-15-1, Sagamihara, Y., Yutsudo, C.H., Kimura, S., M., Tatsuno, I., Abe, H., Iida, T., ii, T., Yasunaga, T., Honda, T., ,M., Kurokawa,K., Ishii,K., ,,E., Nakayama,K., Murata,T., skami,H., Honda,T., Sasakawa,C., ara,S., Shiba,T., Hattori,M. and erohemorrhagic Escherichia coli with a laboratory strain K-12 aLeuGluLeuLys 501
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GGTTAACTTACGC 8348 239 (1999) Ë

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FEATURES

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Alignment Scores:
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// evidence=not_experimental

// transl_table=11

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1588. . 5123
Ohnishi, Keisuke Nakayama (Miyazaki Medical College), Kozo Makino, Ken Kurokawa, Katsushi Yokoyama, Masashi Tanaka, Takeshi Honda, Terno Yasunaga, Hideo Shinagawa (Osaka University), Takahiro Murata (Shinshu University), Chang-Qyun Han, Biichi Ohtsubo, Toru Tobe, Chihiro Sasakawa (University of Tokyo), Hideo Takami (Japan Marine Science and Technology Center), Naotake Ogasawara (Nara Institute of Science and Technology), Satoru Kuhara (Kuyshu University), and supported by the Research for the Puture Program of the Japan Society for the Promotion of Science.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="glucans biosynthesis protein"
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/ KFVNPGRDFWORSFYLLADKVGKLGVADLTSMFLFGFNOESFANNFYFLIFSRDED
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PVWPQWRPELAIALFASTWVLLFLFKLLSILLIWCKGTKEYGGFWRVTLSLLLEVLFS
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FWTALMGFLQLLIGRDKYSISASTYGDEPLNPEHRTALIMPICNEDVNRVFAGLRATW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to membrane glycosyltransferase MDOH ECOLI gi|1787287 percent identity 100 in 847 aa but differs at N-ter (Conserved in E.coli K-12)"
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FEATURES

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AL Submitted (12-JAN-1999) Astra Research Center Boston, 128 Sidney Street, Cambridge, Ma O1319, USA Address all correspondence to: hpearch.us.astra.com or Richard Address all correspondence to: hpearch.us.astra.com or Richard A. Alm, Astra Research Center Boston, 128 Sidney Street, Cambridge, Ma. O2139. Lo-See L. Ling, Donald T. Moir. Douglas R. Smith, Braydon C. Guild, Gilles Carmel, Anthony Caruso, Debra M Mills, Respondence E. Taylor are with he University of Alberta Department of Microbiology and Immunology, Edonotron, Alberta, Canada, TGG 2H7 and the Canadian Bacterial Diseases Network. All other authors are with Astra Research Center Boston, 128 Sidney Street, Canadian Bacter Center Boston, 128 Sidney Street, Canadian Bacter Center Boston, 128 Sidney Street, Canadian Bacter Center Boston, 128 Sidney Street, Canadian Ender Conflage, MA. 02139. Putative identifications sequence alignments and name and sequence search capabiblity are available at ARCB's World Hide Web Site. (URL:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19355 ATTGAGAGTAACAATATTGCGAACGTGAATACCACTGGGTTTAAGTATTCTAGGCTTCT 19296
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                                                                                                                                                         /trānslation="MKKILVIGDLIADYYLMGKSERLSPEAPVPVLEVKKESKNLGGA
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AONQJUKYÜKE DEPLADLE FERTIOFILERIQEIDGVILSDYNGSVLDFEITÜQTI
TLANKHKLILCDPKGKDYSKYSHASLITPNRAELEQALHLKLDSHANLSKALQILQE
                                                                                                                                                                                                                                                  TYHIAMPLVTLSEQGIAFLEKGELVNCPTIAKEVYDVTGAGDTVIASLTLSLLESKŠL
KAGGERAMAAAVVGKNGSALASLESTALINGTHPKI LEBEKLLETLERNQKTVF
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LSCVDYVVVFGEDTPIKLIQALKPDILVKGADYLNKEVIGSELAKETRLIEFEEGYST
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                        gene HP0858"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="similar to H. pylori 26695 gene HP0859"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 PheGlnAspLeuPheSerGlnAspLeuAlaileGlySer----
                     note="similar to H. pylori 26695
codon start=1
transI table=11
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Matches:
Conservative:
Mismatches:
Indels:
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complement(9138. .10127)
                                                                                                                                                                                                                                                                                                                                                                 complement (9138. .10127)
                                                                                                                                                                                                                                                                                                                                             SAIIEKIKRTHND"
                                                                                                                                                                                                                                                                                                                                                                                      gene="gmhD"
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485.00
38.04%
25.03%
18.75%
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Best Local Similarity:
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8230 GATCCTAGTTTAGCGGACAATTATCAAGATTCAGCCGCTTCTATAGGGGTTACAATCAAC 18171
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         18879
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GCGAGTAACCGCATTTCTATGAGGCGAATTTAAACGCTGGAAGGCATGCGGATCAAACA
                                                                                                                                                                                              --- GTATTCGCTTTAGATTCTTCAGCCAAAACCCCTTCAGATGGC
                                                                                                                                                                                                                                                                                                                                     -----SerHisAspileThrValTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18290 CAGTTTAGGACCACTGAAGACTTGCGCGCCTTAATCCAGCATGACGTAATATCGTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18110 AATATCTTTGTGAGTGGGTATTCTTCAGACAGCGTAACGAACAATGTTTTGTTTAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrserThr-----AlaLeuAsnAlaValValAsnLeuGlyAspSerThrAspLysThr
                                                                                                                                                  182 GlnSerGluAlaAsnProTyrPheAlaLeuGluSerTrpLys-----GlyAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                ------ProSer------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerThrGlySerLysThrPheGluTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGly------Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspSerAlaGlyLeuLeuMetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---MetThralaPhe-----ThrProThrGlySerAlaThrLysAspLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 AlaTrpGlnProAlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheVal---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GlyAlaGlyIleGlnProLeuThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- AlagiyAlaProAlaSerAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AlaileGlyThr---
                                                                                                                                                                                                                                          ThrProProlleSerThrSerAsnTyrSerTyrAlaGlnProMetArg-------
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* 7211 7411: gap of unknown length * 7412 27989: contig of 20578 bp in length * 28190 58195: contig of 31786 bp in length * 28190 58175: contig of 31786 bp in length * 58176 59175: gap of unknown length * 58176 59175: contig of 31075 bp in length * Location/Qualifiers Location/Qualifiers Location/Qualifiers 190250 / organism="Leishmania major" //mol_type="genomic DNA" //strain="Friedlin" //db_xref="taxon:5664" //clone="Tokacosome="Unknown" //clone="Tokacosome="Unknown" //lone="Tokacosome="Unknown" //note="Tokacosome="Unknown" nment Scores: 2.05e-20 Length: 90250 Pred. No.: 485.00 Matches: 153 Porcent Similarity: 39.82% Conservative: 74 Best Local Similarity: 26.84% Mismatches: 177 Query Match: 18.75% Indels: 166 DB: 2 Gaps: 19	US-10-009-823A-1 (1-502) x AC095028 (1-90250) OY		Qy 88 AspLeuAlaIIeGlyGlyPhePheGlnValThrLeuGluAspLysVal 105	80668 GGCCTGCAGCTGACCGGCTGCGGGGGGGGGGGGGGGGGG	135 135	\$ \tau_{\text{.}}	
Db 17870 GTGCCTGAGGCAATTAGTAGGGGGTCAGCGCTAATGTTTGAAGGG 17811 Qy 348AspileGlyLysLeuProSerMetMetPro 357 Db 17810 GGCCGTTTGCATTTTAATAACGACGGATCGCTTGCGCCATGAACCCGCCTTTTGCAA 17751 Qy 358	QY 400 GlyLysTyrSerAsnSerGlnValValAspPheTyrAsnIleProLeuAlaArgPheThr 419 Db 17570 GGGGCGTTCAGTAATGGCAACATTTAGCGCTCCAAGTGGCTTTAGCGAATTTGGCT 17511 QY 420 SerGluAspGlyLeuArgArgGluGlyAsnAsnAsnHisTyrSerAlaThrLeuAspSerGly 439 Db 17510 AACGATGCGGGCTTTAGGGAAGGCAATGTCTTTTCTCAAACCGGAAACTCTGGG 17451	QY 440 GlyProGluPheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeu 459. Db 17450 CAAGCCTTAATCGGTGCGGTAATACGGGGCGTAGGGGTTCAATTCAGGATCCAAACTA 17391 QY 460 GluThrSerAsnValAspWetSerArgGluWetValAsnMetlleIleIleGlnArgGly 479 Db 17390 GAGCTTAGTAGATTGAGCCGAGTTTAACAATTTCATTGGTTCAAAGGGGG 17331 QY 480 PheGlnMetAsnSerLysSerArgGATTTTATAATATTATATATTATTATTATTATTATATATTATTATA	Qy 500 LeuLysArg 502	7 5	REFERENCE 1 (Dasses 1 to 90250) AUTHORS Myler, P.J., Siek, E., Cawthra, J., Nelson, S., Vogt, C., Robertson, L., McDonagh, P., Ivens, A., Nguyen, D., Munden, H., Stuart, K., Mack, J., Marty, A., Rinta, J. and Seyler, A. TITLE Direct Submission JOURNAL Submitted (15-SEP-2011) Seattle Biomedical Research Institution, 4	COWMENT ON DECES, 2001 this sequence version replaced gi:15624885. * NOTE: This is a "working draft" sequence. It currently * consists of 4 contigs. Gaps between the contigs * are represented as runs of N. The order of the pieces * is believed to be correct as given, however the sizes * of the gaps between them are based on estimates that have * provided by the submittor. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.	* 1 7210: contig of 7210 bp in length

RBS

CDS

RBS

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetMetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \(\int_0\)note="similar to ABC transporter, ATP-binding protein" \(\)(codon start=1 \)\(\)(trans1_table=11
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Matches:
Conservative:
Mismatches:
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484.50
42.21%
27.02%
18.74%
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Best Local Similarity:
Query Match:
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Pred. No.:
Score:
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                                                                                                                                                                                                                                                                                          | 20m. | 2308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIMALLAIIFFFLRGGKSTSGKAATK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyrAlaGlnProMet 214
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Matches:
Conservative:
Mismatches:
Indels:
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qa	25604	 ATGGGCTTAAACTGGCTTAACA 25630
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KEYWORDS SOURCE ORGANISM	SΜ	r. 4b F2365 r. 4b F2365
REFERENCE		illales, Listeriaceae, Li
AUTHCF		<pre>Mongodin, E. F., Kavel, J., DeBoy, K. T., Angluoli, S., Gill, S. R., Paulsen, I.T., Nelson, W. C., Nierman, W. C., Beanan, M. J.</pre>
	程 H R I	.C., Dodson,R.J., Du an Aken,S., Khouri,F Kathariou,S., Wonder
TITLE	유출합	cn, e.a., Bayles, D.O., Luchansky e genome comparisons of serotype -borne pathogen Listeria monocyl
JOURNAL		the core genome components of this species Nucleic Acids Res. 32 (8), 2386-2395 (2004)

REFERENCE AUTHORS

TITLE JOURNAL

FEATURES

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L. Submitted (27-PEB-2004) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA

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product="PTS system, glucitol/sorbitol-specific,
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175 GlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGluSer 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetMetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20
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                                                                                                                                                                                           Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria
                                                                                                                                                                                                                         Kunst,F. and Glaser,P.
Listeria inocua, genome and applications
Dateria wo 022891-A 4029 11-APR-2002;
INSTITUT PATEUR (FR); CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)
                                                        linear
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137
77
188
105
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Matches:
Conservative:
Mismatches:
Indels:
                                                        DNA
                                                           عوم الاجعبد كم Seguence 4029 from Patent WO0228891.
AX417038
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                                                                                                           AX417038.1 GI:21449648
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484.50
42.21%
27.02%
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6 8 5 8 5 8 5 8 5	8 6 8 6 8 6 8	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	RES AXA AXC DEF ACC VER KEY KEY COU
VERSION KEYWORDS SOURCE ORGANISM Listeria innocua DRCHETERENCE Insteria innocua REFERENCE Insteria innocua REFERENCE AUTHORS TITLE AUTHORS Listeria inocua REFERENCE Insteria inocua REFERENCE TITLE JOURNAL OURNAL AUTHORS LISTERING FR); CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR) LOCATION/Qualifiers In 349980 / Organism="Listeria innocua" / Mol type="unassigned DNA" / Mol type="un	### Scores: 1.16-19	139598 GIGACATCAAATAATTATGCGAACAGGGAACAGGGGTATAAAAAACAAAGGCGTCGTT 41 PheGlnAspLeupheSerGlnAspLeualaileGlySerThrGlySer 52 GIGGLyProAsnGlnAlaGlyNetGlyAlaGlnValGlySerValArgThrIlePheThr 19718 ACAAACCCAATGAGTTCGGTTCGAAAATTGGGGCAATTTTAACCATTATGGG 77 GInGlyAlaPheGluProGlyAsnSerValThrAspLeuAlagIhrIlePheThr 19718 ACAAACCCAATGAGTTCGGGTTCGAAAATTGGGGCAATTTTAACCATTATACA 77 GInGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLySGlyPhe 19718 GCAGGTTCTCCGACATCAACTGGCAAAAATTGGGGCAATTATACA 19818 TTCATTGCTGGCGATAACGCTGGGGGAAAATTCGTTTACAGGCTTTGCA 115 PheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMetGlySerArglle 115 SerAsnAsnProAsnIleLyStysGluThrLeuGluProIleGlnLeuAspPheAsnAsp 115 SerAsnAsnProAsnIleLyStysGluThrLeuGluProIleGlnLeuAspPheAsnAsp 116	Db 39958 GATAAAAATGGCAACGTTTTAAACGGAACTTGCAACCAATTCAAATCGCATTAAATAGC 40017 Qy 155 ProthrValhlaLysSerProAlaLysThrSerThrAlaLeuAsnalaValValAsnLeu 174

215 130373 234 130433 254 130481 274 130523	333 1306 1306 1306 373		Oy 454 LeuServalAsnGlnLeuGluThrSerAsnValAspMetGerArgGluMerValAsnMet 473 ::: ::
AUTHORS Kunst.F. and Glaser.P. IITLE Listeria inocua, genome and applications JOURNAL Patent: WO 0228891-A 4031 11-APR-2002; INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR) FEATURES 1. 349980 / organism="Listeria innocua" //mol_type="unassigned DNA" //mol_type="unassigned D	ignment Scores: 1.1e-19	Db 129803 ATGAATCAAACTATGTATACAGCTATTTCTGGGATGCGTTCCAACAAGCATTATCA 129802 21 ThrvalSerAsnasnilealaAsnahaAsnThrileGlyTyTLySGlnGlnClnValVal 40 22 ThrvalSerAsnasnilealaAsnThrileGlyTyTLySGlnGlnClnValVal 40 23 ThrvalSerAsnaATATTGCCAATGCGACACACACAGCGTGTTAAAACACACGTGTT 129922 41 PheGlnAAATATTTGCAATGCGAACACACAGCGTATTAAAACACAGCGTGTTGCAGGCGTTTTATGCTGGT 129922 Qy 129923 TTCAATGATTTACTTTACCAAACACAAACAGGCGGACTTTATGCTGGA 129982 Qy 57 GlnGlyProAsnGlnAlaGlyMetGlyAlaGlnValGlySerValatgThrilePheThr 76 Db 129983 ACAAACCCAATGAGCTTCGGTTCGGATCGAAAATTGAGGCGAATTTTAACCGATTATACA 130042 Qy 77 GlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLySGlyPhe 96	130043 GLAUSTICLCGRAINSCRIPTION OF THE STATEMENT OF THE S

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REFERENCE AUTHORS JOURNAL

TITLE

AUTHORS

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aa protein from Escherichia
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Shigella flexneri 2a str. 301
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I (bases 1 to 13374)
Si Jin,Q., Yuan,Z.H., Xu,J.G., Wang,Y., Shen,Y., Lu,W.C., Wang,J.H.,
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Qiang,B.Q., Wen,Y.M., Hou,Y.D. and Yu,J.
Qiang,B.Q., Wen,Y.M., Hou,Y.D. and Yu,J.
Genome sequence of Shigella flexneri 2a: insights into
pathogenicity through comparison with genomes of Escherichia coli
K12 and O157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jun, Q., Shen, Y., Wang, J.H., Liu, H., Yang, J., Yang, F., Zhang, X.B., Zhang, J.Y., Yang, G.W., Wu, H.T., Dong, J., Sun, L.L., Xue, Y., Zhang, J.Y., Yang, G.W., Xu, J.P., Chen, S.X., Yao, Z.J., Wang, Y., Lu, W.C., Qiang, B.Q., Wen, Y.M. and Hou, Y.D.
Direct Submission
Submitted (08-MAY-2001) Microbial Genome Center of Chinese Ministry of Public Health, 100 YingXin Jie, XuanMu Qu, Beijing 100052, P.R. China
   AE015135 13-0CT-2002 13374 bp DNA linear BCT 18-OCT-2002 Shigella flexneri 2a str. 301 section 98 of 412 of the complete
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           LOCUS
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FEATURES

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GlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThrAlaLeu 168
                                                                                                                                                                                               AlaileGlyGlyLysGlyPhePheGln---ValThrLeuGluAspLysValHisTyrThr 108
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                                                                                                                                    109 ArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleThrValTyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeu
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GTCTACACCCAGGATAGCAGTGATCCAAACAGCATTGCGAAGACA-
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                                                                                             SFTWDGSLTDGSTAPNGSYNVAISASNGGTQLVAQPLQFALVQGVIRGNSGNTLDLGGT
YGTTTLDFRAQIIKAFTFQDSVWAFSQAVSGLJVAAATNLDVIGNNIAANSATYGFKSGT
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blosynthesis, cell-proximal portion of basal-body rod gi:
1787317 (252 aa). BLAST with identity of 96% in 251 aa.
This CDS contains an in-frame stop codon. The sequence has been checked and is believed to be correct."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /procein_id="AAN42103.1"
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/note="Residues 1 to 260 of 260 are 99 pct identical to residues 1 to 260 of a 260 aa protein from Escherichia coli 0157:H7 EDL933 ref: NP_287212.1"
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  xref="GI:24051371'
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gene="flgF"
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DB:
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Search completed: November 1, 2004, 06:05:13 Job time : 6762 secs

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		42	130	5.0	733 4	US-09-336-115C-4
Scoring table:	SOSOME	43	129.5	5.0	1475 4	US-09-538-092-1160
	Gapop 10.0 Gapext 0.5	44	128	9.	2090 4	US-09-538-092-1081
		45	127.5	4.9	2142 4	US-09-540-236-3459

Sequence 330, App Sequence 45, Appl Sequence 17, Appl Sequence 20, Appl Sequence 302, App Sequence 4, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 6, Appl Sequence 1160, Appl Sequence 1160, Appl Sequence 1160, Appl

ALIGNMENTS

478139

Total number of hits satisfying chosen parameters

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

478139 segs, 66318000 residues

Searched:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Length

% Query Match

Result No.

Issued Patents AA:*

1: /cgn2 6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*

Description

Sequence 19526, A Sequence 8182, App Sequence 1971, App Sequence 10, App Sequence 8, Appli Sequence 5, Appli Sequence 10, App Sequence 10, Appli Sequence 6, Appli Sequence 2, Appli Sequence 67, Appli

US-09-252-991A-19526
US-09-543-681A-8182
US-08-483-857-8
US-09-543-681A-19715
US-08-483-857-10
US-08-483-857-10
US-08-483-857-10
US-08-483-857-7
US-08-483-857-7
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US-08-719-641-2

Sequence Sequence Sequence Sequence Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---- DGGQİGI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 TQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPWRVYDQQGNSHDITVYFDGAPS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----TGDSYHVL 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVPQDLFSQDLAIGST----G 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----VDAĖĠKTQ----
                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: MGG IR7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARS: PARENTE Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,857
                                                                                                                                                                                                                         PROTEIN GENES
us-08-483-857-8
; Sequence 8, Application US/08483857
; Patent No. 6020125
; GENERAL INFORMATION:
; APPLICANT: Chan, Voon Loong
APPLICANT: Louie, Helena
; TITLE OF INVENTION: BASAL BODY ROD PROTEIN C
ITLE OF INVENTION: CAMPYLOBACTER
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTY: Canada
ZIP: M5G 1R7
COMPUTER PERFORMANCE
ZIP: M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                    S-09-543-681A-8182
Sequence 8182, Application US/09543681A
Sequence 8182, Application US/09543681A
Sequence 8182, Application US/09543681A
Sequence 8182, Application US/09543681A
Sequence 8182, Application US/09509

APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: US/09-001
TITLE OF INVENTION: US/09-001
TITLE OF INVENTION: US/09-00-04-09
FILE REFERENCE: 2709-100-04-09
FRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                            -----QDGYPQGDLVDVTITSE 395
                                                                    -----TTQYSTAFAQSNPIQDGYTTGQLAGLEIDDT 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | : | | : | : | : | : | : | : | : | 120 MRITGYPVQNVDGKNVVQKGATPTFIII----PTDMAN-ASATDKMDMTVNLNSAEEAID 174
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                                                                                                                                                                          36 GVIFARYTNGÓSKVQGQVVLÁNFANIQGLTPIGKTSWVQSAESGEÞAVGAÞRSGTLGALQ 425
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                                                                                                                           GKLQGKYSNSQVVDFYNIPLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 FILMGSRISN----NPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLG---DSTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 KDNEWSVYAQDTTTGEPAQDL-----GKLVYKDNGVLDETAPKLKNFTTVAYKGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 PSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 412;
                                                                                                                                                                                                                                                      426 SGALEASNVDISNELVNLIVHQRNYQANAKTIQTEDAVTQTIINLR 471
                                                                                                                                                                                                                              156 VNOLETSNVDMSREMVNMIIIQRGFQMNSKSVTTADTMLQKALELK 501
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18.4%; Score 475.5; DB 4;
Best Local Similarity 26.7%; Pred. No. 3.9e-34;
Matches 136; Conservative 81; Mismatches 165;
                            345 IGTDIGKLPSMMPIQTSSGNSTARNGSSSTRRYS---
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                                                                              328 ISFDMRK----
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61 OAGM--GAOVGS-VRTIFT-----QGAFEPGNSVTDLAIGGKGFFQVTLEDKVH-YTRAG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 VNLGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFD 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 GAPSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 TKDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352 LPSNMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFY 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---NALSITIGRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 21.2%; Pred. No. 1.5e-17;
Matches 108; Conservative 42; Mismatches 101; Indels 258; Gaps
                                                               GENERAL INFORMATION:
APPLICANT: Chan, Voon Loong
APPLICANT: Chan, Voon Loong
APPLICANT: Louis, Helena
TITLE OF INVENTION: BASAL BODY ROD PROTEIN GENES OF
TITLE OF INVENTION: CAMPYLOBACTER
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 GVVSVT-------QQGQAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,857 FILING DATE: 07-UN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               ZIP: MSG IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-483-857-10
; Sequence 10, Application US/08483857
; Patent No. 6020125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REPRENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 261 mnino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 -----PVQVGQLN
                                                                                                                                                                                                                                                                    CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                   Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 -----
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US-08-483-857-10
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Sequence 19715, Application US/09252991A

Sequence 19715, Application US/09252991A

Sequence 19715, Application US/09252991A

PRICE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 19715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 LGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 PSSTGSKTFEYLVAMMPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 PLARFISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNM 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARFISEDGLRREGNNHYSATLDSG-GPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMI 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 DLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93; Indels 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
11.9%; Score 307; DB 4; Length 269;
Best Local Similarity 21.6%; Pred. No. 2.5e-19;
Matches 108; Conservative 46; Mismatches 93; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TqTpT-----
                                                                                                                          475 IIORGFOMNSKSVTTADTMLOKALELKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474 IIIQRGFQMNSKSVTTADTML 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-19715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149
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HONNERSH S HOLDEN HONNORTH	TELEPHONE: (416) 595-1155
OY 412 NIPLARFISEDGLRREGNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREWY 471 Db 175LTTFWANDTGLESIGENLYIETGSSGAPNESTPGLNGAGLLYQGYVETSNVNVAEELV 231 QY 472 NMIIIQRGFQWNSKSYTTADTWLQKALEL 500 Db 232 NMIQVQRAYEINSKAVYTTADTWLQKALEL 500 NS-09-543-681A-8110 SEQUENCE 8110, Application US/09543681A PAPLICANT: GAPL BRETON TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: US/09/543,681A CURRENT APPLICATION NUMBER: US/09/543,681A PRIOR PILING DATE: 1999-04-09 NUMBER OF SEQ ID NOS: 8344 SEQ ID NO 8110 LENGTH: 265 TENGTH: 265 TENGTH: 265 CRACALISM: Proceus mirabilis US-09-543-681A-8110	Query Match 11.11; Score 286; DB 4; Length 265; Bast Local Similarity 19.74; Pred. No. 1.96-17; Matches 100; Conservative 55; Mismatches 98; Indels 234; Gaps 9; GY IMMOSLIFICATORNIAMANTION/OVOUNDLESCOLAIGSTGS 56 In MOSSLIFICATORNIAMANTION/OVOUNDLESCOLAIGSTGS 56 G MIRLWIAMACGLOACHMONISMALANTION/OVOUNDLESCOLLYPRAGE 113 G NAPLQAGMAGAQUSARITETPQAREBONNYDLAIGNORGEPOTILENTH-YPRAGE 113 G NAPLQAGMAGAQUSARITETPQAREBONNYDLAIGNORGEPOTILENTH-YPRAGE 113 G NAPSGLUGTGYREVATERHASGANAQTMOTENDYAIKAGGFEHVOLPDGTANTRGSF 125 QY 114 RTDDGTLUBPGGFLUASSRISMNNHIKKETPEDLUDENDPTVAKSPRATFALMAVYN 173 Db 116 WHORGOLVISSGGTUPAILLETAKKNYNGRDGILSGYFTALMAVYN 173 Db 117 LGDSTDKTGSEANPYFALLESWKGNGTPPISTSNYSYAQPRKYYDQCGNSHDITYFTEDGS 169 QY 234 PSSTGSKTPEYLLVAMPSEDGSAASGTDSAGLLMSGTMTAFTPTGSATK 293 Db 117 LGDSTDKTGSEANFWHASSTLDSGAGLLMSGTMTARTENTSGAUGANTAFTPTGSATK 293 Db 117

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61 IVPTGVQVGGGVKAĞSVYRİTEQGTPTLTDSPLDLAİQGKGYMPILLPSGETAYTRAGNF 120
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                                                                                                                                               413 IPLARFISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVN 472
                                                                                                                                                                                353 PSWMPIQISSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYN 412
---ATAINVATD-GTV 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 -----QAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTL-EDKVHYTRAGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

8.9%; Score 229.5; DB 2; Length 262;
Best Local Similarity 20.6%; Pred. No. 2.2e-12;
Matches 106; Conservative 34; Mismatches 106; Indels 269; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: BASAL BODY ROD PROTEIN GENES OF TITLE OF INVENTION: CAMPYLOBACTER NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Sim & McBurney STREET: Suite 701, 330 University Avenue CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/436,748
FILING DATE: 05-AUG-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                       :| || :: || :: || :| || :| || 234 LITGQRAYEAGSKAITTSDDMLGIVNQLKR 263
                                                                                                                                                                                                                                                         473 MIIIQRGFQMNSKSVTTADTMLQKALELKR 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08436748 Patent No. 5827654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: STEWART, MICHAEL I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIORNEY/AGENT INFORMATION:
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COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                       159 SVMLP---
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                                                                                                                                                                                                        Sequence 5, Application US/08483857
Patent No. 6020125
GENERAL INFORMATION:
APPLICANT: Chan, Voon Loong
APPLICANT: Louie, Helena
TITLE OF INVENTION: BASAL BODY ROD PROTEIN GENES OF
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartable
OPERATING SYSTEM: PC-DOS/KS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/483,857
FILING DATE: 07-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                               5: Sim & McBurney
Suite 701, 330 University Avenue
                                                              : ||||| ||| |:| |:||: ||||
237 VAQRGFQSNSKIVSTTDEILQBLVNLKR 264
                                   475 IIQRGFQMNSKSVTTADTMLQKALELKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-504
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 FIKDNEGNIVNSDGYRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-08-483-857-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sim
STREET: Suite
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Or COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138
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61 IVPTGVOVGGGVKAGSVYRITEQGTPTLTDSPLDLAIQGKGYMPILLPSGETAYTRAGNF 120
-----QAGMGAQVGSVRIIFTQGAFEPGNSVTDLAIGGKGFFQVTL-EDKVHYTRAGNF 113
                                                                             R-----FTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTST 166
                                                                                                                                                            167 ALNAVVNLGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDI 226
                                                                                                                                                                                                                                                                              -----QNATAIT 150
                                                                                                                                                                                                                                                                                                                                                              347 TDIGKLPSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQ 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 407 VVDFYNIPLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDM 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 STNDQGQIVTEDGYLVQP-GITIP------
                                                                                                                                                                                                                                          227 TVYFDGAPSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFT
                                                                                                                                                                                                                                                                                                                       287 PTGSATKDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                             160 ----KL------GQIQ-----GGIQ------
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Patent No. 5827654

GENERAL INFORMATION:
APPLICANT: COUIE, HELENA

TITLE OF INVENTION: BASAL BODY ROD PROTEIN GENES OF
TITLE OF INVENTION: CAMPYLOBACTER

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBLINEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 VSEITALITAQRAYEMNSKVISTADQMLQATSQLKR 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 SREMVNMIIIQRGFQMNSKSVTTADTMLQKALELKR 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
COUNTRY: Canada
COUNTRY: Capada
COUNTRY: Capada
COUNTRY: FRADABLE FORM:
MEDIUM TYPE: Floppy disk
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05-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MIGHAEL I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET UNMER: 1038-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 05-AUG-199
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----PQNATDI 149
                                                       227 TVYFDGAPSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFT 286
                                                                                                                                                                                                                    347 IDIGKLPSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQ 406
                                                                                                                                                                                                                                                                                                 407 VVDFYNIPLARFISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDM 466
                                                                                                                                     287 PTGSATKDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIG 346
                                                                                                                                                                                                                                                                                                                                          -----LANFINEGGLEAIGDNLFLETAASGAATLVRRASRALACCCSTDTEASNVDA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 ----KL-----GDIQ------GDIQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.8%; Score 228.5; DB 3; Length 263; ilarity 20.5%; Pred, No. 2.7e-12; Conservative 32; Mismatches 109; Indels 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Chan, Voon Loong
APPLICANT: Louie, Helena,
TITLE OF INVENTION: BASAL BODY ROD PROTEIN GENES OF
TITLE OF INVENTION: CAMPYLOBACTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NOTABLE
APPLICATION NOTABLE
FILING DATE: 07-JUN-1995
TIGNETON: 435
                                                                                                                                                                                                                                                                                                                                                                                 467 SREMVNMIIIQRGFQMNSKSVTTADTMLQKALELK 501
                                                                                                                                                                                                                                                                                                                                                                                                           227 VSEITALITAQRAYEMNSKVISTADOMLQATSQLR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Sim & McBurney
Suite 701, 330 University Avenue
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Patent No. 6020125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-nne...
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                150 TI-----SK
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
Matches 106; Conserva
                                                                                                                                                                             154 -----
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CITY: Toronto
STATE: Ontario
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US-08-483-857-7
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us-10-009-823a-1.rai

TELEPHONE: (416) 595-1155 TELEFAX: (416) 595-1153 TELEFAX: (416) 595-1163 SEQUENCE CHARACTERISTICS: LENGTH: 260 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear US-08-436-748-10	Query Match Best Local Similarity 19.2%; F Matches 98; Conservative 49;	Qy 1 MMGSLFIGATGMKTHSTGLGT :: : : : Db 1 MISALWIAKSGLDAQQTNMEV	Oy 61 QAGMGAQVGS-VRIIFT	25 1111 811	171			Qy 351 KLPSPMPIQTSSGNSTARNGS	411	471 V 231 V	RESULT 13 US-09-252-991A-30227 ; Sequence 30227 ; Sequence 30227 ; Patent No. 6551795 ; GENERAL INFORMATION: ; APPLICANT: Marc J. Rubenfield 6	TITLE OF INVENTION: NUCLEIC AC: ; TITLE OF INVENTION: AERUGINOSA; ; FILE REFERENCE: 107196.136 ; CURRENT APPLICATION NUMBER: US/ ; CURRENT FILING DATE: 1999-02-11 ; PRIOR APPLICATION NUMBER: US 6; ; PRIOR FILING DATE: 1998-02-18 ; PRIOR FILING DATE: 1998-07-27; ; NUMBER OF SEQ ID NOS: 33142	; IENGHH: 2736 ; IYPE: PRT ; ORGANISM: Pseudomonas aerugino: US-09-252-991A-30227
	QAGMGAQVGSVRIIFTQGAFE-PGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNF : . . .	Qy 114 RFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSFAKTSTALNAVVN 173 Db 109PDGTIEMGNLQKIMK123	Qy 174 LGDSTDKTQSEANPYPALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGA 233 :	Qy 234 PSSTGSKTFEYLVANNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNWTAFTPTGSATK 293	OY 294 DINAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP 353 Db 147ATALNVATD-GTVS 159	354 SMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNI 	414 PLARETSEDGLRREGNNHYSATLDSGGPEFGLEGTSNYGKLSVNQLETSNYDMSREMYNM	IIIORGF : ITGORAY	RESULT 12 US-08-436-748-10	. 28		Can 1R1 ADAB: PE: IBI SYS: Pa Pa Pa Pa Pa Pa Pa Pa Pa Pa Pa Pa Pa P	

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let al.
CID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
A FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                      FSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIG 350
                                                                                                                                                                                                                                                                                                             GSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDF 410
                                                                                                                               MGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNA 170
                                                                                                                                                                           ALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYF 230
                                                                                                                                                                                             PSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGS 290
: | ||
                                                                                                                                                                                                                                       ----QPAITIPA--- 144
                                          Score 220; DB 2; Length 260;
Pred. No. 1.5e-11;
9; Mismatches 103; Indels 260; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   S/09/252,991A
-18
60/074,788
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619 DLTIGHTNSADGTNAKKVTFNQVKDSKISADG-HKVTLHSKVE--TSGSNNNTEDSSDNN 675
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                                                                                                                         124 PSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQS 183
                                                                                                                                                                                                                                                                                         184 EANPYFALLESWKGNGT----PPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSSTG 238
                                                                                                                                                                                                                                                                                                                                              : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 NAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSM 355
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                                                                                                                                                                                 876 ----TTEASSHITSAKGQVNLSAQDGSVACSINAANVTLNTTGTLTTVKGSNINATSGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKTFEYLVAMNPSEDGSAASGTDSAGLL -- - MSGTMTFSSNGELKUMTAFTPTGSATKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 MPIQTSSGNSTARNGSSSTRRYSQDGYPQGDL--VDVTITSEGKL---QGK-----
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ADDRESSEDENCE ADDRESS:
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
ZIP: 2120-1026 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC-COMPUTER: DEP PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRATION NUMBER: US/08/038,682 FILING DATE: US/08/038,682 FILING DATE: US/08/038,682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08038682
Patent No. 554987
GENERAL INFORMATION:
APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               983 -NI-ISKNGINTVLL-KGVKIDVKYIQPGIASVDEVIEAKR 1020
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ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
REGISTRATION TOWNER: 1038-293
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 1536 amino acids
amino acid
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TELEPAK: (703) 415-08:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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US-08-038-682-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1517 DPS-NGTEISGTAEAGATVILTDGGGNPIGQATADGSGNWTFTPGTPLANGTVINAVAQD 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1576 PAGNTSGPASVTVDAIA-PPAPVINPSNGVVISGTAEAGATVILTDGNGNPIGQVTADGS 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AQDAAGNNSSPTSATVDSLAPAAPV 1679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 LESWKGNG--TPPISTSNYSYAQPMRVYDQQGNSHDITVYFDG-APSSTGSKTFEYLVAM 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 SRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANPYFAL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 PTG-----SATKDINAWQPAPLVN-----GLPQFSANFV-----GAGIQPLTLDFG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 IKSQQNMWAGAPASAAIGIDIGKLPSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDL 387
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                                                                                  Indels 142;
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6.8%; Score 176; DB 4; Length 2736; llarity 22.6%; Pred. No. 5.4e-06; Conservative 56; Mismatches 212; Indels 14:
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Patent No. 6432669
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                                       Similarity
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APPLICATION NUMBER:
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                                                                                                                                               Gaps
                                                                       Query Match 6.7%; Score 173.5; DB 1; Length 1536; Best Local Similarity 22.8%; Pred. No. 3.6e-06; Matches 119; Conservative 80; Mismatches 222; Indels 100;
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Sequence 2, Application US/08302832

Patent No. 5603938

GENERAL INFORMATION:

APPLICANT:
Barenkamp, Stephen J

TITLE OF INVENTION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

ADDRESSEE: Shoemaker and Mattare, Ltd.

STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza

STREET: 21691.

CITY: Atlington

STREET: Wighina

COUNTRY: U.S.A.

ZIP: 22202-0286
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FILLING DATE: 16-SEP-1994
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CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: GB 9205704.1
APPLING DATE: 16-MAR.1992
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
           JS-08-038-682-2
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22.8%; Pred. No. 3.6e-06;
tive 80; Mismatches 222; Indels 100;
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US pct/us93/02166
                                            NAME: BETKETEBEET, JETTY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-404
TELEPHONE: (703) 415-0810
TELEPHONE: (703) 415-0810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                      DNA (genomic)
              FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerr
                                                                                                                                                                                                           1536 amino acids
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TOPOLOGY: lin
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                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.7%; Score 173.5; DB 2; Best Local Similarity 22.8%; Pred. No. 3.6e-06; Matches 119; Conservative 80; Mismatches 222;
                                                                                                                                                                                                                                                                                                                      CURRENT AREA TO THE RELEASE H.10, VET CURRENT AREA TO THE APPLICATION NUMBER: US/08/530,198 FILING DATE: 13-DEC-1995 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: BERKSTRESSER, USRRY W REGISTRATION NUMBER: 22,621 REPERRONE, DOCKET NUMBER: JWB-1186 TELECOMUNICATION INFORMATION: TELEPHONE: (703) 415-0810 TELEPHONE: (703) 415-0813 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
1536 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
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RESULT 18 US-08-469-880-2 ; Sequence 2, Application US/08469880

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                          Stephen J.
igh Molecular Weight Surface Proteins
E No. 5876733-Typeable Haemophilus
                                                                                                                                                      ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
CITY: Arlington
CITY: Arlington
COUNTRY: U.S.A.
ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.30
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6.7%; Score 173.5; DB 2;
Best Local Similarity 22.8%; Pred. No. 3.6e-06;
Matches 119; Conservative 80; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 1038-516 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0813
TELEFAX: (703) 415-0813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 68 9205704.1
FILING DATE: 16-MAR-1992
PRIOR APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION DATE: US PCT/US93/02166
APPLICATION NUMBER: US PCT/US93/02166
APPLICATION NUMBER: US 08/302,832
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APPLICATION NUMBER: US/08/469,880
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INPORATION:
NAME: BECKSTRESSER, JOERY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) MOLECULE TYPE: DNA (genomic)
US-08-469-880-2
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                   High .
GENERAL INFORMATION:
APPLICANT: Barenkamp, St
TITLE OF INVENTION: High
TITLE OF INVENTION: of N
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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1116 DITIGNINSADGINAKKVIFNOVKDSKISADG-HKVTLHSKVE--TSGSNNNTEDSSDNN 1116
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                 1011 IXAGVDGENSDSDATNNANLTIKTKELKL-----TQDLNI----SGFNKAEITAKDGS 1059
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Patent No. 5977336

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

ADDRESSEE: Shoemaker and Mattare, Ltd.

STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Alington

STREET: Witiginia

CONTENT: Virington

STREET: U.S.A.

ZIP: 22202-0286
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
COMPUTER: The PC comparatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUBER: .US/08/617,697
FILING DATE: 01-APR-1996
CLASSIPICATION: 424
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-193
ATTORNEY/AGENT INFORMATION:
NAME: Berketreeser, Jerry W
REGISTRATION NUMBER: 22,651
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1275 GGTISGNTVN------VTANAGDLTVGNGAE-----INATEGAATLTTSSGKL--- 1316
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Patent No. 522851
GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 201 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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APPLICATION NUMBER: US/08/728,470
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CLASSIFICATION: 424

PRIOR PAPLICATION 1424

APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832

FILING DATE: 16-MAR-1993

APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166

FILING DATE: 16-MAR-1993

APPLICATION NUMBER: GB 9205704.1

APPLICATION NUMBER: GB 9205704.1

ATTORNEY/AGENT INFORMATION:
NAME: BETKETCSSSEY, JETY W
REGISTRANDN NUMBER: JOSTY W
RECASTRANDN NUMBER: 10319-633

TELECOMMUNICATION INFORMATION:
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (703) 415-0810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TYPE: 1536 amistropics
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US-08-728-470-2
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US-08-728-470-2
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(703) 415-0810

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 MKTHSTGLGTVSNNIANAN-TIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 1536;
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Sequence 2, Application US/08719641

Patent No. 6218141

GENERAL INFORMATION:

APPLICANT: Barenkamp, Stephen J

TITLE OF INVENTION: High Molecular Weight Surface Proteins

TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Shoemaker and Mattare, Ltd.

STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza

STREET: pidg. 1
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                                                                                                                                                                                                                                                                                                                                                                                                      6.7%; Score 173.5; DB 2;
22.8%; Pred. No. 3.6e-06;
tive 80; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: ISH PC COMPATIBLE

COMPUTER: ISH PC COMPATIBLE
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 22.89
Matches 119; Conservative
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OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1536;
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     6.7%; Score 173.5; DB 3;
al Similarity 22.8%; Pred. No. 3.6e-06;
119; Conservative 80; Mismatches 222;
                                               FILING DATE

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/302,832

FILING DATE: 16-SEP-1994

PRIOR APPLICATION NUMBER: US PCT/US93/02166

FILING DATE: 16-MAR-1993

PRIOR APPLICATION NUMBER: GB 9205704.1

FILING DATE: 16-MAR-1992

ATTOMBRY/ABRIT INFORMATION:

NAME: Berketresser, Jesty REGISTRATION NUMBER: 22,651

RESTRENCE DOCKET NUMBER: 22,651

RESTRENCE DOCKET NUMBER: 22,651

RESTRENCE TOOKET NUMBER: 1038-625

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 415-0810

TELEPHONE: (703) 415-0810

INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719,641
                                                                                                                                                                                                                                                                                                                                                                                                                            1536 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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US-09-206-942-67
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Best Local
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Matches
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; Sequence 67, Application US/09206942

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Suite 701, 330 University Avenue
                                                                                                                                                                COMPUTER: IBM PC conpatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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amino acid
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CORRESPONDENCE ADDRESS
ADDRESSEE: SIM & MCE
                                                                                                                      COMPUTER READABLE FORM MEDIUM TYPE: Floppy
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                                                                          Canada
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STATE: Ontario
COUNTRY: Canada
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                                                                                                  APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
TITLE OF INVENTION: Molecular Weight Proteins
FILE REFERENCE: 1038-861 MIS:jb
FILE REFERENCE: 1038-861 MIS:jb
CURRENT APPLICATION UNMBER: US/09/206,942
CURRENT FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: 09/167,568
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 95
SOFIWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 1536;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ee-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.7%; Score 173.5; 22.8%; Pred. No. 3.6e
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Patent No. 5827654
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CHAN, VOON LOONG
APPLICANT: LOUIE, HELENA
                                                           oosmore, Sheena M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 22.83
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-206-942-67
                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 67
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59 KFVMDT---GVRRNFTQGPMTKTGGDYDLAINGMGFFKVQANGGERYTRDGRFTTNFEGI 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 INDPSGFTLM---GSRISNNPNIKKETLEPIQLDFNDPTVAKS-------PAKTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 248;
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 05-AUG-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: STEWART, MICHAEL I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-428 MIS

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 6:

SEQUENCE (416) 595-1163

INPORMATION POR SEQ ID NO: 6:

SEQUENCE CHRRACTERISTICS:

LENGTH: 248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.6%; Score 169.5; DB 2; Best Local Similarity 27.0%; Pred. No. 4.7e-07; Matches 70; Conservative 35; Mismatches 121;
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STREET: Suite 701, 330 University Avenue
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; Sequence 6, Application US/08483857
; Patent No. 6020125
; GENERAL INFORMATION:
APPLICANT: Chan, Voon Loong
; APPLICANT: Chan, Wentena
; TITLE OF INVENTION: BASAL BODY ROD PRC;
ITLE OF INVENTION: CAMPYLOBACTER
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TOPOLOGY: linear US-08-483-857-4
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ZIP: M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 ALNAVVNLGDSTDKTQ----SEANPYFALLESWKGNGTPPISTSNYSYAQPWRVYDQQGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.4%; Score 165; DB 3; Length 247;
Best Local Similarity 27.0%; Pred. No. 1.2e-06;
Matches 70; Conservative 36; Mismatches 119; Indels 34; Gaps
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Patent No. 5827654
GENERAL INFORMATION:
APPLICANT: LOUIE, HELENA
TITLE OF INVENTION: BASAL BODY ROD PROTEIN GENES OF
TITLE OF INVENTION: CAMPYLOBACTER
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCBUTNEY
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROPER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/436,748
FILING DATE: 05-AUG-1995
CLASSIFICATION: 435
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Suite 701, 330 University Avenue
                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,857
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-504
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAR: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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1. TYPE: amino acid
2.TRANDEDNESS: single
1. TOPOLOGY: linear
US-08-483-857-6
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
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US-08-436-748-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MMGSLFIGATGMXTHSTGLGTVSNNIANANTIGYKQQQVV---FQDLFSQ---DLAIGS-
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Patent No. 6020125
GENERAL INFORMATION:
APPLICANT: Cann, Voon Loong
APPLICANT: Louie, Helena
TITLE OF INVENTION: BASAL BODY ROD PROTEIN GENES OF
TITLE OF INVENTION: CAMPYLOBACTER
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/483,857 FILING DATE: 07-UW-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I. REGISTRATION NUMBER: 24,973 REFERENCE/DOCKET NUMBER: 1038-504 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS:
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6.0%; Score 155, DB 2;
Best Local Similarity 30.7%; Pred. No. 1.1e-05;
Matches 46; Conservative 28; Mismatches 64
ATTORNEY/AGENT INFORMATION.

NAME: STEWART, MICHAEL
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-428 MIS
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
IENGTH: 270 amino acids
ITRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
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Suite 701, 330 University Avenue
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 270 amino acids
TYPE: amino acid
STRANDEDNESS: single
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SITSANNQVNLSAKDGSIGGNINAANVTLNTTGALTTVKGSSINANSGTLVINAKDAELN 1034
967 SITSANNQVALSAKDGSIGGNINAANVTLATTGALTTVKGSSINANSGTLVINAKDAELN 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 LDFNDPTVAKSPA-----KTSTALNAVVNLGDSTDKTQS-----BANPYFALLESW--- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SHDITVYFDGAPSSTGSKTFEYLVAMNPSEDGSAASG-----TDSAG 264
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TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
TITLE OF INVENTION: Molecular Weight Proteins
FILE REPERENCE: 1038-861 MIS;196
CURRENT APPLICATION NUMBER: US/09/206,942
CURRENT FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: 09/167,568
EARLIER APPLICATION NUMBER: 09/167,568
EARLIER PILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                              Sequence 63, Application US/09206942
Patent No. 6432669
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Haemophilus influenzae
US-09-206-942-63
                                                                                                                                        NSKSVTTADTMLQKALELKR
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Loosmore, Sheena M. APPLICANT: Yang, Yan-Ping APPLICANT: Klein, Michel H.
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                                                                                                                                                                                 61 TRDASREVNTTIDGIPQVSQEYTDFSLGSLKATNNPLDLAMTREDAFYLVQTKDGEVRT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222
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                                                                                                                                                            54 --TGSQGPNQAGMG-AQVGSVRIIFTQGAFEPGNSVTDLAIGGKGFFQV--TLEDKVHYT 108
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GENERAL INFORMATION:
APPLICANT: Young, Yan-Pari,
APPLICANT: Young, Yan-Pari,
APPLICANT: Young, Yan-Pari,
ITLE OF INVENTION: Michel H.
ITLE OF INVENTION: Molecular Weight Proteins
FILE REFERENCE: 1038-861 Mis.;b
CURRENT APPLICATION NUMBER: US/09/206,942
CURRENT APPLICATION NUMBER: U9/167,568
EARLIER PILING DATE: 1998-10-07
NUMBER: PREDICATION NUMBER: 09/167,568
EARLIER FILING DATE: 1998-10-07
NUMBER: PREDICATION NUMBER: 20/167,568
SOFTWARE: PREDICATION NUMBER: 20/167,568
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SOFTWARE: PREDICATION NUMBER: 09/167,568
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SOFTWARE: PREDICATION NUMBER: 09/167,568
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20.2%; Pred. No. 0.00034;
tive 88; Mismatches 212; Indels 147;
                                             12;
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      Length 270
                                           64; Indels
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      ; DB 3;
1.1e-05;
    6.0%; Score 155; DB 30.7%; Pred. No. 1.1e-tive 28; Mismatches
                                                                                                                                                                                                                                                                 121 KDGNFQLDDEGYLVNKQGYKVLSSDYFNNP 150
                                                                                                                                                                                                                                      109 RAGNFRFTQDGFLNDPSGFTLMGSRISNNP 138
                                                                                                                                                                                                                                                                                                                                                                      Sequence 65, Application US/09206942
Patent No. 6432669
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Best Local Similarity 20.23
Matches 113; Conservative
                                           46; Conservative
      Query Match
Best Local Similarity
Matches 46; Conserv
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                                      392 ITSEGKLOGKYSNSOVVDFYNIPLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNY
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GENERAL INC. 913.20.9
GENERAL INC. 913.20.9
APPLICANT: Loosmore, Sheena M.
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
TITLE OF INVENTION: Molecular Weight Proteins
FILE REFERENCE: 1038-861 MIS.jb
CURRENT APPLICATION NUMBER: US/09/206,942
CURRENT FILING DATE: 1998-12-08
EARLIER PILING DATE: 1998-12-08
EARLIER PILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 95
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                                                                                                                                                                                                      452 GKLSVNQLETSNVDMSREMVNMII
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US-09-206-942-45
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1035 GEASGNHTVVNATNANGSGSVIATTSSRVNITGDLITINGLNIISKNGINTVLL-KGVKI 1093
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Patent No. 6753314

GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR PLING DATE: 1999-04-01

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR FILING DATE: 1990-04-01

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SEQ ID NO 330

LENGTH: 1306
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CTHER INFORMATION: Polypeptide Accession Number YGR014W
US-09-538-092-330
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ORGANISM: Saccharomyces cerevisiae
                                                                                 NSKSVTTADTMLOKALELKR
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; TYPE: PRT
; ORGANISM: Human
US-09-381-656-1
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Sequence 43, Application US/09206942

Sequence 43, Application US/09206942

Sequence 43, Application US/09206942

GENERAL INFORMATION:

APPLICANT: Locsmore, Sheena M.

APPLICANT: Alein, Michel H.

TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
FILE REFERENCE: 1038-861 MIS:jb

CURRENT APPLICATION NUMBER: US/09/206,942

CURRENT FILING DATE: 1998-12-06

EARLIER FILING DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 95

SOFTWARE: PATENTIN Ver. 2.1
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5.5%; Score 142; DB 4; Length 1101;
Best Local Similarity 20.9%; Pred. No. 0.0014;
Matches 101; Conservative 76; Mismatches 229; Indels 78
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US-09-381-656-1
US-09-381-656-1
Parent No. 6645509
GENERAL INFORMATION:
APPLICANT: SERRE, GUY Bruno Rene;
APPLICANT: SIRON, Michel
APPLICANT: SIRON, Michel
                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Haemophilus influenzae
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366 TARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFISED--- 422
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TITLE OF INVENTION: POLYBEPTIDE EXPRESSED IN THE HORNY LAYER OF EPIDERMIS TITLE OF INVENTION: AND USE THEREOF FILE REPERBURE: 01680-336
CURRENT APPLICATION NUMBER: PR 97/03899
PRIOR FILING DATE: 1999-12-29
PRIOR PLING DATE: 1997-03-28
PRIOR PLING DATE: 1997-03-11
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          412 YHPCGSASQSPCSPPG-----SSQSSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SA-----GSFKRQIGYSQVSYSSGSGSSLQGASGSSQLGSSSSHSGSSGSHSGSSSSHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 --GVSSSGQSVSSNQRPCSSDIPDSPCSGGPIVSHSGPYIPSSHSVSGGQRPVVV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.4%; Score 140.5; DB 4; Length 529; Best Local Similarity 20.3%; Pred. No. 0.00062; Matches 108; Conservative 60; Mismatches 182; Indels 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 MSGTMTFSSNGELKNMTAFTPTGSATKDLNAWOPAPLVNGLPQF---
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Sequence 20, Application US/09665479A

Patent No. 6673510N:
GENERAL INFORMATION:
APPLICANT: Itch, Funiko
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
FILE OF INVENTION: ENDO ASSOCIATING FOLYPEPTIDES
CURRENT APPLICATION NUMBER: US/09/665,479A
CURRENT FILING DATE: 1999-09-20
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us-10-009-823a-1.rai

US-09-492-709A-302

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 MRVYDQQGNSHDITVYFDGAPSSTGSKTFEYL-VAMNPSEDGSAASGT-----DSAGLL 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 YNALRRWYTDIQEPMFSAAREOFGNNPFSALAGGSEGSASOPLRTENREPLFNPWSPASP 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 MSGTWITFSSNGELKNWIAFIPIGSATKDLNAWQP---APLVNGLPQFSAN------ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LILDFGIKSQQNMWAGAPASAAIGTDIGKLPSM 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 MPIQTSSGNSTARNGSSSTRRY----SQDGYPQGDLVDVTITSEGKLQGKYSNSQVV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 TGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 ----SSNFMELQQQMQRQLMSNPEMLSQIMENPLVQNMMSNPDLMRQMIIANPQMQQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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APPLICANT: Forsyth, R. Allyn
APPLICANT: Forsyth, R. Allyn
APPLICANT: Forsyth, R. Allyn
APPLICANT: Forsith, Jamie M.
APPLICANT: Grant J.
APPLICANT: Will Howard
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
FILE REPERBURE: ELITRA, 0.014
CURRENT APPLICATION NUMBER: US/09/492,709A
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FRASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                  5.3%; Score 137; DB 4; Length 585;
20.8%; Pred. No. 0.0015;
tive 62; Mismatches 191; Indels 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | | | : : | | NOTE | : : | | NOTE | : : | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | NOTE | 
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GENERAL INPORMATION: APPLICANT: Zyskind, Judith APPLICANT: Chisen, Kari L. APPLICANT: Trawick, John
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.2
SEQ ID NO 20
LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 20.8%
Matches 108; Conservative
                                                                                                                                                                           TYPE: PRT
ORGANISM: Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---FVGAGIQP-
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ORGANISM: E. Coli
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                                                                                                                                                                                                                                   ; ORGANISM: Xend
US-09-665-479A-20
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LENGTH: 2383
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                                                                                                                        :sos atvadtegnalant-----Evtr--tlpedvkanftlsdg-------GKVITDA 1544
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                                                                                                                                                                 ----IFTQGAFEPGNSVTDLAIGGK-----GFFQVTLEDKVHYTRAGNFRFTQDGFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 KNWTAFTPTGSATKDLN-AWQPAPLVNGLPQFSANFVGAGIQPLTL-----DFGIK
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                                                                                       16 STGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVGSVRT--
                                                                                                                                                                                                                                                                                                                      176 DSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPS
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                                                   Gaps
            Length 2383;
                                                 Indels
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APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                236 STGSKTFEYLVAMNPSEDGS-AASGTDSAGLLMSG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSES: Sim & MCBurney
STREET: Suite 701, 330 University Avenue
STATE: Ontario
STATE: Ontario
STATE: Canada
ZIP: MGG 1R7
COMPTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
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APPLICATION NUMBER: US/08/621,944A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 08/478,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08621944A
Patent No. 6440425
GENERAL INFORMATION:
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          Query Match
Best Local Similarity 20.9
Matches 113; Conservative
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Query Match 5.1%; Score 133; DB 4; Length 1833;
Best Local Similarity 20.0%; Pred. No. 0.021;
Matches 126; Conservative 79; Mismatches 222; Indels 204; Gaps 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          552 LDQDKLOVGNVK-ITNTGINAGGKAITGLSPTLPSIADQSSRNIELGNTIQDKDKSNAAS 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             824 QIQVGA-----DGVKFAKVNNNGVVĞAĞIDGTTRITRDEIGFTGTNGSLDKSKPHLSK 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 --LDFGIKSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTSSGNSTARNGSSSTRRYSQDG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   877 DGINAGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSV-A 935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 QAGMGAQVGSVRTIFTQGAFEPGNSVŢDL----AIGGKGFFQV----TLEDKVHYTRAG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 SSTGSKTFEYLVAMNPSED--GSAASGTDSAGLLMSGTMTFSSNG-ELKNMTAFTPTGSA 291
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                                                     ALTOKACH FARMER, INCOMENCE OF ALL MEDISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
REFERENCE/OCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEFORM: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1833 amino acids
                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                        US-08-621-944A-4
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RESULT 36
US-08-945-567D-4
; Sequence 4, Application US/08945567D
; Parent No. 64481386
; GENERL INFORMATION:
; APPLICANT: SASAKI, Ken
; APPLICANT: HARKNESS, Robin E.
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APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
TITLE OF INVENTION: MORAZELLA
FILE REFERENCE: 1038-745 MIS
CURRENT APPLICATION WUMBER: US/08/945,567D
CURRENT FILING DATE: 1995-06-04-29
FRIOR PILING DATE: 1995-06-07
FRIOR APPLICATION NUMBER: 08/431,718
FRIOR APPLICATION NUMBER: 08/431,718
FRIOR APPLICATION NUMBER: 08/421,944
FRIOR PILING DATE: 1995-06-07
FRIOR PILING DATE: 1995-06-07
FRIOR PILING DATE: 1995-06-07
FRIOR PILING DATE: 1995-06-07
FRIOR PILING DATE: 1996-03-26
FRIOR PILING DATE: 1996-04-29
FRIOR FILING DATE: 1996-04-29
FRIOR FILING DATE: 1996-04-29
FRIOR FILING DATE: 1996-04-29
FRIOR FILING DATE: 1096-04-29
FRIOR FILING DATE: 1096-04-29
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FRIOR FILING DATE: 1096-04-29
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5.1%; Score 133; DB 4; Length 1833;
Best Local Similarity 20.0%; Pred. No. 0.021;
Matches 126; Conservative 79; Mismatches 222; Indels 204; Gaps 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Moraxella catarrhalis
LOOSMORE, Sheena M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-945-567D-4
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 4
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us-10-009-823a-1.rai

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APPLICANT: HARKNESS, Robin E.
APPLICANT: HARKNESS, Robin E.
APPLICANT: COOSMORE, Sheena M.
APPLICANT: COOSMORE, Sheena M.
APPLICANT: COOSMORE, Sheela
APPLICANT: COON, Pelea
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
TITLE OF INVENTION: HORANGELLA
FILE REPERENCE: 1038-745 MIS
CURRENT APPLICATION NUMBER: 08/431,718
PRIOR APPLICATION NUMBER: 08/431,718
PRIOR PLING DATE: 1995-06-07
PRIOR PLING DATE: 1995-06-07
PRIOR PLING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1996-04-29
PRIOR FILING DATE: 1996-04-29
PRIOR FILING DATE: 1996-04-29
                                                                                      983 QIQVGA-----DGVKFAKVNNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLSK 1035
                                                                                                                                                                             1036 DGINAGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSV-A 1094
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                                                                                                                                                                                                                                                             928 NQVNTLTIKGENGINIKTDKNGTVTFGINTTSGIKAGKSTLNDGGISIKN-----PTGSE 982
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                                                                                                                                    324 --LDFGIKSQQNMWAGAPASAAAIGTDIGKLPSNMPIQTSSGNSTARNGSSSTRRYSQDG
                                                                                                                                                                                                                                                                                                                     -----GNNHYSATLDSGGPEFGLPGTSN-----YGKLSVNQLETSNV----DMS
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20.0%; Pred. No. 0.023;
tive 79; Mismatches 222; Indels 204;
                                                                                                                                                                                                                           382 YPQGDLVDVIITSEGKLQGKYSNSQVVDFYNIPLARFISEDGLRRE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 20.0%,
Matches 126, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 10
SOFFWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 1992
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-945-567D-3
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                                                                                                APPLICANT: SASAKI, Ken
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOSMORE, Sheena M.
APPLICANT: LOSMORE, Sheena M.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
TITLE OF INVENTION: MEMBRANB PROTEIN OF MORAKELLA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCBUTHEY
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 NFRFTQDGFLND--PSGFTLMGSRISNNP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                     ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REPERENCE/DOCKET NUMBER: 1038-587
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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SOFTMARE: Patencis...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,944A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
            US-08-621-944A-3
; Sequence 3, Application US/08621944A,
Patent No. 6440425
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 07-JUN-1995
CLASSIFICATION:
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linear
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                                                                                                                                                                                                                                                                                                                                                         Ontario
: Canada
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TYPE: amino acid
STRANDEDNESS: sin
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TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
                                                                                                                                                                                                                           8 GATGMK-THSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGA
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5.1%; Score 132; DB 3; Length 2314;
Best Local Similarity 22.8%; Pred. No. 0.036;
Matches 113; Conservative 63; Mismatches 196; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 QVGSVRTIFTOGAFEPG----NSVTDLAIGGKGFF-QVTLEDKVHYTRAGN--
5.1%; Score 132; DB 3; Length 2123;
19.9%; Pred. No. 0.032;
tive 80; Mismatches 243; Indels 164;
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CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 49
LENGTH: 2314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-268-347-49; Sequence 49, Application US/09268347; Patent No. 6335182; GENERAL INFORMATION:
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ORGANISM: Haemophilus influenzae
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                       Query Match
Best Local Similarity 19.9%
Matches 121; Conservative
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US-08-968-685A-10
Sequence 10, Application US/08968685A
Sequence 10, Application US/08968685A
Patent No. 6214981
APPLICANT: TUCKER, KENNETH
APPLICANT: PLOSILA, LAURA
ITILE OF INVENTION: MORAXELLA CATARRHALIS OUTER MEMBRANE
ITILE OF INVENTION: PROTEIN-106 POLYPEPTIDE, GENE SEQUENCE AND USES THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
AUTHOR OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
AUTHOR OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 TKDLNAWQPAPLVNGLPQFSAN---FVGAGIQPLT--------323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 --LDFGIKSQQNMWAGAPASAAIGTDIGKLPSMMPIQTSSGNSTARNGSSSTRRYSQDG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GNNHYSATLDSGGPEFGLPGTSN-----YGKLSVNQLETSNV----DMS 467
                                                                             178 TDXTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHD---ITVYFDGAP 234
                                                                                                                                                                                        878 AENLINTLAKE----IHTTKGTADTALQTFT-----VKKVDENNNADDANALTVGQKNAN 927
                                                                                                                                                                                                                                                                                                         SSTGSKTFEYLVAMNPSED--GSAASGTDSAGLLMSGTMTFSSNG-ELKNMTAFTPTGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 YPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSEDGLRRE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: REALBLE FORDER OF WINDIGHT WITHOUT TYPE: Floppy disk COMPUTER: IBM PC COMPAtible OPERATIOS SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/968,685A FILING DATE: No. 621498lember 12, 1997 CLASSIFICATION: NO 621498lember 12, 1997 ATTORNEY/AGENT INFORMATION: NAME: Baldwin, Geraldine F. REGISCHATION NUMBER: 31,232 REFRENCE/DOCKET NUMBER: 7969-060 TELEPRAKE (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAASIVDVLSAGFNLQGNGEAVDFVSTYDTV 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468 REMVNMIIIQRGFQMNSKS----VTTADTM 493
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2123 amino acids
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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STATE: New York
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STRANDEDNESS:
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GDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNL 1494	HYTRAGNERFTODGELNDPSGFTLMGSRISNNPNIKKETLEPIQLD 151	:	FNDPIVAKSPAKISTALNAVVNLGDSTDKIQSEANPYFALLESHKGNGTPPISTSNY 208	DNDAVNFKQFNEVAKTVNNLANQSNSGASLPFVVTDANGKPINGTDG 1592	SYAQPMRVYDQQGNSHDITVYFDQAPSSTGSKTFEYLVAMNPSEDGSAASGTDS 262	KPQKAIKGADGKYYHANANGVPVDKDGKPITDADKLANLAAHGKPLDAGHQVVASLGGNS 1652	AGLIMSGIMTFSSN-GELKNWTAFTPTGSATKDLNAMQPAPLVNGLPQFS 311	DAITLINIKSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSNAASVKDVLN 1702	312 ANFYGAGIQPLTLDFGIKSQQNWWAGAPASAAAIGTDIGKLPSWMPIQTS 361	1703VGFNLQTNHNQVDF-VKAYDTVNFVNGTGADITSVRSADGTM-SNITVNTALAATDD 1757	SGN STARNGSSSTRRYSQDG-YPQGDLVDVTITSEGKLQGKXSNSQVV 408		TSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQ 458	1814 ALNNLSKAVFKSKDGTTTTTVSSDGISIQGKDNSSITLSKDGLNVGGKVISNVGK-GTKD 1872	NIMI 474	; ; RNLL 1888
GDTGTTAKKLO							AGLLMSGTM	DAITLINIKSTLPQIDTE	ANFVGAGIQPLILDFG	VGFNLQTNHNQVDF			DFYNIPLARF	ALNNLSKAVFKSKDGTTT	LETSNVDMSREMVNMI 474	:: { :: TDAANVQQLNEVRNLL 1888
1444	106	1495	152	1546	209	1593	263	1653	312	1703	362	1758	409	1814	459	1873
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Search completed: October 26, 2004, 09:09:30 Job time : 32 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
               Copyright
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- nucleic search, using frame_plus_p2n model

October 31, 2004, 03:22:21; Search time 477 Seconds (without alignments) 5524.548 Million cell updates/sec

Run on:

US-10-009-823A-1 2586 1 MMGSLFIGATGMKTHSTGLG......NSKSVTTADTMLQKALELKR 502

BLOSUM62 Title: Perfect score: Sequence: Scoring table:

0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext Fgapop Delop 4134886 segs, 2624710521 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model.-DEV=x1h
-MODEL=frame+ p2n.model.-DEV=x1h
-Q=/Cgn2_1/USPTO_spool/US10009823/runat_26102004_100128_1596/app_query.fasta_1.647
-Q=/Cgn2_1/USPTO_spool/US10009823/runat_26102004_100128_1596/app_query.fasta_1.647
-DB=N Geneseq_2586p04 -QFMT=fastap -SUPFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STRRT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORES=pct -THR MAX=100 -THR MIN=0 -ALIGN=40
-MODE=LOCAL -COUTEMT=pcc -NORM=ext -HRAPSIZE=500 -MINLENE=0 -MAXLEN=200000000
-USER=US10009823_@CGN 1 1_352_@runat_26102004_100128_1596 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPPO=10 -XGAPPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

geneseqn1980s:* geneseqn1990s:* Geneseq 23Sep04:* geneseqn2000s:* Database :

geneseqn2003cs:* geneseqn2001as:* geneseqn2001bs:* geneseqn2003as:* geneseqn2002as:* geneseqn2003bs:* geneseqn2002bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aac88037 Lawsonia	Aat69214 Lawsonia	Aat69204 Lawsonia	Aca24087 Prokaryot	Abd04351 Pseudomon	Abd04124 Pseudomon
ei	4 AAC88037	AAT69214	AAT69204	ACA24087	ABD04351	ABD04124
DB	4	~	N	ω	11	디
° Query Match Length DB	100.0 1509 4	568	569	1242	1416	1512
		22.3	22.0	20.5	20.4	20.4
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	7	527.5	20.4	1389	œ	ABT14574	Abt14574 Pseudomon
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		84		110000	ø	ľ.	tion
	15	483	•	2550	~	~	DNA
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	18	469.5		5998	9	ABQ71042	ч
	19	448.5		1215	10	œ	m
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	22	14		110000	ø	ABA92787 3	
	23	360.5	13.9	1912	Ŋ	AAS88896_	
	24	58	•	110000	~	AAX20248_00	∞
	25	307	•	810	11	`₩	0
U	56	302	11.7	1545	1	ABD04219	σ
	27	295	•	783	10		_
υ	28	291	11.3	32768	0	AAX20515	<u>Б</u>
	29	288		816	~	AAT67783	3 H.
	30	288	11.1	816	7	AAT77463	3 H.
	31	288	11.1	837	0	AAT68116	16 H.
	32	286	11.1	798	10	ADF03653	653 Ba
	33	281.5	10.9	1800	m	AAZ88552	25
O	34	279		1398	ហ	AAS88418	~~
	35	7	•	1800	~	AAV58977	Aav58977 FlgFG ope
	36	~	•	789	m	AAZ88554	
	37	237	•	555	9	ABK74597	~
U	38	221	8.5	742	12	16	27
	39	215.5		1524	9	ABK74555	Bacil
	40	201	•	1432	17	ADG32119	19 DNA en
	41	193	7.5	5445	4	AA197965	D.
	42	193	7.5	5445	σ	22	23 Laws
	43	193	7.5	5445	5	ADG33882	œ
	44	193	7.5	5445	9	7	187
ט	45	176	6.8	3129	11	ABD15269	Abd15269 Pseudomon

ALIGNMENTS

AAC88037 standard; DNA; 1509 RESULT 1 AAC88037

BP

(first entry) 07-MAR-2001

AAC88037;

Lawsonia intracellularis flagellar hook protein FlgE gene SEQ ID NO:2.

Lawsonia intracellularis; flgE; flagellar hook protein; vaccine; intestinal disease; immunogenic; diagnosis; antibacterial; swine; pig; infection; detection; identification; ds.

Lawsonia intracellularis

WO200069904-A1.

23-NOV-2000.

11-MAY-2000; 2000WO-AU000437.

99US-0133973P. 13-MAY-1999; (PFIZ) PFIZER PROD INC. (AGRI-) AGRIC VICTORIA SERVICES PTY LTD. (PIGR-) PIG RES & DEV CORP.

Parsons J; Hasse D, Sinistaj M, Rosey EL, Ankenbauer RG; Panaccio M,

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The present sequence encodes the Lawsonia intracellularis flagellar hook protein FIGE. The present invention describes an isolated or recombinant polypeptide (I) that comprises, mimics or cross-reacts with a B- or T-cell epitope of a FIGE flagellar hook) polypeptide from a Lawsonia spp. (I) has antibacterial activity, and induces a specific humoral immune response. (I) are used as antigens in vaccines to prevent or treat infection by Lawsonia, in birds and animals, especially pigs, to raise specific antibodies (Ab) and to detect past or present infection. Ab are also useful in diagnosis, to detect L. intracellularis or immunologically oross-reactive species, also for identification of epitopes in FIGE. Vectors that contain nucleic acids (II) encoding (I) are also useful in genetic vaccines, and fragments of (II) are useful as primers or probes for detecting L. intracellularis or related microorganisms, in
                                                             New immunogenic Lawsonia FlgE peptide, its nucleic acid and antibody, useful in vaccines and diagnosis of Lawsonia infections, particularly in.
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1509 BP; 511 A; 264 C; 316 G; 418 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1509
502
0
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0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                    Claim 32; Page 90-94; 97pp; English.
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2586.00
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              WPI; 2001-016210/02.
P-PSDB; AAB36552.
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Best Local Similarity:
Query Match:
DB:
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US-10-009-823A-1 Oy 1 Mei Db 1 ATK	(1-502) x AAC88037 (1-1509) METGLYSerLeuphelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 	0 0
21	ThrvalSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValVal 40	20
41	PheGlnAspLeuPheSerGlnAspLeuAlaIIeGlySerThrGlySerGlnGlyProAsn.60 	0 80
61 181	GinalagiymetgiyalaginvalgiyserValargThrilePheThrGinGiyalaPhe 80	0 4
81 241	Gluproglyasnservalthraspleualaileglyglytysglyphepheglnvalthr 100	0 0
101	LeugluasplysvalHisTyrThrargalaglyasnpheargpheThrGluaspGlyphe 120	20
121	LeuasnasperosergiypheThrLeuwetGiyserargileserasnasneroasnile 140	4
141	LystysGluthrLeuGluProlleGluLeuAspPheAsnAspProThrValAlaLysSer 160	0 0 8
161	ProalaiysThrSerThrAlaieuAsnalaValValAsnieuGlyAspSerThrAspLys 180 	0 4

yo d	181	ThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGluSerTrpLysGlyAsnGlyThr 200
ζ Q	201	22
Š A	221	24
Sy di	241	ThrPheGluTyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThr 260
yy da	261	luteutys 2 AATTAAAA 8
Sy G	281	ASIMELTHIA BAPHETHI PIOTHIGLY SERALATHILLY SASPLEUASIA BALATIOGLIPIO 300
\delta \delta	301	AlabroLeuvalasnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGln 320
상 업	321	321 ProLeuThrLeuaspPheGlytleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAla 340
<i>장</i> 업	341	SerahaahaalaileglyThraspileglyLysLeuProSermetMetProileglnThr 360
S d	361	SerSerGlyasnSerThralaargasnGlySerSerSerThrargargTyrSerGlnasp 380
& 4g	381.	GlyTyrProglnGlyAspLeuValAspValThrIleThrSerGluGlyLySLeuGlnGly 400
& A	1201	LysTyrSerAsnSerGlnValValAspPheTyrAsnIleProLeuAlaArgPheThrSer 420
& A	421	GlubspGlyLeuArgArgGluGlyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGly 440
\$ g	441	ProgluPheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGlu 460
<i>8</i> ₹	461	ThrserasnValaspmetSerargGluMetValasnMetIleIleIleGlnArgGlyPhe 480
oy Ob	481	GlnMetAsnSeriysSerValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeu 500
& 8	501 1501	01 Lysarg 502 01 Aaggs 1506
RESI AATI XX AC	ULT 2 69214/c AAT692: AAT692:	standard; DNA; 568 BP.

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71 ATTAGAGGATAAAGTACACTATACACGAGCAGGGAATTTTCGTTTTACTCAAGATGGTTT 12
                                                                                                                                                                                                                                                          /*tag= a
/note= "includes in-frame stop codon at 245. .247"
                                                                                                                                                                             Intestinal disease; porcine proliferative enteropathy; vaccine; flagellar basal body rod protein; ss.
                                                                                                                                                        Lawsonia intracellularis vaccine candidate DNA.
                                                                                                                                                                                                                                  Location/Qualifiers
209. .568
                                                                                         ВÞ.
                                                                                                                                                                                                                                                                                                                                                         95AU-00006910
95AU-00006911
                                                                                                                                                                                                                                                                                                                                    96WO-AU000767
                                                                                        AAT69204 standard; DNA; 569
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(PIGR-) PIG RES & DEV CORP.
                                                                                                                                    (first entry)
                                                                                                                                                                                                              Lawsonia intracellularis.
                                                                                                                                                                                                                                                                                                                                                                                                                             Panaccio M, Hasse D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-310605/28.
P-PSDB; AAW16680.
                        eLeuAsnAsp
                                             TTTAAATGAT
                                                                                                                                    20-AUG-1997
                                                                                                                                                                                                                                                                                          WO9720050-A1
                                                                                                                                                                                                                                                                                                                                     29-NOV-1996;
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                                                                                                               AAT69204;
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                                                                                 AAT69204
                                                                     RESULT
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                                             g
                                                                                                                                                                                                                                                                                                                                              DNA molecules (AAT69203-15) were isolated from an immunoscreening of a Lawsonia intracellularis library using experimental sera from vaccinated pigs. These nucleic acids, as well as isolated GroEL and GroES (AAT69201-02) sequences, encode putative vaccine candidates (see also AAW16578-85) useful for protection of animals and birds against intestinal diseases, esp. protection of pigs against porcine proliferative enteropathy (PPE). They can also be used as genetic vaccines
                                                                                                                                                                                                                                                                               Vaccine for treating or preventing Lawsonia intracellularis infection - especially in pigs, containing non-pathogenic form of bacterium or its components.
                                                          Intestinal disease; porcine proliferative enteropathy; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 568 BP; 184 A; 126 C; 72 G; 176 T; 0 U; 10 Other;
                                     Lawsonia intracellularis vaccine candidate DNA
                                                                                                                                                                                                                                                                                                                              Claim 25; Page 71; 94pp; English
                                                                                                                                                                     95AU-00006910,
95AU-00006911,
                                                                                                                                                96WO-AU000767
                                                                                                                                                                                                      (DARA-) DARATECH PTY LID.
(PIGR-) PIG RES & DEV CORP.
                 20-AUG-1997 (first entry)
                                                                               Lawsonia intracellularis.
                                                                                                                                                                                                                                       Panaccio M, Hasse D;
                                                                                                                                                                                                                                                            WPI; 1997-310605/28.
                                                                                                                                                                      30-NOV-1995;
                                                                                                      W09720050-A1
                                                                                                                           05-JUN-1997.
                                                                                                                                                 29-NOV-19967
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DNA molecules (AAT69203-15) were isolated from an immunoscreening of a Lawsonia intracellularis library using experimental sera from vaccinated pigs. These nucleic acids, as well as isolated GroEL and GroES (AAT69201-02) sequences, encode putative vaccine candidates (see also AAW16678-85) useful for protection of animals and birds against intestinal diseases, esp. protection of pigs against porcine proliferative enteropathy (PPE). They can also be used as genetic vaccines. The polypeptide (AAW1668) encoded by the DNA molecule given in AAT69204 has sequence similarity to flagellar basal body rod protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetMetGlySerLeuDheIleGlyAla-ThrGlyMetLysThrHisSerThrGlyLeuGl
                                                                                                                                                                                                                                                                                          BP; 177 A; 72 C; 128 G; 189 T; 0 U; 3 Other;
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Matches:
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Mismatches:
Indels:
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Claim 15; Page 51-52; 94pp; English.
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570.00
95.16%
22.04%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eGluProGlyAsnSerValThrAspLeuAlaileGlyGlyLysGlyPhePheGlnValTh 100
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                                                                                                                                                                                                                                                                                                                                                 251 GTTTCAAGACCTGTTTAGTCAAGATTTAGCAATAGGTTTTACTGGAAGTCAGGGGCCAAA 192
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                                                                                                                                  40 lPheGlnAspLeuPheSerGlnAspLeuAlaileGlySerThrGlySerGlnGlyProAs
                                                                                                                                                                                                                                                                                                                                                                                             nGlnAlaGlyMetGlyAlaGlnValGlySerValArgThrllePheThrGlnGlyAlaPh
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                                                                                                      1 MetMetGlySerLeuPheIleGlyAla-ThrGlyMetLysThrHisSerThrGlyLeuGl
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Vaccine for treating or preventing Lawsonia intracellularis infection especially in pigs, containing non-pathogenic form of bacterium or its components.

Length:
Matches:
Conservative:
Mismatches:
Indels:

1.42e-37 577.00 95.97% 95.97%

Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores:

US-10-009-823A-1 (1-502) x AAT69214 (1-568)

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                                                                                                                80
ATGATGGGGAGTTTGTTTATTGNTGCGAACAGGTATGAAAACCCCATAGNACAGGGNT-GG
                                                                                                                                                             eGlubroGlyAsnSerValThrAspLeuAlaIleGlyGlyLysGlyPhePheGlnValTh
                                                                                                                                                                            TGAACCTGGCAATAGTGTAACAGATCCTGCTATTGGTGGAAAAGGTTTTTTTCAGGTTAC
                                  40 lPheGlnAspLeuPheSerGlnAspLeuAlaileGlySerThrGlySerGlnGlyProAs
                                                                                   GTTTCAAGACCTGTTTAGTCAAGATTTAGCAATAGGTTTTACTGGAAGTCAGGGGCCAAA
                                                                                                                nGlnAlaGlyMetGlyAlaGlnValGlySerValArgThrIlePheThrGlnGlyAlaPh
                                                                                                                             CCAGGCTGGTATGGGAGCACAGGGGGAAGTGTTCGCACAATTTTTACACAGGGTGCTTT
                                                                                                                                                                                                         100 rLeuGluAspLysValHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPh
                                                                                                                                                                                                                        ATTAGAGGATAAAAGTACACTATACACGAGCAGGGAATTTTCGTTTTACTCAAGATGGTTT
                      yThrValSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; ds; prokaryotic essential gene; cell proliferation;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; SEQ ID NO 11957; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Prokaryotic essential gene #5744
                                                                                                                                                                                                                                                                                                                             ACA24087 standard; DNA; 1242 BP.
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Carr GJ,
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06-SEP-2001; 2001US-00949993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                  drug design; gene.
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Wall D,
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polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a product is overexpressed or underexpressed; (12) determining the extent or compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the constitution of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational for identifying proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. prewmoniae or P. aeruginosa. The present sequence is one of the target or provaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the print of the contract of the printed of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 GGCTTGAGGGGATTGGCCGGTGCGTCGAGGAATCTCGACGTCATCGGCAACAACATCGCG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValValPheGlnAspLeuPheSerGln 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1242 BP; 266 A; 421 C; 397 G; 158 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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529.50
44.20%
29.80%
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Best Local Similarity:
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a prometer operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated

è		DE Pseudomonas aerugino
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Q	514514 514 514 515 517 517 517 517 517 517 517 517 517	<pre>KW antibacterial. xx</pre>
λõ	CyrAlaGlnProM	OS Pseudomonas aerugino
Д	538 ACGACGTACAACTACAACTCGTCGATCCAGGTCTACGACACGCTCGGCGCCTCGCAGCAG 597	AA US6551795-B1.
ò	AspGl	XX PD 22-APR-2003.
QQ		XX PF 18-FEB-1999; 99US-
ò	246 ValAlaMetAsnProSerGluAspGlySerAlaAalaSerGlyThrAspSerAlaGlyLeu 265	XX PR 18-FEB-1998; 98US-
QD	634	27-JUL-1998;
ò	266 LeuMetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLysAsnMetThrAlaPhe 285	PA (GENO-) GENOME THERA. XX
Бр		PI Rubenfield MJ, Noll: XX
ò	sn	DR WPI; 2003-615309/58. DR P-PSDB; ABO70780.
g	727 GCCGCGACCGGC 750	XX PT Novel isolated nucle
ò	306 GlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGlnPro 321	PT useful as molecular of PT pathological condition
qq		XX PS Disclosure; SEQ ID N
ઠે	322 LeuThrleuAspPheGlyIleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAlaSer 341	
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DP DP	943 TACTCGAACGCCCAGAGCCCGGTGCTCGGCCTCATCGCGAACTTCAACAACCCG 1002	and the second s
ò	SlyLeuArgArgGluGlyAsnAsnHisTy	No.:
qq	1003 AACGGGCTCGTGAACATCGGCGGCAACCAGTATGCGGAAACGGCCGCGTCCGGCGTGCCG 1062	Score: Percent Similarity: 4
ò	442 GluPheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThr 461	
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ò	SerAsnValAspMetSerArdGluMetValAsnMetIleIleGlnArdGlvPheGln	US-10-009-823A-1 (1-502)
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ABD04351	4351 48D04351 standard: DNA: 1416 BP.	Qy 44 LeuPheSerGli
XX		Db 151 GTCTACGCCGC
ΧE	29-JIII2004 (first ontro)	Qy 64 MetGlyAlaGl
ž	3	Db 196 AGCGGCGTGCT

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elates to Pseudomonas aeruginosa polypeptides and the encoding them. The sequences are useful in diagnosis and ological conditions, as molecular targets for diagnostics, treatment of pathological conditions resulting from a tion, for evaluating a compound, such as a polypeptide, to bind a P. aeruginosa nucleic acid, as components of acterial targets, as tragets for antibacterial drugs, acterial targets, as templates for recombinant.

• aeruginosa-derived peptides or polypeptides, as target diagnosis and/or treatment of P. aeruginosa-caused in detection of P. aeruginosa sequences or other sequences species using biochip technology. Sequences ABD01397-ent P. aeruginosa polymucleotides of the invention. Note: ta for this patent did not form part of the printed ov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                          eac acid encoding Pseudomonas aeruginosa polypeptide, targets for diagnostics, prophylaxis and treatment of ions resulting from bacterial infection.
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                                  .; gene; ds; Pseudomonas aeruginosa infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 A; 509 C; 407 G; 205 T; 0 U; 0 Other;
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Matches:
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Mismatches:
Indels:
osa polynucleotide #2955.
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3-0094190P.
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The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa fuels, so templates for recombinant production of P. aeruginosa nucleic sor polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-CABD17967 represent P. aeruginosa polymucleotides of the invention. Note: The sequence data for this patent did not form part of the printed of Specification but was obtained in electronic format from USPFO at
                                 1242
                                                                                                   1302
444
                                                                    464
                                                                                                                                      484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                       1183 ACGCCGATCCGCAAGACCTCCTGGGTGCAGTCCGCGGAGTCCGGCGAGCCGGCGGTCGGC
                                                                                                   1243 geoccecereccecaecrecasseriscarecassescrissaasecricaasecrecaacers
                                                                                                                                   AspMetSerArgGluMetValAsnMetIleIleIleGlnArgGlyPheGlnMetAsnSer
425 ArgArgGluGlyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyProGluPheGly
                                                                    445 LeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnVal
                                                                                                                                                                                                                               LysserValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeuLys 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection; gene; ds; Pseudomonas aeruginosa infection;
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98US-0094190P.
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Oy 325 ASDPHGIVEUPROGINPHESERALAASNPHEVALGIYALGGINPROLEUTHRLEU 324	345 IleGlyThrAspIleGlyLysLeuProSerMetMetProIleGlnThrSerSerGlyAsn	365 SerThrAlaArgAsnGlySerSerThrArgArgTyrSerGlnAspGlyYyProGln	385 GlyAspleuvalAspvalthrilefinrSerGlüGilyLysleuGlüGiyLyslerAsn	405 SerGinValValAspPheTyrAsnileProGeuAlaArgPheThrSerGiuAspGlyLeu 411 GGCCAGTCCAAGGTGCAGGCCAGGTGGTGTGGCGAACTTCGCCAACATCCAGGGCCTG	425 ArgargGluGlyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGLyProGluPheGly 351 AcgccGaTcGcAagaccrccrggGrGcAgrccgcgaagrccgcgacaaccaaccggcgaagrccgcaagrccgaagrccgaagrccgaagrccgaagrccgaagrccgaagrccgaagrccgaagrccgaagrccgaagrccgaagrccaa	Oy 445 LeuProGlyThrSerAsnTyrGlyLySerValAsnGlnLeuGlUThrSerAsnVal 464	465 AspMetSerArgGluMetValAsnMetIleIleIleGlnArgGlyPheGlnM ::	Oy 485 LysSerValThrThralaAspThrMetLeuGlnLysAlaLeuGluLeuLys 501	3UL	ABIL45/4; 27-FEB-2003 (first entry)	DE Pseudomonas aeruginosa biofilm formation-related gene #16. XX XX XW Gene, ds, biofilm formation modulation, biofilm-associated disease, XW Cystic fibrosis, AlDS; middle ear infection, acne, periodontal disease, XW Cystic fibrosis, AlDS; middle ear infection, acne, periodontal disease,	Pseudomonas aeruginosa.	PN W0200285295-A2. XX PD 31-OCT-2002. XX XX	PF 19-APR-2002; 2002WO-US012532. XX PX	XX PA (IOWA) UNIV IOWA RES FOUND. PA (HARD) HARVARD COLLEGE. XX	PI Whiteley M, Bangera MG, Lory S, Greenberg EP; XX DX DX WPI, 2003-075601/07. DR P-PSDB; ABJ18752.	
ed. No.: 3.96e-33 ze: 528.50 rcent Similarity: 45.84% st Local Similarity: 29.21% 20.44%	US-10-009-823A-1 (1-502) x ABD04124 (1-1512) QY. 4 SerLeuPheIleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGlyThrValSer 23	Qy 24 AsnasılleAlaAsnalaAsnThrIleGlyTyrLysGlnGlnGlnValValPheGlnAsp 43	Oy 44 LeuPheSerGlnAspLeuAlaileGlySerThrGlySerGlnGlyProAsnGlnAlaGly 63 :::::::: :: ::	Qy 64 MetGlyAlaGlnValGlySerValArgThrIlePheThrGlnGlyAlaPheGluProGly 83	OY 84 ASISERVALThrAspLeualaileGlyGlyLySGlyPhePheGlnValThrLeuGluAsp 103	•	SLYSGlu 143 : GAACGGC 109	44 ThrLeuGluProIleglnLeuAspPheAsnAspProThrValAlaLysSerProAla 1 	. Oy 163 LysThrSerThrAlaLeuAsnAlaValValAsnLeuGlyAspSerThrAspLysThrGln 182 :::	Qy 183 SerGluAlaAsnProTyrPheAlaLeuLeuGluSerTrpLy8GlyAsnGlyThrProPro 202	1 leserThrSerAshTyrSerTyralaGlnProMetargValTyrAspGlnGlnGlyAsh	Qy 223 SerHisBASDILEThrValTyrPhe85pGlyAlaProSerSerThr 237	Qy 238GlySerLysThrPheGluTyrLeuValAlaMetAsnProSerGluAsp 253	254 GlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPhe 27.	Oy 274 SerSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySer 290 TAS CAPTERCAST	291AlaThrLysAspheuAsnAlaTrpGlnProAlaProLeuVal 30.	

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biofilm
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modulating biofilm formation by ssistance, useful for treatment
  Identifying compound capable of modulating bacteria/bacterial antibiotic resistance, associated disease.
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Claim 1; Page 70; 154pp; English

The invention comprises a method for identifying a compound capable of modulating biofilm formation by bacteria. The method of the invention is useful for identifying a compound capable of modulating biofilm formation by bacteria or modulating bacterial antibiotic resistance. The method of the invention is also useful for diagnosing and treating a subject (especially an immunocompromised human) that is afflicted with a biofilm-associated disease or disorder, such as: oystic fibrosis, AIDS; middle ear infections; acne; periodontal disease; catheter-associated infections; and medical device-associated infections. The present DNA sequence represents a gene that is used in the invention

Sequence 1389 BP; 291 A; 501 C; 396 G; 201 T; 0 U; 0 Other;

	1389	151	98	202	75	16
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	4.29e-33	527.50	45.84%	29.21%	20.40%	60
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

US-10-009-823A-1 (1-502) x ABT14574 (1-1389)

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	4	AGTITCAACATCGGCCTGAGCGGCATCCAGGCGGCCTTTCAACGTCACGTCACCGGC 63
	24	AsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValValPheGlnAsp 43
	64	AACAACATCGCCAACGCCGCCACCGTAGGCTTCAAGCAATCCCGCGCGGAGTTCGCCGAC 123
	44	LeuPheSerGlnAspLeuAlalleGlySerThrGlySerGlnGlyProAsnGlnAlaGly 63
	124	
	64	MetGlyAlaGlnValGlySerValArgThrIlePheThrGlnGlyAlaPheGluProGly 83
•	169	AGCGGCGTGCTCTCGGACGTCTCGCAGATGTTCAAGCAGGGCAACATCGACTCGACC 228
	84	AsnSerValThrAspLeuAlaileGlyGlyLysGlyPheBleGlnValThrLeuGluAsp 103
•	229	
	104	LysValHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAsp 123
•	289	GCGATCAGCTACACCCGCGCCCCCACTACATACCGACAGGATTTCATCGTCGAC 348
	124	ProSerGlyPheThrLeuMetGlySerArglleSerAsnAsnProAsnIleLysLysGlu 143
	349	349 AACAACGGCTACCGCCTGCAGGGCTATGCCGTCGGGCCGAACGGCCAGTTGCAGAACGGC 408
	144	ThrLeuGluProlleGlnLeuAspPheAspAspProThrValAlaLysSerProAla 162
	409	GIGGICACCGACTCAAGGTCAAGGCGCGCGCAGGCGCCGCAGGCACCTCGAGCATC 468
	163	
•	469	CAGCAGTCGTACAACCTCAACTCGACGCTGAAG
	183	SerGluAlaAsnProTyrPheAlaLeuLeuGluSerTrpLysGlyAsnGlyThrProPro 202
•	505	
	203	IleSerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsn 222
	529	TCCGACGCCGTACCTACAACTCGTCCTCTTCGCTGGGCATCTATGACAGCCAGGGCAAC 588

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from base 600001 (Borrelia burgdorferi polynucleotide 1 LOCUS AAX20248 Accession Aax20248
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                                                                                                                      New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease.
                                                                                                                                                                                            AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borralia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borralia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes, epidemic and endemic relapsing
                                                                                                                                                                                                                                                                                                          Sequence 111309 BP; 35956 A; 13151 C; 19075 G; 43117 T; 0 U; 10 Other;
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Matches:
Conservative:
Mismatches:
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WPI; 2003-029926/02.
P-PSDB; ABU22839.
                       Burkholderia mallei
                   drug design; gene
                           WO200277183-A2.
                                                                                                                                            Sequence 1239
         19-JUN-2003
             Prokaryotic
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IlecinleuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThrAla
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Alignment Scores:
Pred. No.:
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(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide, (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway compared for proliferation or that has an activity against a biological pathway in which a proliferation or the the test compound that inhibits expoliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a gene required for required gene or its gene product lies or agene on which the test compound that inhibits spoilferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound,'s activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous mucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. prewnyoliferation in cells other than S. aureus, S. typhimurium, conform part of the printed specification, but was obtained in cell ectronic format directly from WIPO at the print pot the print bot between the print sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                        ds; prokaryotic essential gene; cell proliferation;
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Yamamoto R, Forsyth RA,
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                                                                                                                                                                                                      essential gene #8366
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
ACA26709 standard; DNA; 1239
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Trawick JD,
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1239 137 81 180 105

Length:
Matches:
Conservative:
Mismatches:
Indels:

(1-1239)

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288 ThrglySerAlaThrLysAspLeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeu,307 308 ProGlnPheSerAlaAsnPheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGly 327

Kapur V, Gadgil M; XX XX XX XX XX XX XX XX XX XX XX XX X	Alignment Scores: 2.89e-30 Length: 1209 Pred. No.: 491.50 Matches: 143 Score: 43.95\$ Conservative: 75 Best Local Similarity: 28.83\$ Mismatches: 173 Query Match: 19.01\$ Indels: 105 DB: 12.10-009-823A-1 (1-502) x ADK13720 (1-1209)	10 ThrGlyMetLysT ::: ::: 22 AGCGATTAAACC 30 ASHThrIleGlyT	Oy 50 AlaileGlySerThrGlySerGlnGlyProAsnGlnAlaGlyMalaGlyAlaGlnValGly 69	Oy 109 ArgalaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr 128
Db 732	Qy 438 SerGlyGlyProGluPheGlyLeuProGlyThrSerAenTyrGlyLysLeuSerValAen 457		ADX13720 ID ADX13720 XX AC ADX13720; XX AC ADX13720; XX XX DT 20-MAY-2004 (first entry) XX XX XX XX XX XX XX XX XX XX XX XX XX	Key CDS WO2004018638 04-MAR-2004 21-AUG-2003 21-AUG-2002 (MINU) UNIY (KAPU/) KAPY (GADG/) GADG/)

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WP ABG69245_05 S00001 610000 WP ABG69245_06 600001 710000 WP ABG69245_07 700001 810000 WP ABG69245_09 900001 1010000 WP ABG69245_10 1000001 1110000 WP ABG69245_11 1000001 1210000 WP ABG69245_13 1300001 131000 WP ABG69245_14 1400001 151000 WP ABG69245_15 1600001 171000 WP ABG69245_16 1600001 171000 WP ABG69245_19 1800001 171000 WP ABG69245_19 1800001 171000 WP ABG69245_20 2000001 2110000 WP ABG69245_21 2000001 210000 WP ABG69245_22 2000001 210000 WP ABG69245_24 2400001 210000 WP ABG69245_25 2500001 271000 WP ABG69245_26 <th>Alignment Scores: 3e-27 Length: 110000 Pred. No.: 484.50 Matches: 137 Score: 484.50 Conservative: 77 Best Local Similarity: 27.02% Mismatches: 168 Query Match: 6 Gaps: 11 US-10-009-823A-1 (1-502) x ABQ69245_07 (1-110000)</th> <th>Lyst Lyst 31 yr 56 Gr Ceua 57 T G</th> <th>29983 ACAAACCCATCGGTTCCGGTTCGAAATTGGGGCATTTTAACCGATTATAAC 77 GINGlyalaPheGluProGlyAsnSerValThrAsDLeulalalleGlyGlyLySGlyPhe 96 77 GINGlyalaPheGluProGlyAsnSerValThrAsDLeulalalleGlyGlyLySGlyPhe 96 78 GAGGTTCTCCGACATCAACTGGCAGAAACAAAGATGCAGCACCACAAGGCCGGCGCGCTTT 30 97 PheGlnValThrLeuGluAspLySValHiSTYTThrAspAlaGlyAsnDheArg 11 10103 TTCATTGCTGGCGATAACGCTGGGAGATATCGTTTACACACGAGACGGTAGCTTTGCA 30 115 PheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuWetGlySerArglle 13 115 PheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuWetGlySerArglle 13 115 PheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuWetGlySerArglle 13</th> <th>154 174 3034 3034</th>	Alignment Scores: 3e-27 Length: 110000 Pred. No.: 484.50 Matches: 137 Score: 484.50 Conservative: 77 Best Local Similarity: 27.02% Mismatches: 168 Query Match: 6 Gaps: 11 US-10-009-823A-1 (1-502) x ABQ69245_07 (1-110000)	Lyst Lyst 31 yr 56 Gr Ceua 57 T G	29983 ACAAACCCATCGGTTCCGGTTCGAAATTGGGGCATTTTAACCGATTATAAC 77 GINGlyalaPheGluProGlyAsnSerValThrAsDLeulalalleGlyGlyLySGlyPhe 96 77 GINGlyalaPheGluProGlyAsnSerValThrAsDLeulalalleGlyGlyLySGlyPhe 96 78 GAGGTTCTCCGACATCAACTGGCAGAAACAAAGATGCAGCACCACAAGGCCGGCGCGCTTT 30 97 PheGlnValThrLeuGluAspLySValHiSTYTThrAspAlaGlyAsnDheArg 11 10103 TTCATTGCTGGCGATAACGCTGGGAGATATCGTTTACACACGAGACGGTAGCTTTGCA 30 115 PheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuWetGlySerArglle 13 115 PheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuWetGlySerArglle 13 115 PheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuWetGlySerArglle 13	154 174 3034 3034
Db 499	326 PheGlylleLysSerGlnGlnAsnMetTrpAlaGl		446 ProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAsp 4	RESULT 12 ABG69245 Or 10 of ABG69245 from base 700001 (Listeria innocua DNA sequence #684. Continuation (8 of 31) of ABG69245 from base 700001 (Listeria innocua DNA sequence #684. WP Sequence split into 31 fragments LOCUS ABG69245 Accession Abg69245 WP ABG69245 00 100001 100000 WP ABG69245 01 100001 310000 WP ABG69245 03 300001 410000 WP ABG69245 03 400001 510000

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WP ABG67197_00 1100001 210000 WP ABG67197_01 200001 210000 WP ABG67197_02 200001 310000 WP ABG67197_03 300001 310000 WP ABG67197_04 400001 510000 WP ABG67197_06 600001 510000 WP ABG67197_06 600001 710000 WP ABG67197_06 600001 710000 WP ABG67197_09 900001 110000 WP ABG67197_09 100001 110000 WP ABG67197_01 100001 1100001 110000 WP ABG67197_10 1000001 110000	ignment Scores: 3e-27 add. No.: 784.50 rcent Similarity: 7.02\$ st Local Similarity: 18.74\$	10-009-823A-1 (1-502) x ABQ67197_06 (1-110000) 1 MetMetGlySerLeuPhelleGlyAlaThrGlyMetLysT	21 ThrValSerAsnAsnIleAlaAsnAhaAsnThrIleGlyTyrLysGlnGlnGlnValVal 4 39598 GTGACATCAAATAATATTGCCAATGCGAACACGACAGGTATAAAAAAAA	41 PheGlnAspLeuPheSerGlnAspLeuAlaileGlySerThrGlySer 5 39658 TICAATGATTACTTTACGAAAGGAAGGGATCTGTGGAGGGGGATTTATGCTGA	OY STOLEY FOR THE STATE OF THE	97 PheGlnValThrLeuGluAspLysValHisTyrThrArgAlaGlyAsnPheArg 114 ThrLeuGluAspLysValHisTyrThrArgAlaGlyAsnPheArg 114	Oy 115 PheThrGlnAspGlyPheLeuAshAspProSerGlyPheThrLeuMetGlySerArglle 134	135 SerAsnAsnProAsnIleLysLysGluThrLeuGluProIleGlnLeuAspPheAsnAsp 15	155 ProThrValAlaLysSerProAlaLysThrSerThrAlaLeuhsnalaValValAsnLeu	175 GlyAspSerThrAspLysThrGlnGerGluAlaAsnProTyrPheAlaLeuLeuGluSer 19	Oy 195 TrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyrAlaGlnProMet 214 1:: Db 40105	Oy 215 ArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPheAspGlyAla 233 bb 40108 TCTGTATACGATAATGCTGGGAAAACATAAACTTCAAGTCAATATGAAAGCTGCGACA 40167 Ov 234 ProSerSerThrGlySerLysThrPheGluTyrLeuValAlaMetAsnProSerGluAsp 253	
175 30343 195 30370 215	234 30433 254 30481	Oy 274 SerSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySerAlaThrLys 293 :::::	314 30592	Oy 334 MetTrpAlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLysLeuPro 353	Oy 354 SerMetMetProlleGlnThrSerSerGlyAenSerThrAlaArgAenGlySerSer 373 ::: Db 30631 AACTAC	Db 30649 GTATTCTCACCAACTTCTGACGAAAAGGCGCTGCAACTGTAAAAGACTACGCAGTTAC 30708 Oy 394 SerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValValValAspPheTyrAsnIle 413 10709 GATTPCTCACTTATTATTCAACTTAATTAAAAAAAAAAAA	414 ProlectalaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAshHisTyrSer 433 30769 GCGGTTACTTTCTCCAATGAAGACGCTTAGTCAAATGAGGCGAATGAGAATGAGACGCTTAGTCAAATGAGGCGAATGAAGACGCGTTAGTTCAAAATGACGAATGAAGATCAAATGACGCTTAGTTCAAAATGACGAATGAAA		Qy 454 LeuServalAsnGlnLeuGluThrSerAsnValAspWetSerArgGluMetValAsnMet 473 :::	Qy 474 IleIleGlnArgGlyPheGlnMetAsnSertySSerValThrThrAlaAspThrMet 493 30949 ATGACATACCAAGTGGTTTCCAAGGCAATACAAAGTTATCCGTGTTGCAGTGATGACGTG 31008	Oy 494 LeuGlnLysAlaLeuGluLeu 500 ::::::::::::::::::::::::::::::::::::	SULT 13 267197 06 ntinuation (7 of 12) of ABQ67197 from Sequence split into 12 fragments LOC	WP Fragment Name Begin End

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2	Db 40504 GCGCTTGCTACATGAAGACGCGTTAGTCAAAATGCGCAATAGTT 40563 Oy 434 AlaThrLeuAspSerTGTGTAGTCAAAATGCGCGAATGCCGAATGCTGAAGATGCGGAATGCTGTGGGGGAATGCTGTGGGGGAATGCGGGGGAATGCTGGGGGGAATGCGGGGAATGCGGGAATGCGGGGAATGCGGGGAATGCGGGGAATGCGGGGAATGCGGGGGAATGCGGGGAATGCGGGGAATGCGGGGGAATGCGGGGGAATGCGGGGAATGCGGGGAATGCGGGGAATGCGGGAATGCGGGGAATGCGGGGAATGCGGGGAATGCGGGAATGCGGGAATGCGGGAATGCGGGAATGCGGGAATGCGAAGTGCTTAGGGGGTCAAACGTGAATTAGGGGGTCAAACGTGAATTAGGGGGTCAAACGTGAACTGCTAAACGGGAATTAGGGGGCTAAACGGAATTAGGGGCTCAAAACGTGAATTAGGGGCTCAAAACGTGAATTAGGGGCTCAAAACGTGAATTAGGGGCTAAAACGAAATTAGGGGCTAAAAACGAAACTAGGTTTCCAAGGCAAATTAGGGGAATTAGGGAATTAGGGGAATTAGGGAATTAGGGGAATTAGGGGAATTAGGGAATTAGGGAATTAGGGAATTAGGGAATTAGGGAATTAGGGAATTAGGGAATTAGGGAATTAGGGAATTAGGGAATTAGGGAATTAGGGAATTAGGAATTAGGGAATTAGGAATTAGGGGAATTAGGAAAGTTAGGAATTAGGGAATTAGGAATTAGGGAATTAGGAATTAGGGAATTAGGAATTAGGAATTAGGAATTAGGAATTAGGGAATTAGGAATTAGGGAATTAGGAATTAGGGAATTAGGGAATTAGGAATTAGGGAATTAGG

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31482 GCGGTTGCTACGTTCTCCAATGAAGACGGTTTAGTCAAAATGGGGAAACGGCGAATATGTT 31541 31602 ATTÄGTGGTICTTCCCTÄGÄÄÄGGATCÄÄÄÄGGTÄGÄCTTGTCCGTGÄÄÄTTCGTTÄÄCTTA 31661 414 ProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyrSer 434 AlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGlyLys LeuSerValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMetValAsnMet

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AAV99813 standard; cDNA; 2550 DNA encoding 12-APR-1999 AAV99813; AAV99813
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(first entry)

FlgB; flagellar hook; vaccine; infection; therapy; ulcer; ds. Helicobacter pylori FlgE flagellar hook Helicobacter pylori

Location/Qualifiers

New Helicobacter pylori F1gB polypeptide - useful for inducing protective immune response to H. pylori infection. Disclosure; Page 20-23; 36pp; English 98WO-SE001093 321. .2477 /*tag= a Berglindh T, Mellgard B; WPI; 1999-080888/07 (ASTR) ASTRA AB. P-PSDB; AAW80991 08-JUN-1998; WO9856816-A1 17-DEC-1998

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31304

-----AAACAAGTCAAT 31316

This cDNA sequence codes for Helicobacter pylori FIGE flagellar hook protein (see AAW80991). FIGE cDNA can be cloned from the J99 strain of H. protein (see AAW80991). FIGE cDNA can be cloned from the J99 strain of H. pylori by PorR amplification using primers (see AAV9814-15) specific for the 5 and 3' ends of the open reading frame. The FIGE polypeptide is used in a claimed vaccine, which further comprises an adjuvant (a pharmaceutically as a prophylactic vaccine in mammals (especially husses) infected by H. pylori. It is additionally used to form a composition in the treatment and diagnosis of H. pylori infection, and in eliciting a protective immune response against such infection. Diagnostic kits are formed for diagnosis and detection of H. pylori infection. The polypeptide elicits an immune response towards both the coccoidal and mechanisms locally in the stomach, which is important because systemic immunity only plays a limited role in protection against mucosal

413

433

Sequence 2550 BP; 757 A; 499 C; 607 G; 687 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: 3.57e-29 483.00 37.34% 24.90% Similarity: Percent Similarity: Alignment Scores: Query Match:

US-10-009-823A-1 (1-502) x AAV99813 (1-2550)

493

473

|||::: ||||||::: |||||321 AIGCTTAGGTCTCTTATGGTCTCTGGTTGGATGCAAGCCCACCAAATCGCTTTGGAT 380 440 1 MetMetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20 40 PheGlnAspLeuPheSerGlnAspLeuAlaIleGlySer-----ThrGlySer 56 381 ATTGAGAGTAACAATATTGCGAACGTGAATACCACTGGTTTTAAGTATTCTAGGGCTTCT ThrValSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValVal 41 141 ઠે ద d g à ò

74 94 57 GlnGlyProAsn-----GlnAlaGlyMetGlyAlaGlnValGlySerValArgThrile PheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLys gcaedecaeaarearrrrrcrerecedecrreedecraecedrecareceaceacraaaare 501

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TTTTCACAAGGCAATATCCAAAACACAGATGTCAAAACCGATCTAGCGATTCAAGGCGAT 620 GlyPhePheGlnValThrLeuGluAspLysVal----HisTyrThrArgAlaGlyAsn 112

reponema pallidum. WO9859034-A2 05-MAY-1999 400 2286 2166 2226 440 2346 344 366 380 420 2466 347 347 348 358 AAX20553 8 6 8 6 8 6 8 6 8 ठ हे ठ 음 상 음 ò q g 6 6 6 1385 |||:::::: | ATIATCTTTGTGAGCGGGTATTCTTCAGACAGCGTAACGAACAATGTTTTGTTTAAAAAT 1685 ::: ||| ||| ||| 206 GIGGCGGCTAAAAATGCGATCAAAGCCAAAAGCCAAACAGGCATTGAAGCTTATTA 1265 :::||| | S66 CAATACGGCATGTTTGAAATCAACAATAAAGACAATAAAAATGTCATTAAAGAAAATCTT 1625 |||::: 966 AITAATCCGGIGIATGATTCAGGCACGAATCTIGCTCAAGICGCCGAAGACAIGGGATCT 1025 446 CAGITIAGGACCACIGAAGACITGCGCGCCTTAAICCAGCAIGACGTAATAICATAAA 1505 1506 GATCCTAGCCÍAGCGGACAATTACCAAGACTCAGCCÓCTTCTÁTÁGGAGTTACAATCAAC 1565 740 207 TyralaGlnProMetArgValTyraspGlnGlnGlyAsnSerHisAspIleThrValTyr 229 -----AlaPheThrProThrGlySerAlaThrLys 293 294 AspleuAsnAlaTrpGln----- 305 -----GlyAlaGlyIleGlnProLeuThrLeu 324 AspPheGly-----IleLysSerGlnGln 332 -----AlaGlyAlaProAlaSerAlaAla 343 143 741 GTGAGAAATGGGAGCGATACCGGCAATAAAGGGAGGGATACAGACGCTTTAAAAGTGGAT 800 ThrLeuGluProileGinLeuAspPheAsnAspProThrValAlaLysSerProAlaLys 163 801 AACACCGGTCCTTTAGAAAACATTAGGATTGATCCTGGAATGGTG---ATGCCAGCCAGA 857 230 PheAspGlyAlaPro------SerSerThrGlySerLysThrPheGluTyr 244 LeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGly------Thr 260 |||||||||| ::: ::||||| GGCTTTTTTATCATTAGAGAGATCACGCGCAATTTCACTAGAGATGGGGGA 680 164 ThrSerThr-----AlaLeuAsnAlaValAsnLeuGlyAspSerThrAspLysThr 181 182 GlnSerGluAlaAsnProTyrPheAlaLeuLeuGluSerTrpLys-----GlyAsnGly 199 131 --------GlySerArgileSerAsnAsnProAsnIleLysLysGlu ----GlyLeuProGlnPheSerAlaAsnPheVal---AspSerAlaGlyLeuLeuMetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys 1326 AACATTGTAGTTACTCAAGCCGGAACCGGAGCGTTCGCTAACTTTTAGACGGGGATAAA PheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMet-----200 ThrProProlleSerThrSerAsn-----AsnMetTrp------AsnMetThr------333 1146 245 325 113 144 210 281 261 621 셤 QQ 8 8 ò g 임 ઇ g δ g 8 6 ⋧ g 8 යි සි G · & 셤 6 B 6 점상 . d B & B & ⋩ . Q Š ઠે

||| :::|||||| ::: |GAAGCGTTCAGTAATGGCAGGACTTTAGCGCTCCACTCAAGTGGCTTTAGCGAATTTCGCT 2225 1686 GCGATGAAAGGGCTTAATACCGCTTCTTTAATTGAAGGGGGAGCGTCAGCGAGCAGTTCT 1745 806 CACGCCATGCGCATTGAGTTTTATAGGAGTGGGGGAGCGGATTGGAATTTTAGAGTGATC 1865 1866 GTGCCTGAGCCTGGGGAATTAGTAGGGGGGGCTAGGGCTAGGCCTAATGTGTTTGAAGGA 1925 AspGlyTyrProGlnGlyAspLeuValAspValThrIleThrSerGluGlyLysLeuGln 399 GlyLysTyrSerAsnSerGlnValValAspPheTyrAsnIleProLeuAlaArgPheThr CAAGCCTTAATCGGTGCGGCTAATACGGGGCGTAGGGGTTCAATTTCAGGATCTAAACTG 1926 GGCCGTTTGCACTTCAATAATGACGGATCGCTTGCAGGCATGAACCCGCCTCTTTTGCAA :::||||||| 2106 AACGGCTATCAAGCGGGCGATTTGATGGATGTCCGCTTTGATTCAGATGGGGTGCTTTA -----IleglnThrSerGlyAsnSer GlyProGluPheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeu ----AspileglyLysLeuProSerMetMetPro------ThralaArgAsnGlySerSerSerThrArgArgTyrSer------[||||||| CTTAAGCAA 2474 500 LeuLysArg 502

AAX20553 standard; DNA; 10461 BP. (first entry)

Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds. Polynucleotide sequence from the genome of Treponema pallidum

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1779 ACTGTTCACTATGCCTGTAATTTAGACAAGCGTCTGCCTGAGCTTGCTGCAGATGCGAAC 1720
                                                                                                                                                                                                             GACTTT------CAAGTGTATGATAGTCTTCGGGCAGCAGCATACGTTG 1645
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|111 TCGAACAACTCAGGGATAGCGAACATTAGCACGTCGGGGGGGTGATGGGGGAAGGGGAAAGTTG 1052
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                                                                                                                                                                                                                                                  for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetMetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10461 BP; 2325 A; 3411 C; 2493 G; 2213 T; 0 U; 19 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 ThrGlnAspGlyPheLeuAsnAspProSer---------
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                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 491-497; 1150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biosynthetic products such as enzymes
     98WO-US013041
                                                     97US-0050667P
                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to new Proteus mirabilis polypeptides and polymucleotides. The invention also relates to antibodies against the polypeptides, amethod for producting the polypeptides, amethod of per producting the polypeptides, amethod for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polynucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial accines, as targets for antibacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drags or as bio-control agents for plants. This sequence represents a Proteus mirabilis polymucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                         New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for plants.
                                                                                                                   Proteus mirabilis infection; bacterial infection; antibacterial; immunostimulant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1239 BP; 398 A; 246 C; 262 G; 333 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 4010; 870pp; English.
                                                                                                                                                                                                                                                                           (GENO-) GENOME THERAPEUTICS CORP.
                          BP.
                                                                                               Bacterial polynucleotide #4010.
                          ADF03725 standard; DNA; 1239
                                                                                                                                                                                                                            05-APR-2000; 2000US-00543681
                                                                                                                                                                                                                                                    99US-0128706P.
                                                                       (first entry)
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P-PSDB; ADF07897.
                                                                                                                                                       Proteus mirabilis
                                                                        12-FEB-2004
                                                                                                                                                                               US6605709-B1.
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Alignment Scores:

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353 ProSerMetMetProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSer 372 127 PheThrLeuMetGlySerArglleSerAsn------AsnProAsnIleLysLys 142 462 ::: :::: ||||
463 AGTGCAACCGATAAATGGATATGACTTAACTTGAATTCAGCTGAAGGCTATCGAT 522 LysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGluSerTrpLysGlyAsnGly 199 200 ThrProProlleSerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAspGln 219 LysThrPheGluTyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGly 259 -------GluLeuLysAsnMetThrAlaPheThrProThrGlySerAlaThr 292 293 LysaspleuasnalaTrpGlnProalaProLeuValasnGlyLeuProGlnPheSerala 312 313 AsnPheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGln 332 333 AsnMetTrpAlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLysLeu 352 373 SerThrargargTyrSerGlnAspGlyTyrProGlnGlyAspLeuValaspValThrlle 392 --GGTGCAGGCTTGGTGTAAAAGTATCA 183 AlaileGlyGlyLysGlyPhePheGlnValThrLeuGluAspLys------ValHis 143 GluThrLeuGluProlleGlnLeuAspPheAsnAspProThrValAlaLysSerProAla ::||||||| 336 GATGAAACAGCACCTAAGCTGAAAACTTTACTACCGTTGCTTATAAAGGTTCA-----SerValArgThrIlePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeu GCATTAGCCAAAACTTTAAAGATGGTAGTATCACTACTACTAACGCCCCAACCGATGGTAGTG ATGCGTATTACAGGTTATCCAGTACAAACGTAGACGGTAAAAAAGGG 163 LysThrSerThrAlaLeuAsnAlaValValAsnLeuGly------AspSerThrAsp ThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPheSerSerAsnGly------GGCTCT--916 817

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                                                    The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-listeria vaccines. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from MIPO at ftp, wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                  452
                                                                                                                                                                                                            LysLeuSerValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMetValAsn 472
                                                                                                                                                                                                                                                                                                      MetilellelleGlnArgGlyPheGlnMetAsnSerLysSerValThrThrAlaAspThr 492
                        IleProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyr 432
                                                                                                                  SeralaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; Listeria; food contamination; mutational analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Listeria monocytogenes 4b contig DNA sequence #984
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1210 ATCCTGCAAACACTAGTTAGCATGCGC 1236
                                                                                                                                                                                                                                                                                                                                                                                                     MetLeuGlnLysAlaLeuGluLeuLys 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes ATCC 19115.
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(CNRS ) CNRS CENT NAT
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| S247 GCAATICCAGGAGAAAGGAAAAAGGTAGCTIAAAGGGGTAACATICCACIAGACIGG 5306
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|5568 ATG------GGCTTAAACCTAAGTGGCTTAACC 5594
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                                                                                                                                                                                                                         334 MetTrpAlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLyBLeuPro 353
                                                                               354 SerMetMetProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSerSer 373
                                                                                                                        374 ThrArgArgTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAspValThrIleThr 393
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314 PheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsn 333
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5595 AACTAC-----
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(first entry) 20-NOV-2003

Photorhabdus luminescens nucleotide seguence #6950.

Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; whooping cough; gene; ds.

Photorhabdus luminescens

WO200294867-A2.

28-NOV-2002.

07-FEB-2002; 2002WO-IB003040.

07-FEB-2001; 2001FR-00001659.

(INSP) INST PASTEUR. (CNRS) CNRS CENT NAT RECH SCI.

Danchin A; œ, Frangeul L, Kunst ď, Taourit S, Glaser Duchaud E, Ta Buchrieser C;

WPI; 2003-148459/14.

S. A.

Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.

Claim 2; SEQ ID NO 6950; 1205pp; French

The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. Luminescens and related species, to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of the genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microrganisms other than P. Luminescens and are able to alter response or sensitivity to toxins and antibocics produced by P. Luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes proteins, vectors containing the genes and Ab are also useful are sensitive to P. Luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence facts and for identifying targets of human diseases for which P. Luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. Luminescens genes

Sequence 1215 BP; 342 A; 257 C; 304 G; 312 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	8.58e-27	Length:	1215
Score:	448.50	Matches:	141
Percent Similarity:	40.75%	Conservative:	99
Best Local Similarity:	27.76%	Mismatches:	174
Ouery Match:	17.34%	Indels:	127
DB:	10	Gaps:	17

US-10-009-823A-1 (1-502) x ACF68483 (1-1215)

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10	ThrGlyMetLysThrHisSerThrGlyLeuGlyThrValSerAsnAsnIleAlaAsnAla 29
22	22 AGTGGTTTGAATGCCGCGGCAGGTAATTTGGATGTTATTGGTAATAATATGGCTAACGCG 81
30	30 AsnThrileGlyTyrLysGlnGlnGlnValValPheGlnAspLeuPheSerGlnAspLeu 49
82	eccacataricatritaaarccaccaccatrititcraacatrititcc 132
50	50 AlalleGlySerThrGlySerGlnGlyProAsnGlnAlaGlyMetGlyAlaGlnValGly 69
133	133GGTTCTCAGGTGGGACTGGGGGTAAAAGTATCG 165
70	70 SerValArgThrIlePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeu 89
166	166 GGTGTTAATCAGAATTTTAAAGATGGTACGCCAACGACGACTAACCGAACACTTGATCTG 225
06	90 AlaileGlyGlybvpysGlyPhePheGlnValThrLeuGluAspLysValHisTyrThr 108
226	GCGATCACGCAGGCGGTTTTTTCCGTATGCAAGGCGGTGATGGCGGGATTTATTATTATCC 285
109	109 ArgalaglyasnPheargPheThrGlnaspGlyPheLeuAsnAspProSerGlyPheThr 128
286	
129	129 LeuMetGlyGlu 143
346	TIGACCGGCTATCCCGCTGCCAGCGTCAATGGTGGCGCGCCGCGGAGATCAGAAAGGGGCT 405
144	144 ThrLeuGluProlleGlnLeuAspPheAsnAspProThrValAlaLysSerPro 161
406	406 AACCCAGAGCCAATTACAATACCTCAAGGTATATTGATG 444
162	162 AlalysThrSerThrAlaLeuAsnAlaValValAsnLeuGlyAspSerThrAspLysThr 181

셤 ઠે ద 8 g ò g ò 셤 ACF65378 standard; DNA; 102644 BP.

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949 GTTCTGACTAACTTTGCTAACCCAGAAGGACTGGCAGCGAAGGGGTGATAACGTTTGGGTA 1008
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RESULT 20 ACF65378/c

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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the geneme of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/damplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/damplification of the genes are used for detection/damplification of the genes are used for detection/damplification of arry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibicties produced by P. luminescens. Cells transformed to express the genes are useful for ecombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes proteins, vectors containing the genes and Ab are also useful are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens genes
                                                                                                                                                Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; whooping cough; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic sequence of Photorhabous luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides
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	sp. genomic DNA SEQ ID NO:1 Aba92787
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242 PheGluTyrLeuValalaMethanProSerGlu 242 PheGluTyrLeuValalaMethanProSerGlu 1	2787 3 inuation (4 of 7) of ABA92787 from base 300001 (Buchnera inuation (4 of 7) of ABA92787 from base 300001 (Buchnera equence split into 7 fragments LOCUS ABA92787 Accession ABA92787 1 10000 210000 ABA92787 1 100001 310000 ABA92787 300001 410000 ABA92787 4 400001 510000 ABA92787 5 500001 640681
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310 PheSerAlaAsnPheValGlyAlaGly 72927	imaging; diagnostic jene mapping; gen imaging; diagnostic 217. 3167. 3 YT; gen end encoded poly gene mapping, identi
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The invention relates to isolated polymuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primeras, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving direction normal useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving abbrrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and or oproduce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences. AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the printed specification, but was obtained in the printed specification.
responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                              Claim 1; SEQ ID NO 24700; 103pp; English
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Sequence 1912 BP; 573 A; 501 C; 518 G; 320 T; 0 U; 0 Other;

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                                                                                                        85 SerValThrAspleuAlaIleGlyGlyLysGlyPhePheGlnValThrLeuGluAspLys 104
                                                                                                                                                                                 105 ValHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspPro 124
                                                                                                                                                                                                                                                                                                                                LeuGluProIleGlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThr 164
                                                                                                                                                                                                                                                                                                                                                                                                       SerThrAlaLeuAsnAlaValValAsnLeuGlyAspSerThrAspLysThrGlnSerGlu 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 AlaAsnProTyrPheAlaLeuLeuGlu-----SerTrpLysGlyAsnGlyThrPro 201
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                               65 GlyAlaGlnValGlySerValArgThrIlePheThrGlnGlyAlaPheGluProGlyAsn
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94072 TCAGACCCCAAAAGACTTGTTAGCGAGTATGAAAATTCTTGGGAA-----
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93754 CTTGAAACAGCTCCGGTTGTGGGCAAAATAGGAACA-
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                                                                                                                                                                                                                                                                                                                                                                      94024 TTTAAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bo can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease.
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                                                                                                                           Borrella burgdorferi, spirochete; bacterium, pathogen, Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 910715 BP; 327171A; 129646C; 130753G; 323091T; 0U; 540ther;
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Matches:
Conservative:
Mismatches:
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                                                                                          Borrelia burgdorferi polynucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 157-671; 1128pp; English.
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97US-0053377P.
97US-0057483P.
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358.50
38.39%
22.90%
13.86%
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                                                                                                                                                                                                      Borrelia burgdorferi
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Best Local Similarity:
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22-JUL-1997;
03-SEP-1997;
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                   AAX20248;
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Query Match:
DB:
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                                                                                                                                                                             94774 GGGTCATTTAAAATCGATTCTAATCGAGAGCTTGTAACAAGGCCAAGGATACAAAGTATTG
                                                                                                                                                                                                                                                                          94834 CCTAATATACTCTTCCCAGAAGAATATATCCAAAACTCAATTACAATATCTGAAGAGGA
-SerSerThrArgArgTyrSerGlnAsp
                                                                                                                                                                                                                                       ------TyrProGlnGlyAspLeuValAsp----ValThrileThrSerGluGly
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antibacterial.
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P-PSDB; ABO70969.
AsnGlySer-
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polymocleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polymetride, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa attuges as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target or production of P. aeruginosa-derived peptides or polypeptides, as target infection, and in detection of P. aeruginosa sequences or other sequences of Resudomonas species using biochip technology. Sequences ABD01397-ABD1997 represent P. aeruginosa polymucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html

Sequence 810 BP; 166 A; 299 C; 226 G; 119 T; 0 U; 0 Other; *8888888888888888888888888

Alignment Scores: Pred. No.: Score: Becrent Similarity: Best Local Similarity:	1.35e-15 307.00 30.74% 21.56%	Length: Matches: Conservative: Mismatches:	810 108 46 93
Query Match:	11.87%	Indels:	254
DB:	11	Gaps:	11

US-10-009-823A-1 (1-502) x ABD04540 (1-810)

20	84	0	144
1 MetMetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20	ATGTTATCGGCACTGTGGGTCAGCAAGACCGGTCTGTCCGCCCAGGACATGAACCTGACC	21 ThrvalSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnValVal 40	85 ACCATTTCCAACAACCTGGCCAACGTATCCACCACCGGCTTCAAGCGCGCGC
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204 PheglnAspLeuPheSerGlnAspLeuAlaIleGlySerThrGlySerGlnGlyProAsn 145 iriccadeaccrecateraccadarccedecedecedecedecedecedecade 41

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61 GlnAlaGlyMetGlyAlaGlnValGlySer---ValArgThrIlePheThrGlnGlyAla

94 80 PheGluProGlyAsnSerValThr------AspLeuAlalleGlyGlyLys

113 324 GlyPhePheGlnValThrLeuGluAsp --- LysValHisTyrThrArgAlaGlyAsnPhe 95

134. IleSerAşnAsnProAsnIleLysLysGluThrLeuGluProIleGlnLeuAspPheAsn 153 385 CACCTGAACTCCGACGGGCAGATCGTCACCTCCAACGGCTTCGCCCTG <u>අ</u> 8 432 154; AspProThrValAlaLysSerProAlaLysThrSerThrAlaLeuAsnAlaValValAsn

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LeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGlu 193 GAGCCAGCGATC------433 à 엄 ò

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Disclosure; SEQ ID NO 3144; 455pp; English

194 SerTrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyrAlaGlnPro 213

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Nolling J,

98US-0074788P. 98US-0094190P.

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The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a careferial infection, for evaluating a compound, such as a polypeptide, of for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial dargs, as templates for antibacterial dargs, including anti-P. aeruginosa dargs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-Captesent P. aeruginosa polymucleotides of the invention. Note: The sequence data for this patent did not form part of the printed sequence. The sequence in the patent did not form part of the printed sequence. The sequence capta for this patent did not form part of the printed sequence. The sequence them
                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1545 BP; 226 A; 447 C; 568 G; 304 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 2823; 455pp; English.
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            Pseudomonas aeruginosa.
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P-PSDB; ABO70648.
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27-JUL-1998;
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42 GlnAspLeuPheSerGlnAspLeuAlaIleGlySerThrGlySerGlnGlyProAsnGln 61 MetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGlyThr 1545 107 46 93 254 11 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-10-009-823A-1 (1-502) x ABD04219 (1-1545) 7.66e-15 302.00 30.60% 21.40% 11.68% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: N g ò 셤 ઠે

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Bacterial infection; gene; ds; Pseudomonas aeruginosa infection; antibacterial.

Pseudomonas aeruginosa polynucleotide #2823.

(first entry)

29-JUL-2004

ABD04219

Alignment Scores: 1.2e-14 Pred. No.: 295.00	#35 Learnspace of the control of	충 名
XX SQ Sequence 783 BP; 235 A; 163		면 (
	AArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyrSerAla	ò
therapeutically are sensitive to biopesticides. Factors and for	395 GluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValValAspPheTyrAsnIlePro 414	සි ර
CC antibacterials useful as ins CC acterials useful as ins CC genes, proteins, vectors con	375 ArgArgTyrSerGinAspGiyTyrProGinGiyAspLeuvalAspValinfileiniser 374 	දු දු
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carry a gene-containing modulate, regulate, indu	355 MetMetProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThr 374	ઠે
polypeptides encoded by of P. luminescens, e.g.	1093 1093	ф
	335 TrpAlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLysLeuProSer 354	ò
CC The invention relates to the CC proteins from Photochabdus 1 CC entres of probes and primes	 	유
PS Claim 2; SEQ ID NO 6948; 120	1099 1099 1099 1099 1099	a (
PT Genomic sequence of Photorha PT useful e.g. as therapeutic a	LeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPhe	ò
DR WPI; 2003-148459/14.	1099 1099	q
PI Duchaud E, Taourit S, Glass PI Buchrieser C; xx	275 SerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySerAlaThrLysAsp 294	ઠે
(INSP) INST PASTEUR. (CNRS) CNRS CENT NAT RE	255 SeralaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPheSer 274 1113ACCAACGTTCACC 1099	& E
PR 07-FEB-2001; 2001FR-00001659	1128	q
AA PF 07-FEB-2002; 2002WO-IB003040	235 SerSerThrGlySerLysThrPheGluTyrLeuValAlaMetAsnProSerGluAspGly 254	ò
AA PA 28-NOV-2002.	1129 1129	셤
AA WO200294867-A2.	215 ArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPheAspGlyAlaPro 234	ò
XX OS Photorhabdus luminescens.	'	급
KW antibiotic; biopesticide; vi	1129 1127 1129 1127 1129 1129 1129 1129 1129 1129 1129	දු ද
	GlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGluSer	ò
Photorhabdus	1137 CCAGCGATC 1129	q
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906 GCCCAGAA	1245 TTCTTCCAGGTCCTGCTGCCACGGCACGGCACCGTGCCTACACCCGCGACGGCAGCTTCCAC 1186	음 전
Qy 455 SerValAsnGlnLeuGluTi		ć

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tes to the isolation of genes and their encoded brhabdus luminescens. The isolated sequences are ning primers for detecting the genome of P. luminescens; to study polymorphisms; for gene analysis and for their of the genes. Antibodies (Ab) raised against the day the genes are used for detection/identification e.g. in foods. The genes, proteins, Ab and cells that induce or inhibit expression of the genes in plants, anisms other than P. Luminescens and are able to altervity to coxins and antibiotics produced by P. transformed to express the genes are useful for ion of the proteins, particularly toxins and infection by bacteria or fungities. The setors containing the genes and Ab are also useful intection by bacteria or fungities. Intent microbial infection by bacteria or fungit hat luminescens-encoded toxins or antibiotics) and as ruses of the genes and the proteins are as virulence intifying targets of human diseases for which P. this one of the isolated P. luminescens genes
   474
                            de; insecticide; polymorphism; genetic analysis; expression; plant; animal; microorganism; toxin; de; virulence factor; disease model; plague; ds.
455 SerValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMetValAsnMetIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               otorhabdus luminescens and encoded polypeptides,
utic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glaser P, Frangeul L, Kunst F, Danchin A;
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374 ThrargargTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAspValThrIleThr 393 | | | | ::: | | | | | | | ::: 42 ------GACCTCACCATTAGC 456

29971 GGCAGATTGTGGAACGAAGTGGTGCGTGCAAAGTAG 201	229 rpheaspdlyalaproser	yy 251 rGluAspGlySerAlaAlaSerGlyThrAspSerAl 	263 a-GlyLeuLeuMetSerGlyThiMetThrPheSerSerasn 	282	287 roThrGlySerAlaThrLySAsp29533 gAACCTATGCTTATACCGGGACGATGGTT	303	318 29413	29408	<pre>// 358 leClnThrSerSerThrAlaArgAshGlySerSerserinfArgAshGlyTs //</pre>	yy 378 erGlnAspGlyTyrProGlnGlyAspLeuValAspValThrIleThrSerGluGlyLySr 	y 398 euGlnGlyLysTyrSerAsnSerGlnValValAspPheTyrAsnIleProLeuAlaArgP	418	N 438 erGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnG	y :458 InLeuGluThrSerasnValaspMetSerargGluMetValasnMetIleIleIleGlna	y 478 rgGlyPheGlnMetAsnSerLysSerValThrThrAlaAspThrMetLeuGlnLysAlaL
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US-10-009-823A-1 (1-502) x AAT67783 (1-816)

DB:

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AAT67783 standard; DNA; 816 BP

AAT67783;

29-JUL-1997 (first entry)

H. pylori flagella associated protein ORF 29298130.aa.

Vaccine, prevention, treatment, infection, identification, binding compound; bacterium, life cycle, activator, bacteria, inhibitor, duodenal ulcer disease, chronic gastritis, diagnosis, flagella, associated, flagellum, ds.

Helicobacter pylori

Location/Qualifiers 1. .816 /*tag= a

WO9640893-A1

19-DEC-1996

96WO-US009122. 06-JUN-1996; 95US-00487032 96US-00630405 07-JUN-1995; 01-APR-1996;

(ASTR) ASTRA AB.

Mellgaerd BL; Smith D, Berglindh OT,

WPI; 1997-052306/05. P-PSDB; AAW20373.

Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.

Claim 1, Page, 1481pp; English.

The present sequence encodes a Helicobacter pylori flagella associated protein. The protein may be used in a vaccine to prevent or treat H.

Dyori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homelogy to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts. Note: This DNA sequence is not reproduced in the specification and has been derived from the related specification, W09719098

Sequence 816 BP; 237 A; 199 C; 183 G; 197 T; 0 U; 0 Other;

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arity: 28.68%	,,,,,,	4.65e-14	Matches:	CO)	
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ઠે	21 T	ThrValSerAsnIeAlaAsnAlaAsnThrlleGlyTyrLysGlnGlnGlnValVal 4	0
Q	88 A	ccacticaaacaacaicgccaaigtcaaiaaccacceeerriaaaaaarctcececeer 1	47
ò	41 —	PheGlnAspLeuPheSerGlnAspLeuAlalleGlySerThrGlySerGlnGlyProAsn (0
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δ	61 -		4.
ΩÞ	208 T	TATCGCCAGATGGCATGGAAGTGGGCCTTGGCGTACGCCCTAGTGCGATTACCAAAATG 2	63
ò	75 P	PheThrGlnGlyAlaPheGluProGlyAenSerValThrAspLeuAlaileGlyGlyLys 5	94
qq	268 T		327
ò	95 6	GlyPhePheGlnValThrLeuGluAspLysValHisTyrThrArgAlaGlyAsnPhe 1	13
Ωp	328 G	-ti	387
ò	114 A	ArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMetGlySerArg	133
a a	388 A		438
à	134 I	IleSerAsnAsnProAsnIleLysLysGluThrLeuGluProIleGlnLeuAspPheAsn 1	153
Dp	439 -	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	453
Š	154 A	SpProThrValAlaLysSerProAlaLysThrSerThrAlaLeuAsnAlaValAsn	173
Dp	454 -		477
ģ	174 L	${\tt AspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGlu}$	193
ф	478 A		483
ò	194 S	erTrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyrAlaGlnPro	213
셤	483 -		483
ò	214 M	ValTyrAspGlnGlyAsnSerHisAspIleThrValTyrPheAspGlyAla	233
gg	484 -	GTGGATGGCACG	495
ò	234 P	sThrPheGluTyrLeuValAlaMetAsnProSerGluAsp	253
QC	496 G		507
ζō	254 G	laAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPhe	273
qq	507 -		507
È	274 S	erSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySerAlaThrLys	293
qa	507 -		507
È	294 A	spLeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuProGlnPheSerAlaAsn	313
qu	507 -		507
ò	314 F	PheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsn	333
QQ Q	507 -		507
δ	334 N	MetTrpAlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLySLeuPro	353

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114 ArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMetGlySerArg 133
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ThrvalSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValval

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-------GlnAlaGlyMetGlyAlaGlnValGlySerValArgThrIle

113 387 438

AspProThrValAlaLysSerProAlaLysThrSerThrAlaLeuAsnAlaValValAsn 173

------ACTTAAATC-----ACTTTA----

GlyPhePheGlnValThrLeuGluAsp---LysValHisTyrThrArgAlaGlyAsnPhe

PheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLys

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The present sequence encodes a Helicobacter pylori flagella associated protein, which was found to be homologous to flagellar basal body rod protein, which was found to be homologous to flagellar basal body rod corresponding following BLAST protein analysis. H. pylori has been strongly linked to chronic gastrifis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators of hubbitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The mucleic acid sequences, and corresponding proteins, are also useful for generating vaccines for immunising subjects against H. pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and conduct a median size of 2000 bp. Purified DNA fragments were bluntened and ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker adapter inserts were ligated to each of the 20 pWPX vectors to construct a series of shotgun subclone libraries. The purified DNA concatements has obtained from the related specification, W09640893
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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434 AlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGlyLys 453 999 667 İTAAGGCAAGGCTTTİTGGAGCTTAGTAACGTCAGATTGGTAGAAATGACAGATCTA 726 413 433 LeuServalAsnGlnLeuGluThrSerAsnvalAspMetSerArgGluMetValAsnMet 473 354 SerMetMetProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSerSer 373 374 ThrArgArgTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAspValThrlleThr 393 214 MetArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPheAspGlyAla 233 ------GTGĠÀŤĠĠĊACG 495 234 ProserserThrGlySerLysThrPheGluTyrLeuValAlaMetAsnProSerGluAsp 253 GlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPhe 273 274 SerSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySerAlaThrLys 293 294 AspLeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuProGlnPheSerAlaAsn 313 MetTrpAlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLysLeuPro 353 394 SerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnvalValAspPheTyrAsnIle 414 ProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyrSer 547 ACTITIGGCIAATITIGICAATCCGGCGGGCTTCATTCTATGGGGGATAATTTGTTTTCC 314 PheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsn ilellelleginargGlyPheGlnMetAsnSerLysSerValThrThrAlaAspThrMet 194 SerTrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyrAlaGlnPro LeuGlnLysAlaLeuGluLeuLysArg 502 crecahacagreantrecerchahacee 813 196 GTGAGCGTGACT-------------ATCGGT-474 787 508 494 478 483 254 207 507 507 507 507 484 507 507 셤 qq ద g ठ ò ð 8 8 6 8 8 8 8 合 8 셤 ⋧ 8686 \$ 8 \$ 셤 ò ď 8 6 8 8

AAT68116 AAT68116 ID AAT6 XX AC AAT6 XX

RESULT 31

AAT68116

(first entry) 16-JUL-1997 pylori flagella-associated membrane protein ORF 12ge20305orf11.

Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope; membrane; flagella; ds.

Helicobacter pylori.

Location/Qualifiers

/*tag= a /note= "no stop codon given in sequence"

WO9640893-Al

19-DEC-1996

96WO-US009122. 1996;

95US-00487032. 07-JUN-1995; 01-APR-1996;

(ASTR) ASTRA AB.

BĽ; Mellgaerd Smith D, Berglindh OT,

WPI; 1997-052306/05. P-PSDB; AAW20863.

Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.

Claim 1; Page 909; 1481pp; English.

The present sequence encodes a Helicobacter pylori flagella-associated comembrane protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial CC from overlapping contigs generated by computer sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify CC likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant compounts of the known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in B. coli hosts

Sequence 837 BP; 240 A; 201 C; 186 G; 210 T; 0 U; 0 Other;

837 107 339 109 254 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 4.8e-14 288.00 28.68% 21.02% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. No.:

US-10-009-823A-1 (1-502) x AAT68116 (1-837)

1 MetMetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly ò 용

ACCACTICABACAACAICGCCAAIGICAATACCACGGGGITIAAAAAAICTCGCGCGGAI 171 40 21 ThrValSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTVrLysGlnGlnGlnValVal

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41 PheGlnAspLeuPheSerGlnAspLeuAlaileGlySerThrGlySerGlnGlyProAsn 60	Db 532
	Oy 414 ProLeualaargPheThrSerGluaspGlyLeuargan
PheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLys	Oy 434 AlaThrLeuAspSerGlyGlyProGluPheGlyLeuP:
TTTTCGCAAGGCAGCCCTRAAGAAACGGAGAAATAATTTAGATATTGCTATTACAGGTAAA 35 GlyPhepheGlnValThrLeuGluAspLysValHisTyrThrArgAlaGlyAsnPhe 11 [Qy 454 LeuSerValAsnGlnLeuGluThrSerAsnValAspMe
114 ArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMetGlySerArg 133 114 ArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMetGlySerArg 133 115	Oy 474 IleIleIleGlnArgGlyPheGlnMetAsnSerLyS6
itysgluthrieuglubrolleglnieuAspPheAsn	Oy 494 LeuGlnLysAlaLeuGluLeuLysArg 502
AspProThrValAlaLysSerProAlaLysThrSerThrAlaLeuAsnAlaValValAsn	RESULT 32 ADF03653 ID ADF03653 standard; DNA; 798 BP. XX
ProTyrPheAlaLeuLeuGlu	AC ADF03653; XX DT 12-FEB-2004 (first entry)
194 SerTrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyrAlaGlnPro 213	Bacterial polymucleotide #3938.
507	KW Proteus mirabilis infection; bacterial infection KW immunostimulant; gene; ds. xx
214 MetargvalTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPheAspGlyAla 233	OS Proteus mirabilis. XX XX TREFARENO.B
	XX PF 05-APR-2000; 2000US-00543681.
254 GlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPhe 273	XX PR 09-APR-1999; 99US-0128706P. XX
531 531	PA (GENO-) GENOME THERAPEUTICS CORP. XX
274 SerSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySerAlaThrLys 293	PI Breton GL;
531 531 531 531 531 531 531 531	DR WPI; 2003-895291/82. DR P-PSDB; ADF07825. xx
	New Proteus mirabilis polypeptides and reagents for diagnosis of bacterial dis
314 PheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLyșSerGlnGlnAsn 333	
531 531	PS Disclosure, SEQ ID NO 3938; 870pp; English.
334 MetTrphlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLysLeuPro 353	CC The invention relates to new Proteus mirabilis CC polynolectides. The invention also relates to CC polynoatides methods for invaling the nolynoatides methods for invaling the nolynoatides.
SerMetMetProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSer	CC generating vaccines for immunished an individual CC method for evaluating a compound for the abilit
531 531	CC polypeptide and a method for screening test com CC activity. The polypeptides and polynucleotides
374 ThrArgArgTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAspValThrIleThr 393	CC resulting from bacterial infection, as reagents CC besulting from bacterial infection, as reagents CC bacterial diseases, as components of antibatter.
	CC for antibacterial drugs or as bio-control agent CC sequence represents a Proteus mirabilis polynuc
394 SerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValValAspPheTyrAsnIle 413	

lis polypeptides and to antibodies against the ypeptides, a method of didual against P. mirabilis, a illty to bind a P. mirabilis, a compounds for anti-bacterial des are useful as molecular ting pathological conditions ents for diagnosis of cterial vaccines, as targets gents for plants. This ynucleotide of the invention. | |||::: |PACGTGATCGGG-----CAAATC 570 ServalThrThrAlaAspThrMet 493 ProGlyThrSerAsnTyrGlyLys 453 |||| ::: |CCGGATTCTCAAGGCTTAGGCAAG 690 MetSerArggluMetValAsnMet 473 ::: |||||| ::::::
ATTGGTAGAAGAAATGACAGATCTA 750 cleotides, useful as as components of cterial drugs, or as ion; antibacterial;

SQ Sequen	quence 798 BP; 233 A; 163 C; 189 G; 213 T; 0 U; 0 Ot	her;
Alignment S Pred. No.: Score: Percent Sim: Best Local (Query Match DB:	nnt Scores: 6.55e-14 Length: 798 Vo.: 286.00 Marches: 100 Similarity: 30.57* Conservative: 55 cal Similarity: 19.72* Mismatches: 98 Aatch: 11.06* Indels: 254	
US-10-009-8	09-823A-	
8 6	1 MetMetGlySerLeuPheileGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly	erThrGlyLeuGly 20 :: ::
	,	•
<i>장</i> 옵	21 ThrvalSerAshashideAlaAshalashashashartilediyiyyydindindindarval 	inginginyalyal 40 :: :: :cccAGcGTGCGGTT 135
ð	41 PheGlnAspLeuPheSerGlnAspLeuAlalle	ilySerThrGlySer 56
11.	:::	 CATCCGAGCAGACG 195
λo	57 GlnGlyProAsnGlnAlaGlyMetGlyAlaGlnValGlySerValArgThrll	74
Db 1	96	GGACAGAACGITTA 255
ò	75 PheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyUyB	MaileGlyGlyLys 94
Db 2	99	SCTATCAAAGGGCAA 315
ò	95 GlyPhePheGlnValThrLeuGluAspLysValHisTyrThr	TyrThrArgAlaGlyAsnPhe 113
33	 TTCCATGTTCAATTACCTGATGGTACGGATGCT	Greatecterri 375
Qy 1	114 ArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMetGlySerAr;	9 13
DÞ 3	376 CAAATGGACCAAAATGGGCAACTAGTGACCTCCAGTGGCTTTCAA	ATCGTCCCAGCG 432
oy 1	34 IleSerAsnAsnPro	AspPheAsn 15
Db 4	433ATTATTTTGCCAGAAACCGCTAAAAAGGTGATGGTA	ATGGTA 468
0y 1	54 AspProThrValAlaLysSerProAlaLysThrSerThrAl	aLeuAsnAlaValValAsn 173
Db 4	468	468
Oy 1	174 LeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAl	pheAlaLeuLeuGlu 193
Db 4	468	468
Oy 1	194 SerTrpLysGlyAsnGlyThrProProlleSerThrSerAsnTy	rSerTyrAlaGlnPro 213
Db 4	468	468
ο _γ	214 MetArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrVal	ч.
Db . 4	469GGTCGTGATGGTATTGTCAGTGT	GGAGATTGAAGGATCG 507
δ δ	erSerThrGlySerLysThrPheGluTyrLeuValAl	aMetAsnProSerGluAsp 253
Db S	508 CCTGCA	513
0y 2	254 GlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSer	GlyThrMetThrPhe 273
qq	513	513
δ,	274 SerSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThr	GlySerAlaThrLys 293
Dp 92	513	513
2	294 AspLeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuProGlnPhe	GlnPheSerAlaAsn 313

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	ిం	314 PheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsn 333
	d d	
	ò	334 MetTrpAlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLysLeuPro 353
	Д	520CAAGTAGGGCAATTA 534
C [2]	ò	354 SerMetProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSer 373
	q 0	534
ACAACTAACATGGAT 75	ò	374 ThrargargTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAspValThrIleThr 393
	අු	
	ò	394 SerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValValAspPheTyrAsnIle 413
	qa	
	ò	ProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyrSer
	ор	
	8 8	434 AlamhrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGlYVs 453
: :TGCTATCAAAGGGCAA 315	8 8	
	i 8	
	λο	474 ilellellaglnArgGlyPheGlnMetAsnSerLysSerValThrThrAlaAspThrMet 493
<pre>irLeuMetGlySerArg 133 ir::: :::::</pre>	යි	
AATCGTCCCAGCG 432 LeGlnLeuAspPheAsn 153	ò	LeuGlnLysAlaLeuGluLeu
:: ::: rganggra468	셤	775 TTACAGAAACTCACGCAACTC 795
ValValAsn	RESULT AAZ8855	LT 33 8552 AA288552 standard; DNA; 1800 BP.
468	XX	
yrPheAlaLeuLeuGlu 193	X	04-MAY-2000 (first entry)
468	XX MX	lgF and f
yrSerTyrAlaGlnPro 213	XX	r.
468	Z & X	
alTyrPheAspGlyAla 233	SO	Campylobacter jejuni.
IGGAGATTGAAGGATCG 507	E 5	Key Location/Qualifiers
etAsnProSerGluAsp 253	: E	
513	r F	/product= "ilgr" 9421733
erGlyThrMetThrPhe 273	EE	/*tag= b /product= "flgg"
	×	US6020125-A.
hrGlySerAlaThrLys 293	X & I	01-FEB-2000,
513	PF	07-JUN-1995; 95US-00483857.
roGlnPheSerAlaAsn 313	# H	08-MAY-1995; 95US-00436748.
Trans	> *** * *****	
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P-PSDB; AAY51376, AAY51377 (CONN-) CONNAUGHT LAB LTD WPI; 2000-146875/13. Louie H,

Recombinant basal body rod protein producible by a transformed host for use in immunological vaccine compositions for in vivo administration to protect against diseases caused by bacterial pathogens.

Claim 1a; Col 15-20; 28pp; English

This invention describes a novel recombinant basal body rod protein (I) producible by a transformed host containing an expression vector comprising a nucleic acid selected from; (a) an entire nucleic acid sequence of 1800 base pairs (bp), or the nucleic acid sequence of the FigF gene having 810 bp, both given in the specification; (b) a nucleic acid sequence, given in the specification; (c) a nucleic acid sequence acid sequence of the FigF protein, a 270 residue sequence, given in the specification; (d) a nucleic acid sequence according a functional FigF basal body rod protein of a flagellum of a protein of (ampylobacter; or (d) an immunogenic fragment of an FigF protein of (a), (b) or (c), and expression means operatively coupled to the nucleic acid molecule for expression means operatively coupled to the nucleic acid molecule for expression means operatively coupled to protein of a flagellum of a strain of Campylobacter. (I) is useful in immunological vaccine compositions for in vivo administration to protect against diseases caused by bacterial pathogens that produce basal body of monosasays, or for procedures for the detection of antibacterial, campylobacter, basal body rod protein and/or peptide antibodies. The product of the invention has immunostimulatory activity. This sequence encodes the Campylobacter jejuni flgF and flgG proteins described in the method of the invention

Sequence 1800 BP; 636 A; 251 C; 363 G; 550 T; 0 U; 0 Other;

221 ATTGCAGATTTTAAAAGAATTTTTAAAGAAACTCAGGATGAGTTGCCTATAGAAAATCAC 280 281 ACAAGAGATGCATCTCGTTTTGTAAATACTACAATAGATGGAATCCCACAAGTTCTCAA 340 341 GAATATÁCGGATTTTAGCCTAGGTTCTTTAAAGGCCACAÁACAATCCTTTGGÁTTTGGCA 400 109 ArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr 128 101 ATGCAAAATGGATATTATCAAGCAACTGGCGGAATGGTAACTCAGTTTAATAAACTTGAT 160 91 IleGlyGlyLysGlyPhePheGlnVal-----ThrLeuGluAspLysValHisTyrThr 108 41 -----PheglnAspLeuPheSerGln-----AspLeuAlaIleGlySer-- 53 71 ValArgThrIlePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAla 90 1 MetMetGlySerLeuPheIleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20 -----ThrGlySerGlnGlyProAsnGlnAlaGlyMetGly---AlaGlnValGlySer 70 21 ThrValSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValVal 1800 133 94 228 136 22 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-10-009-823A-1 (1-502) x AAZ88552 (1-1800) 4,18e-13 281,50 38,41% 22,50% 10,89% Percent Similarity: Best Local Similarity: Alignment Scores: 54 Query Match: DB: g ઠે ò d à ò a ద g 8 ò

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Д	461 AAAG	AAAGATGGAAATTTTCAACTTGATGATGAGGTTATTTGGTAAATAAGCAAGGATACAAG 520
ò		LeuMetGlyserArgIleSerAsnAsnProAsn139
QQ	521 GTAT	:: TAAGTAGTATTTTTAATAATCCTCAGAATGCTGGCATACGCATTCCTAATAGT 580
ò	13,9	139
셤	581 GCTGTT	TTCAAATTAGCGTTGATAAAAACGGAAGCATTGAAGTTGATGGAGCTCAAAATGCA 640
አ _. . զ	140 641 AGATTA	IleLysLysGluThrLeuGluProlleGlnLeuAspPheAsn 153 ::: :: :: :: :: TATTTGTAGGAGATAATGTC 700
ò	154	AspBroThrValAlaLysSerProAlaLysThrSerThrA
ДQ	701 TATA	
ζ		ValValAsnLeuGlyAspSerThrAspLysThrGlnSer
đ	761 GGTT	ti
රු සි	186 AsnP1 821 AAC	<pre>roTyrPheAlaLeuLeuGluSerTrpLysGlyAsnGlyThrProProlleSerThr 205 ::::: ::::: :::::AGAATGGTAGAAATGTATCAAAAGTTATGACAGCTCATATGGATGAC 871</pre>
ò	206 SerA	SerAsnTyrSerTyrAlaGlnProMet 214
q _O	872 TTAA	 TTAAATCAAGAAGCTATCAATAAGCTTGCAGCTGTTAAATAATTAAATAAA
ර යි	215 ArgV : 932 AGGA	ArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPheAspGlyAlaPro 234 :: :: :: 34 AGGATTAAAAATGATGAGATCACTTCATACTGCTGCTACAGGAATGGTAGCGCA 985
ò		erThrGly-SerLysThrPheGluTyrLeuValAlaMetAsnProSerGluAspGl 254
q _Q		
δλ	254 ySer	ySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGl 269
οp	1040 TTT	AAGAAAAGTCGCGCAGAATTTGCTGATCTTATGTATCAAGTTATGAAGTATGCAGG 1099
δ	>-	LysAsnMetThrAlaPheThrProThrGl 289
qq	4	TCTTTCTCCTTCGGG 11
ò	289 yser	SeralaThrLysAspLeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuProGl 309
do .	1136 TATAGAA	GAA
ò	309 nPhe	SerAlaAsnPheValGlyAlaGlyIleGlnProLeuThrLeu 324
q _O	1143	GTGGGTGTGGGTGTGCGTCCAACAGCGGTAACTAAAGTTTTTAC 1186
δ,	325 -Aspl	-AspPheGlyIleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAlaSerAlaAlaAl 344
дд	1187 TGAAG	GGAAATTTAAAATCACAACAAGTACTGATGGTCTTGATATGGCTATTGCAGG 1240
ŏ	344 alle	GlyThrAspileGlyLySLeuProSerMetMetProlleGlnThrSerSerGlyAs 364
qq	1241 TAATO	GGGTTTTTTCAAATACAACTTCTGATGGCACTATAGGATATACTAGAAATGGGCA 1300
ò	364 nSer	ThralaArgAsnGlySerSerSerThrArgArgTyrSerGlnAspGlyTyr 382
qq	1301 ATTT	ATTTACAAAAGATAATGAAGGTAATATTGTAAATTCAGATGGTTATAGACT 1351
ò	383	
qq	1352 TTTA	cctgaaatgacaatacctgaaggcgcaacagcaattaatgttgctacagatgg 1408
ò	396 y	ybysLeuGlnGlyLysTyrSerAsnSerGlnValValAspPheTyrAs 412
qq	1409 AACC	STITCTGTAATGCTACCAGGGGGGCAACAAGAAGTCAAATTGGCCA 1459

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food pupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
                               1519
                                                                                               1579
                                                                                                                                                                                                                     432
                                                                                                                                472
                                                                                                                                                                                                nMetilellelleGlnArgGlyPheGlnMetAsnSerLysSerValThrThrAlaAspTh 492
                     1520 TCTTGAAACAGGAGCAAGTGGTGCACCTGTTGCGGGTATAGCAGGACAAGATGGGCTTGG
                                                                                                                                                              1580 AACAATAAGACATGGATTTATAGAACTTAGTAATGTTCAGCTTGTTGAAGAAATGACAGA
                                                                                                                                452 yLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMetValAs
   nlleProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTy
                                                               432 rSerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       novel human diagnostic protein #24222.
                                                                                                                                                                                                                                                                                        1700 TATGCTAGGAATTGTAAATCAGCTTAAGCGA 1730
                                                                                                                                                                                                                                                                   492 rMetleuGlnLysAlaLeuGluLeuLysArg 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 24222; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                    AAS88418 standard; cDNA; 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-00540217
2000US-00649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-2002, (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; ABG24231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1386 THGTGAAGACCGGGAT------AATAACTGGCAGGTCTACACCCCAGGAT 1342
                                                                                                                                                                                                                                                                                                                                                                                                                             325 AsppheGlyIleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAlaSerAlaAlaAla 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 IleGlyThrAspileGlyLysLeuProSerMetMetProlleGlnThrSerSerGlyAsn 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerThralaargasn---GlySerSerSerThrargargTyrSerGlnaspGlyTyrPro 383
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 responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AASG4197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this spetent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the Campylobacter flgFG operon of the invention. The encoded flgF and flgG proteins are basal body rod proteins of the flagellum of the Campylobacter. The nucleic acid and host cell containing it, are useful for the recombinant production of Campylobacter, especially C. jejuni, basal body rod proteins. This bacterium is the especially C. jejuni, basal body rod proteins. This bacterium is the produced can be used to raise antibodies, which in turn can be used to produced can be used to raise antibodies, which in turn can be used to Additionally, the peptides, and specifically the live vectors (e.g. poxor vaccinia virus) can be used as vaccines against the bacterium, and the antibodies can be used for passive immunisation. The nucleic acids can also be used to detect the presence of the bacterium
                                                                                                                                                                                                                                                                                                                                DNA encoding Campylobacter flagellum basal body rod proteins - useful for recombinant production of the proteins for use as vaccines against the bacterium, and for its detection, additionally with antibodies raised
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 ThrValSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 GTGATTACTAATAATCTTGCCAATATCAATACAAGTGGATATAAAAGAGATGATGTGGTT
          FlgFG operon; flgF protein; flgG protein; basal body rod protein; flagellum; secretory diarrhoea; enteritis; vaccine; therapy; ds.
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Matches:
Conservative:
Mismatches:
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                                                                    Location/Qualifiers
                                                                                       /*tag= a /product= "flgF" 942. .1733 /*tag= b /product= "flgG"
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277.50
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P-PSDB; AAW73072, AAW73073.
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                                            Campylobacter jejuni
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                                                               281 ACAAGAGATGCATCTCGTTTTGTAAATACTACAATAGATGGAATCCCACAAGTTTCTCAA 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                          461 AAAGATGGAAATTTTCAACTTGATGATGAGGGTTATTTGGTAAATAAGCAAGGATACAAG 520
                                                                                                                                                                                                                                                                 IleGlyGlyLysGlyPhePheGlnVal-----ThrLeuGluAspLysValHisTyrThr 108
                                                                                                                                                                                                                                                                                                                                                                                                       ArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr 128
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AGGATTAAAAATGATGAGTCACTTCATAC-----TGCTGCTACAGGAATGGTAGCGCA 985
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-----ThrGlySerGlnGlyProAsnGlnAlaGlyMetGly---AlaGlnValGlySer
                                                                                                                                                                                                                                                                                                           ::: ||| ::: ||| 401 ATGACTAGABABATGGAAGATTAGATCAGACCAAAGATGAGAAGTAAGATTAACC
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|------AGAATGGTAGAAATGTATCAAAAAGTTATGACAGCTCATATGGATGAC
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|||| | 1241 TAATGGGTTTTTTCAAATACAACTTCCTGATGGCACTATAGAAATGGGCAATTTACAAAA 1300 1380 -GCAACAGCAATTAAIGTIGCIACAGAIGGAACCGITICTGIAAIGCTACCAGGGGAGCA 1438 1490 GGGTCTTCATCTATGGGTGATAATCTTTATCTTGAAACAGGAGCAAGTGGTGCACCTGT 1549 1550 TGCGGGTATAGCAGGACAAGATGGGCTTGGAACAATAAGACATGGATTTATAGAACTTAG 1609 354 rMetMetProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSerTh 374 -----ProGlnGlyAs 386 386 pLeuValAspValThrIleThrSerGluGly------LysLeuGlnGlyLysTy 402 rSerAsnSerGlnValValAspPheTyrAsnIleProLeuAlaArgPheThrSerGluAs 422 422 pGlyLeuArgArgGluGlyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyProGl 442 442 uPheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSe 462 rAsnValAspMetSerArgGluMetValAsnMetIleIleIleGlnArgGlyPheGlnMe 482 482 tAsnSerLysSerValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeuLysAr 502 Recombinant basal body rod protein producible by a transformed host for use in immunological vaccine compositions for in vivo administration to protect against diseases caused by bacterial pathogens. immunogen; Basal body rod protein; flgG; flagellum; vaccine; pathogenic bacteria; detection; antibacterial; ss. 1301 GATAATG -----AAGGATAATGAAGGTAATATTGTA-374 rArgArgTyrSerGlnAspGlyTyr----AAZ88554 standard, DNA; 789 BP. 95US-00483857 95US-00436748 04-MAY-2000 (first entry) (CONN-) CONNAUGHT LAB Campylobacter jejuni WPI; 2000-146875/13. P-PSDB; AAY51377. C. jejuni flgg DNA Chan VL; 1730 Å 1730 g 502 07-JUN-1995; 08-MAY-1995; US6020125-A. 402 462 1332 502 AAZ88554; Louie H, AAZ8855 셤 8 셤 ò 요 ò g à g a δ 엄 셤 g ò ઠ à

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Example 1; Col 21-22; 28pp; English. $\overset{\alpha}{\times}\overset{\times}{\times}\overset{\circ}{\circ}{\circ}\overset{\circ}$

producible by a transformed host containing an expression vector.

Comprising a muclaic acid selected from; (a) an entire nuclaic acid sequence of the FigF gene having Bio base pairs (bp), or the nuclaic acid sequence of the FigF gene having Bio by, both given in the specification; (b) a nuclaic acid sequence.

Sequence, given in the specification; (c) a nuclaic acid sequence of the recoding a functional FigF basal body rod protein of a flagellum of a strain of Campylobacter; or (d) an immunogenic fragment of an FigF protein of (a), (b) or (c), and expression means operatively coupled to protein of a flagellum of a strain of Campylobacter; (I) is useful in immunological vaccine compositions for invivo administration to protect against diseases caused by bacterial pathogens that produce basal body rod proteins. (I) are also useful as immunogens, as antigens in immunosassy, or for procedures for the detection of antibacterial, immunosassy, or for procedures for the detection of antibacterial, immunosassy, or for procedures for the detection of antibacterial, immunosassy, or for procedures for the detection of antibacterial, immunosassy, or for procedures for the detection of antibacterial, the product of the invention has immunostimulatory activity. This sequence encodes the Campylobacter jejuni flgg protein described in the method of the invantion has immunostimulatory activity. invention describes a novel recombinant basal body rod protein (I) the invention

Sequence 789 BP; 260 A; 127 C; 179 G; 223 T; 0 U; 0 Other;

ment	Scores:)
Pred. No.: Score: Percent Simi Best Local S Query Match:	No.: :: int Similarity: Local Similarity: Match:	5.29e-10 237.50 27.45% 18.63% 9.18%	Length: Matches: Conservative: Mismatches: Indels:	789 95 45 115 255
DB: US-10-009-823A	(3A-1 (1-502)	3 x AAZ88554	Gaps: (1-789)	σ.
Š	1 MetMetGly	MetMetGlySerLeuPhelleGlyAlaThr	31	MerlysThrHisSerThrGlyLeuGly
QC	1 ATGATGAGA	 TCACTTCATACTGC	 TGCTACAGGAATGGTA(atgatgagatcacttcatactgctgctgctagaaatggtagcgcagcaaacacaaattgat
Qy 2	21 ThrValSerAsnA	snIleA	laasnalaasnThrileGly	yTyrLysGlnGlnGlnValVal
9 90	61 GTTACTTCA	AATAACATCGCCAA	 	TTTAAGAAAAGTCGCGCAGAA
ço 4	41 PheGlnAsp	LeuPheSerGlnAs	preualalledlyser	PheGlnAspLeuPheSerGlnAspLeuAlalleGlySerThrGlySerGlnGlyProAsn
Db 121	1 TTTGCTGAT	CTTATGTATCAAGT	::: TATGAAGTATGCAGGA	 CTTATGTATCAAGTTATGAAGTATGCAGGAACTTCAACTTCAGCTACTACT
ογ 6	61 GlnAlaGly	GlnAlaGlyMetGlyAlaGlnValGly	1G1y	ServalArgThrIle
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ο,	75 PheThrGln	GlyAlaPheGlu	-ProGlyAsnSerVal	PheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGly
Db 241	-	 GGAAATTTAAAATC	aacaagtactgatggt	
٥ <i>γ</i>	4 Lysgl	yPhePheGlnValThrLeuGluAsp	uGluAsp LysvalHi	HisTyrThrArgAlaGlyAsn
Db 30	ä	TTTCAAATACAACT	rccrgarggcacrara	AATGGGTTTTTTCAAATACAACTTCCTGATGGCACTATAGGATATACTAGAAATGGGCAA
Oy 11	13 PheArgPhe	ThrGlnAspGlyPhe	eLeuAsnAspProSer	PheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMetGlySer
36 Db 36	61 TTTACAAAA	GATAATGAAGGTAA:	 TTACAAAAGATAATGAAGGTAATATTGTAAATTCAGATGGTTATAGACTT	SGTTATAGACTT
Oy 13	3 Argiles	AsnAsnProAsnIle	elyslysGluThrLeu(erAsnAsnProAsnIleLysLysGluThrLeuGluProIleGlnLeuAspPhe
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Qy 15	Α Α	snAspProThrValAlaLysSei	SerProAlaLysThrSer	erThrAlaLeuAsnAlaValVal
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173 AsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeu 192

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Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
           Bacillus licheniformis genomic sequence tag (GST) #1888.
                                                                                                                                05-OCT-2001; 2001WO-US031437.
                                                                                                                                                  06-OCT-2000; 2000US-00680598.
27-MAR-2001; 2001US-0279526P.
                                                                      Bacillus licheniformis
                                                                                                                                                                                                                              WPI; 2002-416684/44.
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                  GluSerTrpLysGlyAsnGlyThrProProIleSerThrSerAsnTyrSerTyrAlaGln 212
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BIOTECH INC.

Clausen IG;

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The invention describes a method of monitoring differential expression of genes in a first Bacillus cells relative to expression of the genes in other bacillus cells to a substrate containing array of Bacillus cells to a substrate containing array of Bacillus cells to a substrate containing array of Bacillus genemic sequenced tags (GST), examining the array, and determining containing array of Bacillus cells useful for measuring the expression of a spot in the array. The method is useful for measuring the expression of a spot in a first Bacillus cell relative to expression of the same genes of in one or more second Bacillus cells. The method is useful for monitoring gene copy number variation and stability. Monitoring can copy number variation and stability. Monitoring can copy number variation and stability. Monitoring can copy number variation and stability. Monitoring can copy number variation and stability. Monitoring can consist of the way in expression of genes may be used to provide a representation of the way in expression of genes may be used to provide a representation of the way on that a stress or other physiological provocation. Extensive follow up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence date (or this patent did not form part of the printed specification, but, was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrSerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGln 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      part of the printed specification, but was obtained in electro
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 555 BP; 163 A; 145 C; 129 G; 118 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                               Claim 4; SEQ ID NO 1888; 200pp; English.
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ABK74597 standard; DNA; 555

(first entry)

13-AUG-2002

ABK74597

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RESULT 38

BP ADM91627 standard; DNA; 742 ADM91627;

(first entry) 15-JUL-2004 Lawsonia intracellularis specific nucleotide sequence SEQ ID NO:28

Lawsonia intracellularis; infection; antibacterial; immunotherapy; gene;
ds; proliferative enteropathy.

Lawsonia intracellularis

402004033631-A2

22-APR-2004

01-OCT-2003; 2003WO-US031318

04-OCT-2002; 2002US-0416395P.

(MINU) UNIV MINNESOTA

Kapur V, Gebhart CJ;

2004-340902/31. P-PSDB; ADM91689 New nucleic acid that generates an amplification product from L. intracellularis nucleic acid using an appropriate second nucleic acid molecule, useful for treating and preventing L. intracellularis

Disclosure; SEQ ID NO 28; 87pp; English

The present invention describes an isolated nucleic acid comprising a nucleic acid molecule of at least 10 nucleotides in length having at least 75% identity to SEQ ID NO:8741 (ADM91733), where any of the amplecule that is 10-29 nucleotides in length, under standard amplification conditions, generates an amplification product from Lawsonia intracellularis nucleic acid using an appropriate second nucleic acid molecule. Also described: (1) a vector comprising the nucleic acid;

cc comprising the vector; (3) an isolated polypeptide encoded by the nucleic acid; (4) an article of manufacture comprising the colypeptide; (5) an antibody having specific binding affinity for the colypeptide; (6) a method for detecting the presence or absence of intracellularis in a biological sample; (7) a method of preventing intracellularis in an animal; (8) a composition of comprising a first oligonucleotide primer and a second oligonucleotide primer, where the first and second primers are each 10 to 50 nucleotides in length, and where in the presence of I. intracellularis nucleic acid, generate an amplification product in the presence of nucleic acid from an organism other than I. intracellularis; and (9) an article of manufacture comprising the composition. The nucleic acid comprising the composition. The nucleic acid comprising the composition. The nucleic acid comprising the composition of in immunotherapy. The nucleic acid and polypeptides are useful for treating and preventing C intracellularis infection e.g. proliferative enteropathy. The present sequence represents an L. intracellularis specific nucleic acid molecule, compliant in the exemplification of the present invention.

Sequence 742 BP; 213 A; 149 C; 133 G; 245 T; 0 U; 2 Other;

493 527

IleIleIleGlnArgGlyPheGlnMetAsnSerLysSerValThrThrAlaAspThrMet

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742 62 33 87 12 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.05e-08 221.00 48.97% 31.96% 8.55% Percent Similarity:
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US-10-009-823A-1 (1-502) x ADM91627 (1-742)

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448 578 388 458 408 398 428 338 468 429 AsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThr ||| ||| :::::: 277 GAAAACTTAGGGACTATAGCTCAAGGATTCCTTGAAATGTCTAATGTAGAGGTTGTTGAT GlumetValAsnMetIleIleIleGlnArgGlyPheGlnMetAsnSerLysSerValThr GlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGinGlnAsnMetTrp AlaglyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLysLeuProSerMet ::: |||| :: GTTGGTGATTAATGTATACAGAGCAGGTGCTTTTAAACTTAATCAGATGGGACT AspvalThrileThrSerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValVal gcrgcrggagaaraccrrraragcrrrgrraarccagcgggacrggaaaagga 337 cgraarctatartcccacagaagcarccagaagcgragaaggrgracagaggractagaa 449 SerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMetSerArg MetProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSerThrArg -----GlnGlyAspLeuVal AspPheTyrAsnIleProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGly 376 ArgTyrSerGlnAspGlyTyrPro-------316 336 356 577 389 409 397 g ъ g 8 g ò ò

RESULT 39 ABK74555

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Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds. sequence tag (GST) Claim 4; SEQ ID NO 1846; 200pp; English Bacillus licheniformis genomic (NOVO) NOVOZYMES BIOTECH INC (NOVO) NOVOZYMES AS. DNA; 1524 06-OCT-2000; 2000US-00680598, 27-MAR-2001; 2001US-0279526P. 05-OCT-2001; 2001WO-US031437 (first entry) Bacillus licheniformis Clausen IG; WPI; 2002-416684/44. standard; directly from WIPO WO200229113-A2 Sequence 1524 ABK74555

The invention describes a method of monitoring differential expression of genes in a first Bacillus cells. Comprising hybridising labelled nucleic acid probes isolated from Bacillus cells. Comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cells ribe expression of the same genes in one or more second Bacillus cells The method is useful for monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, environmental stress or other physiological provocation. Extensive follow-up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence cate (GST) used in the method of the invention. Note: The sequence data for this patent did not form a first in the method of the invention when the data for this patent did not form a first in the method of the invention when the data for this patent did not form the data for this patent did not form the contract of the particle dependence data for this patent did not form and the data for this patent did not form and the data for this patent did not form the data for this patent did not form the data for this patent did not form the data for this patent did not form the data for the data for this patent did not form the data for this patent did not form the data for the data for the data for the data for the data for the data for the data for the data for the data for the data for the data for the data for the data for the data at ftp.wipo.int/pub/published_pct_sequences

BP; 466 A; 341 C; 376 G; 341 T; 0 U; 0 Other;

LeuPheIleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGlyThrValSerAsn 24 Length:
Matches:
Conservative:
Mismatches:
Indels: JS-10-009-823A-1 (1-502) x ABK74555 (1-1524) 7.18e-08 215.50 37.21\$ 22.93\$ 8.33\$ Percent Similarity: Best Local Similarity: Query Match:

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144 190 ---CAGATGGGTACAGGCGTTGAAATCGGTTCGGTTGAAAGGGTT-----AGGGACAGC 240 172 246 100 ThrLeuGluAspLysValHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGly 119 306 123 127 426 144 486 158 543 187 663 84 43 -----AspleuPheSerGlnAspLeuAlalleGlySerThrGlySerGlnGlyPro 59 79 ტ ტ 207 723 227 771 247 261 --SerAlaGlyLeuLeuMetSer-----GlyThrMetThrPhe 273 294 AspLeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuProGlnPheSerAlaAsn 313 SerSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySerAlaThrLys 293 CTGGAAATCGCAAAAAGAGGCTTGTCCGCGCAGCAATCAGCTCTGAGCGTGACAAAC AsnGlnAlaGlyMetGlyAlaGlnValGlySerValArgThrIlePheThrGlnGlyAla ::: |||::::|||::: 208 TyrSerTyrAlaGlnProMetArgyalTyrAspGlnGlnGlyAsnSerHisAspIleThr 80 PheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLysGlyPhePheGlnVal 247 GACTATCAATACAGGACGCAGAATACAAAGGCCGGCTATTACAATGCAAAAGTGGACGCT ThrieuMet-----GlySerArglleSerAsnAsnProAsnIleLysLysGluThr LeuGluProIle-------GinLeuAspPheAsnAspProThrValAla ------AsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnPro GGCTATCTCCCGAACGATTTGTACGATAAGCGTGATCAGCTCCTTGATGAACTGTCTTCA 188 TyrPheAlaLeuLeuGluSerTrpLysGlyAsnGlyThrProProlleSerThrSerAsn GGCATTGTGTCA-----ATAGAAGTCCTTGACGTAAACGGCCAGTCT------CTGGGC ValTyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeuValAla -----GTCAAA 248 MetAsnProSerGluAsp-----GlySerAlaAlaSerGlyThrAsp---GGCATCGATTCGTTTACTAGCAAAGGGTCCCTGCTCGGTTTAATCGAATCTTACGGATAT 25 AgnileAlaAgnAlaAsnThrileGlyTyrLysGlnGlnGlnValValPheGln----159 LysSerProAlaLysThrSerThrAlaLeuAsnAlaValval----------IreuAsnAsp----772 AAGGITCITGACGGCCAAACITCACGACTGAAACI-----241 TTT-----9 128 120 145 124 604 724 974 173 262

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| 1231 ACCAAG-----AAAATICAAATCGGTGACAAACGACGACCGTTTTAGACTATTAC 1281
                                                                                                                                                                                                                                                                                                        -----GGCAAAATCAAA 1128
                                                                                                                                                                                                                                                                GlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMetVal 471
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                                                                                                                                                                                           392 IleThrSerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValValAspPheTyr 411
                                                                                                                                                                                                                                          412 AsnileProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHis 431
PhevalGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsn 333
                                              334 MetTrpAlaGlyAlaProAlaSerAlaAlaIleGlyThrAspIleGlyLySLeuPro 353
                                                                                             354 SerMetMetProlleGlnThrSerSerGlyAsnSerThrAlaArg-----AsnGlySer 371
                                                                                                                                          SerSerThrArgArgTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAspValThr 391
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                                                                                                                                                                                                                                                                                         432 TyrSerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding a mutant B_licheniformis secreted polypeptide SeqID 89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutant; host cell; production yield; shelf life; product stability; purity; secreted; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clausen IG;
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                                                                     ------ecraagócrácáaagggagócó
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                                                                                                                                                                                                                                                                                                                                                                                                                                         492 ThrMetLeuGlnLysAlaLeu 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG32119 standard; DNA; 1432 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Bacillus licheniformis.
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483 AsnSerLysSerValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeuLysArg

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This invention relates to a novel Bacillus licheniformis (B. licheniformis) mutant host cell derived from a parent B. licheniformis host call that is mutated in genes encoding secreted polypeptides.

Specifically, it refers to the generation of an improved Bacillus host that reduces the need for product purification caused by contaminant secreted native polypeptides in the outlare medium. Accordingly, the present invention describes reducing the expression of these native present invention describes reducing the expression of these native protecties (e.g. proteclytic enzymes, nutrient uptake factors and signal molecules), which in turn makes it easier to purify the heterologous product of interest and therefore improving the production process.

Further benefits of a mutated host cell include an increase in total product stability and purify. This polymucleotide is a DNA sequence product stability and purify. This polymucleotide is a DNA sequence encoding a mutant B. licheniformis secreted polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnvalaspMetSerArgGluMetValasnMetIleIleIleGlnArgGlyPheGlnMet 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 PheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSer
more secreted polypeptides than the parent host cell, useful fo
producing a product of interest e.g. polypeptides, amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1432 BP; 477 A; 287 C; 335 G; 333 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                   Disclosure; SEQ ID NO 89; 422pp; English
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66.25%
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Best Local Similarity:
Query Match:
DB:
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October 26, 2004, 09:35:12; Search time 195 Seconds (without alignments) 531.115 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

US-10-009-916A-1 950 1 MXIKLFFVTSIVTISLLTSI......DXPLPLGGGGARIACGVIPN 180

Title: Perfect score: Sequence:

Run on:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	[] ellerida Aerico	shidella	P53635 escherich	08fh80	Q704s6 sa	Caf0653	O68901 sa	salmonell	Q887£8	Y P53636	Q704s7 sa	Caf0653	P58645 br	Q6d531	Q9krg3 vibrio chol			~		~	Q7aeal escherichia	escher		Q87g06 vibrio para	vibrio		yersinia	æ	Д	07wh53 bordetella	
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ALIGNMENTS

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Name=sodC; OrderedLocusNames=b1646, z2661, ECs2355

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).
-!- CATALYMIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-!- COFACTOR: Binds I copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 ŚLAILALV--VATGAQAAŚEKVEMNLVTSQGVGÓŚIĠSVTITETDKGLEFSPDĹKALPPĠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
-:- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
EMBL; AID15188; AAN43254.1; -.
HSSP; P55635; 1ESO.
128 KATDAVIAPRLKSLDBIKDKALMVHVGGDNMSDQPKPLGGGGERYACGVI 177
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P53.635; P96756;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1)
                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-MR-2004 (TrEMBLrel. 26, Last ann
Superoxide dismutase (Cu.Zn).
Name=sodC, OrderedLocusNames=SF1673;
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les 92; Conserv
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Escherichia Coli Complete genome sequence of enterohemorrhagic Escherichia coli O15:H7 and genomic comparison with a laboratory strain K-12.";
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                                                                                                                                                                                                                                                                                       STRAIN-KL2 / MG1655,
MEDLINE-97426617, PubMed-9278503,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                          SEQUENCE FROM N.A.
STRAIN=K12 / W3110;
MEDLINE=56196162; PubMed=8626323;
MEDLINE=565196162; PubMed=87073;
MEDLINE=765196162; FubMed=8626323;
MEDLINE=7619619 of sodo, encoding the copper-zinc superoxide dismutase of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=97156972; PubMed=9003353;
Battistoni A., Folcarelli S., Gabbianelli R., Capo C., Rotilio G.;
"The Cu.Zn superoxide dismutase from Escherichia coli retains
monomeric structure at high protein concentration. Evidence for
altered subunit interaction in all the bacteriocupreins.";
Biochem. J. 320:713-716(1996).
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SEQUENCE FROM N.A.

MEDLINE-21074935, PubMed=11206551; DOI=10.108135054089;

MEDLINE-21074935; PubMed=11206551; DOI=10.108135054089;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasher J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Agodaca G., Anantharaman T.S., Linn A., Dimalanta E.T., Potamousis K.,

Welch R.A., Blattner F.R.;
                                                      Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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MEDLINE=21156231; PubMed=11258796;
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                                                                                                                                                                                                                                          J. Bacteriol. 178:2564-2571(1996).
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Unpublished results, cited by:
Unlay K.R.C., Imlay J.A.;
J. Bacteriol. 178:2564-2571(1996)
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MEDLINE=95305591; PubMed=7786035;
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MEDLINE=96196162; PubMed=8626323;
              Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria, Proteobacteria; Gammap
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334;
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                                                                                                                                                                                                    Battistoni A., Rotilio G.; "Isolation of an active and heat-stable monomeric form of Cu,Zn superoxide dismutase from the periplasmic space of Escherichia coli."; FESS Lett. 374:199-202(1995).
Jenov L.T., Chang L.Y., Day B., Fridovich I.;
"Copper, zinc superoxide dismutase in Escherichia coli: periplasmic
localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Periplasmic.
-!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
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Copper and zinc.
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EMBL, AE00259; AAC74718.1; --
EMBL, AB00258; BAB53778.1; --
EMBL, A800258; BAB53778.1; --
EMBL, C99023; C9023.2; C9023.2; C9023.1; --
PIR, UC6004; UC6004.
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CHARACTERIZATION.
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STRAIN=66.H1 / CFT073 / ATCC 700928 / UPEC;
STRAIN=66.H1 / CFT073 / ATCC 700928 / UPEC;
MEDLINE=22388234; PubMed=12471157;
A. MEDLINE=22388234; PubMed=12471157;
A. MEDLINE=22388234; PubMed=12471157;
A. Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
T. Extensive mossic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

I. Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

C. -! FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems (By similarity).

C. -! CATALYTIC ACTIVITY: 2 supercivide + 2 H++) = O(2) + H(2)O(2).

C. -! COFACTOR: Binds I copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 EHGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGPLGNGHKGDLPRLVVKADG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 EHGFHIHARGSCQPATKDGRASAABSAGGHLDPQNTGKHEGPEGAGHLGDLPALVVNNDG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 SIVTISLLTSITSVVLACSVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKGLPAG 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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-- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.

EMBL, AED16761, AAN80498.1; -.

HSSP, P53635, 1ESO.

GO; GO:0004785; F:copper, Zinc superoxide dismutase activity; IEA.

GO; GO:0064872; F:meral ion binding; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0006801; P:superoxide metabolism; IEA.
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01-MAR-2003 (TrEMBLrel. 23, Last se
01-MAR-2004 (TrEMBLrel. 26, Last an
Superoxide dismutase (EC 1.15.1.1).
Name=sodC; OrderedLocusNames=c2038;
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MEDLINE=99307419; PubMed=10377444;
MEDLINE=99307419; PubMed=10377444;
Fang F.C., DeGroote M.A., Foster J.W., Baumler A.J., Ochsner U.,
Testerman T., Bearson S., Glard J.C., Xu Y., Campbell G., Laessig T.;
"Virulent Salmonella typhimurium has two periplasmic Cu, Zn-superoxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 VTISLLTSITSVVLAC----SVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKG
126 KADGIAKETLLAPRI-TVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enterica subsp. enterica serovar Choleraesuis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella; Salmonella enterica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ASO; Apello M., Pasquali P., Kroll J.S., Langford P.R., Rotilio G., Valenti P., Battistoni A.; Rotilio G., Valenti P., Battistoni A.; Estimo G., Valenti P., Battistoni A.; Estimo G., Valenti P., Sattistoni A.; Sulmonella and sodC2 to intracellular survival and pathogenicity of Salmonella enterica subsp. enteric serovar Choleraesuls.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
26-FEB-2004 (Rel. 44, Last annotation update)
Superoxide dismutase [Cu-2n] 2 precursor (EC 1.15.1.1) (sodCII).
Name=sodC; Synonyms=sodC2; OrderedLocusNames=STM1440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
superoxide dismutase [Cu-Zn].
511A19E8057F1255 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ620904; CAF06532.1; ...
Oxidoreductase; Signal.
                                                                                                                                                                                                                                          10-MAY-2004 (TrEMBLrel. 27, Created)
10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Superoxide dismutase precursor (EC 1.15.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dismutases.";
Proc. Natl. Acad. Sci. U.S.A. 96:7502-7507(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.6%; Score 452; DB 2;
52.3%; Pred. No. 1e-32;
tive 22; Mismatches 49.
                                                                                                                                                                                        A
                                                                                                                                                                                     173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN 20 173 S1
SEQUENCE 173 AA; 17721 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=119912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                    CAF06532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                     CAF06532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 EHGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGPLGNGHKGDLPRLVVKADG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 EHGFHIHAKGSCQPATKDGKASAAESAGGHLDPQNTGKHEGPEGAGHLGDLPALVVNNDG 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ammendola S., Ajello M., Pasquali P., Kroll J.S., Langford P.R., Rotilio G., Valenti P., Battistoni A.; Submitted (JAN-2004) to the EMB/GenBank/DDBJ databases.

-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).

-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).

-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                   10 SIVTISLLTSITSVVLACSVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKGLPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 VTISLLTSITSVVLAC----SVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 LPAGEHGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGPLGNGHKGDLPRLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 LPPGEHGFHIHANGSCQPAIKDGQAVAAEAAGGHLDPQNTGKHEGPEGQGHLGDLPVLVV
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
-!-SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
EMBL; AJ620904; CAF06532.1; --
GO, GO:0016491; F:Oxforeductase activity; IEA.
GO; GO:0004784; F:Superoxide dismutase activity; IEA.
InterPro; IPR001424; SOD_CU_ZN.
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                                                                                                                         al-binding; Oxidoreductase; Zinc. 6217F2DAAE1A8E23 CRC64;
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                                                                                                                                                                                                                 Length 190;
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ilarity 52.3%; Pred. No. 1e-32;
Conservative 22; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 173 superoxide dismutase [Cu-Zn].
173 AA; 17721 MW; 511A19E8057F1255 CRC64;
                                                                                                                                                                                                                                                                            51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enterica subsp. enterica serovar Choleraesuis.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Superoxide dismutase precursor (EC 1.15.1.1).
                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                             49.8%; Score 473.5; DB 2
53.5%; Pred. No. 1.3e-34;
tive 25; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 AA
   InterPro; IPR001424; SOD_CU_ZN.
Pfam; PF00080; Sod_Cu; 1
Probom; PD000469; SOD_CU_ZN; 1.
Complete proteome; Copper; Metal-binding; SEQUENCE 190 AA; 19617 NW; 6217F2DAABI
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                                                                                                                                                                                                             Query Match
Best Local Similarity 53.5*
Matches 91; Conservative
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Best Local Similarity
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF056931; AAC13559.1; -.

EMBL; AF056931; AAC13559.1; -.

EMBL; AE008762; AAL20362.1; -.

EMBL; AE008762; AAL20362.1; -.

EASTP PSSSTS; ESOC.

InterPro; IPR001424; SOD. CU_ZN.

EASTP PSSOC CU_ZN.

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                                                                                                                                                                                      Nature 413:852-856(2001).

-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).

-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).

-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                           -1- SUBBRIT: Monomer (By similarity).
-1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 KADGIAKETLLAPRL-TVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                                                                                                                      (Potential). 
 -!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFDCF9F6EF64B3EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.5%; Score 451; DB 1;
52.3%; Pred. No. 1.2e-32;
live 22; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17737 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 91; Conserv
                                                                                                                                                                                                                                                                                              similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
Q8Z6P6
ID Q8Z6:
AC Q8Z6:
DT 01-M
        셤
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118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMedt G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Batteriol. 185:2330-2337(2003).

-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).
-!- CATALYNIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).
-!- COPACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By similarity).
-!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
EMBL; AL621271; CAD01927.1; -.
EMBL; AE016838; AAO68958.1; -.
                                                                                                                                                                                                                                                                                                                                                            ARAINE-CIES.
MEDINE-2153497; PubMed=11677608; DOI=10.1038/35101607;
MEDINE-2153497; PubMed=11677608; DOI=10.1038/35101607;
MEDINE-2153497; PubMed=11677608; DOI=10.1038/35101607;
Churcher C.M., Mungall K.D., Jentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davies R.M., Dowd L., White N., Farrar J., Fellwell T., Hamlin W., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Parrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serowar Typhi (T18.")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 LPPGEHGFHIHAKGSCQPAIKDGKAVAAEAAGGHLDPQNTGKHEGPEGQGHLGDLPVLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LSLAMVT-----LLACAGAQAASEKVEMNLVTAQGVGQSIGTVVIDETEGGLKETPHLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 VTISLLTSITSVVLAC----SVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 LPAGEHGEHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGPLGNGHKGDLPRLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 NNDGIATEPVTAPRLKSLDEVKDKALMIHVGGDNMSDQPKPLGGGGTRYACGVI 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 KADGIAKETLLAPRL-TVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL627271; CAD01927.1; -.
EMBL; AE016838; AA068958.1; -.
EMBL; AE016838; AA068958.1; -.
HSSP; P53635; IESO.
GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
GO; GO:0004887; F:metal ion binding; IEA.
GO; GO:0006801; P:superoxide metabolism; IEA.
InterPro; IPR001424; SOD_CU_ZN.
                                                                                                                                             Salmonella typhi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Promo, PR0080; Sod Cu; 1. – Promo, PR0080; Sod Cu; 1. – ProDon; PD00469; SOD Cu Zu; 1. PR0SITE; PR00312; SOD Cu Zu; 1. Complete proteome; Copper; Metal-binding; Oxidoreductase; Zinc. SEQUENCE 173 AA; 17735 MW; 00A5A8B6AF25B4EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.3%; Score 449; DB 2; Length 173
52.3%; Pred. No. 1.9e-32;
ive 22; Mismatches 49; Indels
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Copper-zinc supervoid dismutase.
Namescodt, OrderedLocusNames=STY1682, t1308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0887F8;
01-JUN-2003 (TrEMBLrel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:848-852(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        NCBI_TaxID=601;
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Q887F8
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'n

173 AA.

QBZ6P6; Q7CA25; 01-MAR-2002 (TrEMBLrel. 20, Created)

PRELIMINARY;

Q8Z6P6

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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
       DAR REPRESENTE TRANSPORTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY REPRESENTED FOR THE PROPERTY FOR THE PROPERTY FOR THE PROPERTY FOR THE PROPERTY FOR THE PROPERTY FOR THE PROPERTY FOR THE PROPERTY FOR THE PROPERT
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WEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;

WEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;

WEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;

Weaking M. L., Doddson R. U., Dandy T. T., Color M., Beanan M. J., Haft D.H.,

Radupu R., Daudherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,

RA Medupu R., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,

RA Mchouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,

BAND W. L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterfee A.K.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer A.,

RA Bender C.L., White O., Fraser C.M., Collmer B.,

RA Bender C.L., White O., Fraser C.M., Collmer B.,

RA Bender C.L., White O., Fraser C.M., Collmer B.,

RA Bender C.L., White O., Fraser C.M., Collmer B.,

RA Bender C.L., White O., Fraser C.M., Collmer B.,

RA Bender C.L., White O., Fraser C.M., Collmer B.,

RA Bender C.L., White O., Fraser C.M., Collmer B., Fraser C.M., Carlyllyll B.,

RA Bender C.L., White O., Fraser C.M., Carlyll B.,

RA Bender C.L., White O., Fraser C.M., Carlyll B.,

RA B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 HVHENGSCEAGTKDGVKVAALAAGGHFDPAKTGKHLGPYARGHLGDLPALYVTADGTADY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO: 0004785; F:copper, zinc superoxide dismutase activity; IEA. GO: GO:0046872; F:metal ion binding; IEA. GO: 0006801; P:superoxide metabolism; IEA. INCORP.; IPRO01424; SOD CUZ. ZN. INCORP.; IPRO01424; SOD CUZ. ZN. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
-!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
EMBL, AE016860; AA054860.1; -.
                                                                                                                                            Pseudomonas syringae (pv. tomato).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SODI_SALTY STANDARD; PRT; 177 AA.
P953656, 033803; O50545;
01-OCT-1996 (Rel. 34, Created)
28-PBB-2003 (Rel. 41, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Superoxide dismutase [Cu-Zn] 1 precursor (EC 1.15.1.1) (sodCI).
Name=sodC1; Synonymas=sodC; OrderedLocusNames=STM1044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR010916; TONE BOX N.
Proposition PR01080; Scd Cu; 1.
Proposition PD000469; SCD Cu Zn; 1.
PROSITE; PS00087; SCD Cu Zn; 1; UNKNOWN 1.
PROSITE; PS00332; SCD Cu Zn 1; UNKNOWN 1.
PROSITE; PS00430; TONE DEPENDENT REC 1; UNKNOWN 1.
COMPLETE Proceeme; Corper; Metal-binding; Oxidoreductage; Zinc. SEQUENCE 172 AA; 17465 MW; C829BC408590A472 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 TLLAPRI-TVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57; Indels
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
1-JNAR-2004 (TrEMBLrel. 26, Last annotation update)
Superoxide dismutase, Cu-Zn.
Name=sodC; OrderedLocusNames=PSPTO1338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.8%; Score 435.5; DB 2; 51.8%; Pred. No. 3.1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.8%; Prec. ...
                                                                                                                                                                                                                              Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P53636; 1EQW.
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                  NCBI_TaxID=323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Sim-
86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR;
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SOD1 SALTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=98054349; PubMed=9391141;

MEDLINE=98054349; PubMed=9391141;

De Groote M.A., Ochsner U.A., Shiloh M.U., Nathan C., McCord J.M.,

Dinauer M.C., Libby S.J., Vazquez-Torres A., Xu Y., Fang F.C.;

"Periplasmic superoxide disamutase protects Salmonella from products of phagocyte NADPH-oxidase and nitric oxide synthase.";

Proc. Natl. Acad. Sci. U.S.A. 94:13997-14001(1997).
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-1- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to bloogical systems.

-1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).

-1- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit.

-1- SUBGELLULAR LOCATION: Periplasmic.

-1- SUBCELLANBOUS: Encoded by a cryptic bacteriophage.

-1- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
MCCIelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Mguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional and crystallographic characterization of Salmonella typhimurium Cu, Zn superoxide dismutase coded by the sodCI virulence
                                                                                                                                                                                                                                                                         Farrant J.L., Sansone A., Canvin J.R., Pallen M.J., Langford P.R., Wallis T.S., Dougan G., Kroll J.S.;
Bacterial copper., and zinc-cofactored superoxide dismutase
contributes to the pathogenesis of systemic salmonellosis.";
Mol. Microbiol. 25:785-796(1997).
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MEDLINE-20428907; PubMed=10970746; DOI=10.1006/jmbi.2000.4074;
Pesce A., Battistoni A., Stroppolo M.E., Polizio F., Nardini M.,
Kroll J.S., Langford P.R., O'Neill P., Sette M., Desideri A.,
Bolognesi M.;
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                                                                                                                                                                                                                             MEDLINE=98025474; PubMed=9379906;
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EMBL; AE008743; AAL19978.1; --
EMBL; X9437; CAA63988.1; --
PDB; 1EQW; X-ray; A/B/C/D=22-177.
StyGene; SG10705; sodC1.
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602;
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                                                                                                                                    FROM N.A.
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us-10-009-916a-1.rup

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69 GEHGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGPLGN-GHKGDLPRLVVKA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 GIHGFHVHTNPSCMPGMKDGKEVPALMAGGHLDPEKTGKHLGPYNDKGHLGDLPGLVVNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enterica subsp. enterica serovar Choleraesuis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=119912;
                                                                                                                                                                                                                                                                                                                                            44.7%; Score 425; DB 2; Length 177;
51.2%; Pred. No. 2.8e-30;
cive 22; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                               SLEWALL 1 20 POTENTIAL.
CHAIN 21 177 SUPEROXIDE DISMUTASE [Cu-Zn].
SEQUENCE 177 Aa; 18370 MW; IEC743EE2AB38CAE CRC64;
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1EC743EE2AB38CAE CRC64;
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10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Superoxide dismutase precursor (EC 1.15.1.1).
SODC1.
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hes 88; Conservative
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                                                                     Copper; Metal-binding;
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               | Reproperties | Proposed | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproperties | Reproper
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Superoxide dismutase precursor (EC 1.15.1.1).
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           InterPro; IPR001424; SOD_CU_ZN
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Gaps

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STRAIN-A50;
Amendola S., Ajello M., Pasquali P., Kroll J.S., Langford P.R., Rotilio G., Valenti P., Battistoni A.;
Rotilio G., Valenti P., Battistoni A.;
Polfferential contribution of sodol and sodo to intracellular survival and pathogenicity of Salmonella enterica subsp. enterica survival and pathogenicity of Salmonella enterica subsp. enterica submitted (JAN-2004) Lot the EMBL/GenBank/DDBJ databases.
EMBL; AJ620903; CAF06531.1;
Detartial Salmonella enterica subsp. enterica serovar Choleraesuis. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella; Salmonella enterica. Length 177; DB 2; 44.7%; Score 425; Query Match

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Potential.

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1 MKIKLFFVTSIVTISLLTSITSVVLACSVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIK 60
                                       HSEP, PS3656; IEGW.

TIGR: BRA0703; -.

TIGR: BRA0703; -.

TICR: BRA0703; -.

TICR: BRA0703; -.

Fram: PF00080; Sod Cu; 1.

ProDom; PD000469; SoD CU ZN, 1.

PROSITE; PS00087; SOD CU ZN, 2; 1.

PROSITE; PS00332; SOD CU ZN, 2; 1.

Antioxidant; Complete proteome; Copper; Metal-binding; Oxidoreductase; Periphasmic; Signal; Zinc.

PROSITE: PS00332; Sol Cu ZN, 2; 1.

PROSITE: PS00332; Sol Cu ZN, 2; 1.

PROSITE: PS00332; Sol Cu ZN, 2; 1.

PROSITE: PS00332; Sol Cu ZN, 2; 1.
   EMBL; AE009694; AAL53823.1; -.
EMBL; AE014566; AAN33888.1; ALT_INIT.
FIR; AD3582; AD3582.
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                                                                                                     127
                                                                                                                             GIHGFHVHTNPSCMPGMKDGKEVPALMAGGHLDPEKTGKHLGPYNDKGHLGDLPGLVVNA 123
                                              68
                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                               The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts.";

Proc. Natl. Acad. Sci. U.S.A. 99:13149-13153 (2002).

-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to blological systems (By similarity).

-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).

-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                           SLLTSITSVVLACSVTSE----VHMID--DNGIKQSIGTVTFTDTDKGLQIKTDLKGLPA
                                                                                                   GEHGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGPLGN-GHKGDLPRLVVKA
                  Gaps
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SPECIES=B. auis; STRAIN=1330 / Biovar 1;
SPECIES=B. auis; STRAIN=1330 / Biovar 1;
MEDLINE=2224741; PubMed=12271122; DOI=10.1073/pnas.192319099;
Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Real T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A., Van Aken S.B., Riedmuller S., Tettelin H., Gill S.R., White O., Faraser C.M.; Roover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
                                                                                                                                                           128 DGIAKETLLAPRL-TVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                          similarity).
--- SUBUNIT: Homodimer (By similarity).
--- SUBCELULIAR LOCATION: Periplasmic (By similarity).
--- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
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                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                Indels
                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1).
Name=sodC; OrderedLocusNames=BMEII0581, BRA0703;
               54;
51.2%; Pred. No. 2.8e-30; ive 22; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
                                                                                                                                                                                                                                                              174 AA.
                Conservative
                                                                                                                                                                                                                                                                                                                                                             Brucella melitensis, and
                                                                                                                                                                                                                                                                                                                                                                                                          Brucellaceae, Brucella.
NCBI_TaxID=29459, 29461;
                                                                                                                                                                                                                                                              STANDARD;
Best Local Similarity
             88;
                                                                                                                                                                                                                                                              BRUME
                                          15
                                                                                                                               64
                                                                                                                                                                                      124
                                                                                                                                                                                                                                 RESULT 13
SODC_BRUME
            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 ENGFHINEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGPLGNGHKGDLPRLVVKADG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 YHGFHVHENPSCAPGEKDGKIVPALAAGGHYDPGNTHHHLGPEGDGHMGDLPRLSANADG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 SLLTSITSVVLAC----SVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKGLPAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SCRII043;
Bell K.S., Sebalaida M., Pritchard L., Holden M., Hyman L.J.,
Holeva M.C., Thomson N.R., Bentley S.D., Churcher C., Mungall K.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Barrell B.G., Parkhill J., Toth I.K.;
Submitted (FBS-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 SLFIASTWVLMAFPAFAESTIVKMYEALPIGPGKEVGTVVISSAPGGLHFKVNMEKLIPG
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erwinia carotovora subsp. atroseptica SCRI1043.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                 .
9
Superoxide dismutase [Cu-Zn].
Copper (By similarity).
Copper and zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 KVSETVVAPHLKKLAEIKQRSLMVHVGGDNYSDKPEPLGGGGARFACGVI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 IAKETLLAPRI-TVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI
                                                                                                                                                                                                                                                                                                                                                                                           58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63; Indels
                                                                                                                                                                                                          Copper (By similarity).

By similarity.

08B355A9A6F7F67A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BX950851; CAG75112.1; -.
SEQUENCE 174 AA; 17907 MW; 3655E6E2C8355949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
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43.9%; Score 417.5; DB 2;
Best Local Similarity 47.8%; Pred. No. 1.3e-29;
Matches 86; Conservative 22; Mismatches 63;
                                                                                                                                                                                                                                                                                                                            44.2%; Score 420; DB 1;
49.4%; Pred. No. 7.8e-30;
tive 22; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae; Pectobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copper-zinc superoxide dismutase, ORFNames=ECA2211;
                                                                                                                                                                                                                                                                         18262 MW;
                                                                                                                                                                                                                                                                                                                                                        Local Similario,
nes '84; Conservative
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ng-To-coa-a-co-oT-gn

Created)

PRT;

PRELIMINARY;

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Q7AFX5
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                                                              119
                                                                                                                               113
                                                                                                                                                                                          178
                                                                                                                                                                                                                             DFFVTSIVTISLITSIVILACSVTSBVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LFAVVAFFSSSVLAQEMTVVMT------DLSSGQSVGTVTVTDSEYGTVFTPQLT 54
   23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c similarity).

C -!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.

E EMBL; AB0183; AP94737.1; -.

R PIR; A82183; AP0446; IYAI.

R TIGR; VC1583; -.

GO; GO: 0004785; F: copper, zinc superoxide dismutase activity; IEA.

GO; GO: 0004785; F: superoxide metabolism; IEA.

R GO; GO: 00048612; F: metal ion binding; IEA.

R GO; GO: 0004861; F: superoxide metabolism; IEA.

R HORDOR SOURCE IN PROMON SOUL ZN.

R PRODOR; PROMON SOUL ZN.

R PRODOR; PROMON SOUL ZN.

R PROSITE; PS000087; SOUL ZN. 1.

R PROSITE; PS000087; SOUL ZN. 1.

R PROSITE; PS000087; SOUL ZN. 1.

R PROSITE; PS000087; SOUL ZN. 1.

R PROSITE; PS000087; SOUL ZN. 1.

R PROSITE; PS000087; SOUL ZN. 1.

R PROSITE; PS000087; SOUL ZN. 1.

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R PROSITE; PS000087; SOUL ZN. 1.

R PROSITE; PS000087; SOUL ZN. 1.
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                                                                 TDLKGLPAGEHGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGPLGN-GHKGD
                                                                                                                            54 PNIKGLEAGIHGFHVHENASCEPAEQDGKSVPALAAGGHFDPKKTGKGLGPYDDQGHVGD
                                                                                                                                                                                             120 LPRLVVKADGIAKETLLAPRL-TVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholerae.";
Nature 406:477-483(2000).

Nature 406:477-483(2000).

-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).

-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).

-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 48.6%; Pred. No. 2.7e-29;
Matches 85; Conservative 19; Mismatches 59; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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01-0CT-2000 (TEMBLEEL 15, 1
01-MAR-2004 (TEMBLEEL 15, 1
Superoxide dismutase, Cu-Zn.
OrderedLocusNames=VC1583;
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cholerae.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Escherichia.
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-:- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.

-:- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.

-:- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.

-:- SIMILARITY: Belongs to the Cu-Zn Superoxide dismutase family.

-:- SIMILARITY: SOD CU ZN Superoxide dismutase family.

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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative copper-zinc superoxide dismutase encoded within
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47.8%; Pred. No. 2.7e-29;
Live 27; Mismatches 53; Indels
                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Putative copper/zinc-superoxide dismutase. OrderedLocusNames=ECs1120;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 47.8
Matches 88; Conservative
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05-JUL-2004
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Enterobacteriaceae; Escherichia

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Pfam; PF00080; Sod Cu; 1. ProDom; PD000469; SOD CU ZN; 1.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 HPGDLPALFVTHDGKANYPVLAPRLNSLKEIKGRSLMLHAGGDNHHDHPEPLGGGGARMA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 HKGDLPRLVVKADGIAKETLLAPRL-TVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
                                                                                                                                                                                                                                                                                   -1- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).
-1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-1- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKIKLFFVTSIVTISLLTSITSVVLACSVTSE----VHMIDDNGIKQSIGTVTFTDTDKG
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                                                      SEQUENCE FROM N.A.

STRAIN=015:H7 / EDL933 / ATCC 700927 / EHEC;

MEDLINE=21074935; PubMed=11206551;

Perna NT., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.,

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.",
                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00080; Sod Cu; 1.
Probom; PP00086; Sod Cu Zn; 1.
Probom; PD000469; SoD Cu Zn; 1.
Complete proteome; Copper; Metal-binding; Oxidoreductase; Zinc. SEQUENCE 274 AA; 28777 MW; SIDFIFA7BFES0989 CRC64;
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Beck B.L., Tabatabai L.B., Mayfield J.E.;
"A protein isolated from Brucella abortus is a Cu-Zn superoxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.6%; Score 414; DB 2; Length 274; 47.8%; Pred. No. 4.6e-29; ative 27; Mismatches 53; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brucella abortus.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
VCBI_TaxID=215,
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01-ARR-1990 (Rel. 14, Created)
01-ARR-1990 (Rel. 14, Last sequence update)
02-UUL-2004 (Rel. 44, Last annotation update)
Superoxide dismutase (Cu-Zn] (EC 1.15.1.1).
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les 88; Conservative
                                                                                                                                                                                                                                                                    Nature 409:529-533(2001).
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                        NCBI_TaxID=83334;
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                                                                                                                                                                                                                                                                                                                                                                         similarity).
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                                                                                                                                   produced within the
dismutase.";

Biochemistry 29:372-376(1990).

Calle and which are toxic to biological systems.

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Calle and which are toxic to biological systems.

Calle and which are toxic to biological systems.

Calle and which are toxic to biological systems.

Calle and which are toxic to biological systems.

Calle and which are toxic to biological systems.

Calle AndryIIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).

Calle Andriak Binds 1 copper ion and 1 zinc ion per subunit (By similarity).

Calle SubceLiarak LoCATION: Periplasmic.

Calle SubceLiarak LoCATION: Periplasmic.

Calle Andriak LoCATION: Periplasmic.

Calle Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andria Andri
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MEDLINE=21065122; PubMed=11136448;
MEDLINE=21065122; PubMed=11136448;
Figueroa-Bossi N., Uzzau S., Maloriol D., Bossi L.;
Figueroa-Bossi N., Uzzau S., Maloriol D., Bossi L.;
Forthable assortment of prophages provides a transferable repertoire of pathogenic determinants in Salmonella.";
Mol. Microbiol. 39:260-271(2001).
MSPSP; P53645; AAF824841.; -.
HSSP; P53636; 1EQW.
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Copper (By similarity).
Copper and zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
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By similarity.

4672C31481704468 CRC64;
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Last annotation update)
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01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
Putative Cu/Zn superoxide dismutase.
Name=sodCIII;
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5 LMTLAVFL-FSSAASAASTDATVNLVNANGTGQKIGNITITETEYGLLFTPHLSSLPAGI
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Q8X6B6
ID Q8X6B0
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                                                                                                                                    70
                                                                                                                                                        -i-FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).
-i-CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-i-COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By similarity).
-i-SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
HSSP: P53636: 1EQW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=21534946; PubMed=11677609;
MCClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P.,
MCClelland M., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan B., Sun H., Florae L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R EMBL; AE008337; AAL19860.1; -.. RSP; P53636; 1EQW.
R GO; GO:00046875; F:copper, zinc superoxide dismutase activity; IEA.
GO; GO:0016491; F:copper, zinc superoxide dismutase activity; IEA.
GO; GO:0016491; F:copper, zinc superoxide metabolism; IEA.
GO; GO:0016801; P:superoxide metabolism; IEA.
InterPro; IPRO1424; SOD_CU_ZN.
R ProDom; PF00080; SOD_CU_ZN.
R PROSITE; PS00087; SOD_CU_ZN: 1.
R PROSITE; PS00087; SOD_CU_ZN: 1.
R PROSITE; PS00332; SOD_CU_ZN: 2.
R PROSITE; PS00332; SOD_CU_ZN: 3.
R PROSITE; PS00332; SOD_CU_ZN: 3.
R PROSITE; PS00332; SOD_CU_ZN: 3.
R PROSITE; PS00332; SOD_CU_ZN: 3.
R PROSITE; PS00332; SOD_CU_ZN: 3.
R PROSITE; PS00332; SOD_CU_ZN: 3.
R PROSITE; PS00332; SOD_CU_ZN: 3.
R PROSITE; PS00332; SOD_CU_ZN: 3.
R PROSITE; PS00332; SOD_CU_ZN: 3.
R PROSITE; PS00332; SOD_CU_ZN: 3.
R PROSITE; PS00332; SOD_CU_ZN: 3.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative Fels-1 prophage Cu<sup>2</sup>n superoxide dismutase (EC 1.15.1.1)
(Superoxide dismutase [Cu-Zn]).
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                   124 NADYPVLAPRLKSISQVKGHAIMIHTGGDNHEDHPNPLGGGGARIACGVI 173
                                                                                                                                                                                                                                                                  130 IAKETLLAPRI-TVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                     3;
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49.4%; Pred. No. 3e-29;
live 21; Mismatches 62; Indels 3.
                                                                   43.5%; Score 413.5; DB 2; Length 174;
49.4%; Pred. No. 3e-29;
ive 21; Mismatches 62; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00087; SOD_CU_ZN_1; UNKNOWN_1.
PS00332; SOD_CU_ZN_2; 1.
174 AA; 17995 WW; 557DE7F2B5DB76D0 CRC64;
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                                                                          Query Match
Best Local Similarity 49.4%
Matches 84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 413:852-856(2001)
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Best Local Similarity
Matches 84; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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PROSITE; E
SEQUENCE
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STRAIN-CLESTING TRIMD 0509952 / EHEC;

MEDLINE-21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayawa K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete ganome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

-: FUNCTION: Destroys radicals which are normally produced within the

cells and which are toxic to biological systems (By similarity).

-: CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).

-: COPACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKIKLFFVTSIVTISLLTSITSVVLACSVTSE----VHMIDDNGIKOSIGTVTFTDTDKG
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71 НGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDXTGKHEGPLG-NGHKGDLPRLVVKADG
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
07-JUL-2004 (TrEMBLrel. 27, Last annotation update)
07-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                 124 NADYPVLAPRLKSISQVKGHAIMIHTGGDNHEDHPNPLGGGGARIACGVI 173
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Best Local Similarity 47.8%; Pred. No. 3.46-29;
Matches 88; Conservative 27; Mismatches 53; Indels
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STRAIN-0157.H7 / EDL933 / ATCC 700927 / EHEC;

MEDLINE-21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Miller L.,

A Gorbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

A Modaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Netch R.A., Blattner F.R.;

Nature 409:529-533(2001).

I. Nature 409:529-533(2001).

I. Calls and which are toxic to biological systems (By similarity).

C.I. CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).

SINGLE ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).

SINGLE ACTIVITY: 2 superoxide and 1 zinc ion per subunit (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 HKGDLPRLVVKADGIAKETLLAPRL-TVKEIKGRTVMIHAGGDNYSDKPLPLGGGGGARIA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 HLGDLPALFVTHDGKANYPVLAPRLNSLKEIKGRSLMLAGGGDNHHDHPBPLGGGGARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKIKLFFVTSIVTISLITSITSVVLACSVTSE----VHMIDDNGIKQSIGTVTFTDTDKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53; Indels 16; Gaps
                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.5%; Score 413; DB 2; Length 328; 47.8%; Pred. No. 6.9e-29; ive 27; Mismatches 53; Indels
                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                            Putative superoxide dismutase.
OrderedLocusNames=z3312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.88;
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Matches 88; Conservative
                                                                                                                                                                                             Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 CGVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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SSEPPE

PRELIMINARY;

Q7MFM9

Name=VVA0291; Vibrio vulnificus (strain YJ016).

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70 EHGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGP-LGNGHKGDLPRLVVKAD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 SIVTISLLTSITSVVLACSVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKGLPAG 69
                                                                                                                                                                         Genome Res. 13:2577-2587(2003).

-!- FUNCTION: Destroys radicals which are normally produced within the FUNCTION: Destroys radicals which are toxic to biological systems (By similarity).
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).
-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C -:- Similarity)

C -:- Similarity)

C -:- Similarity)

C -:- Similarity Belongs to the Cu-Zn superoxide dismutase family.

R EMBL; APO05345; BAC96317.1; -.

R GO; GO:0004785; F:recpper, zinc superoxide dismutase activity; IEA.

R GO; GO:0004801; P:rmetal ion binding; IEA.

R GO; GO:0006801; P:superoxide metabolism; IEA.

R GO; GO:0006801; P:superoxide metabolism; IEA.

R GO; GO:0006801; P:superoxide metabolism; IEA.

DR FODOm; PD000469; SOD_CU_ZN; 1.

DR PRODOM; PD000469; SOD_CU_ZN; 1.

DR PROSITE; PS00087; SOD_CU_ZN 1; UNKNOWN 1.

KW COPPET; Metal-binding; Oxidoreductase; Zinc.

SEQUENCE 170 AA; 17613 MM; SAA2C93F1176704A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Pubmed 1. Chang V.-C., Chang C.-H., Tsai H.-C., Chang C.-H., Tsai H.-C., Liao C.-Y., Wu K.-M., Chang Y.-C., Shen A.B.-T., Li J.-C., Su T.-L., Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F., Li J.-C., Su T.-L., Tsai S.-F., Li J.-C., Su T.-L., Tsai S.-F., Li J.-C., Su T.-L., Li J.-Comparative genome analysis of Vibrio vulnificus, a marine pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 GIAKETLLAPRLTVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-UNN-2003 (TrEMBLrel. 24, Created)
01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-UNN-2004 (TrEMBLrel. 26, Last annotation update)
Superroxide dismutase, Cu-Zn.
OrderedLocusNames=VPA1514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.3%; Score 411; DB 2;
48.2%; Pred. No. 4.9e-29;
ative 26; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 48.2%
les 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                NCBI_TaxID=196600;
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SIVTISLLTSITSVVLACSVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKGLPAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBirel. 23, Created)
01-MAR-2003 (TrEMBirel. 23, Last sequence update)
01-WAR-2004 (TrEMBirel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 KQHALMIHAGGDNYSDHPMPLGGGGARMACGVI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superoxide dismutase (Cu-Zn).
Name=sodC; OrderedLocusNames=y0815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 54.2
nes 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=632;
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             20
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Q8D1A0;
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Q8D1A0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 ITSVVLACSVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKGLPAGEHGFHIHEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 MIPNALAOSIT-----WIDLGINQAVGIVDLSESDYGIVFIPNLSGIPAGLHGFHYHANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Destroys radicals which are normally produced within th cells and which are toxic to biological systems (By similarity).
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
             c similarity).

C -:-SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.

EMBL; AP005089; BAC62857.1; -.

R HSSP; P00446; 1YAI.

R GO; GO:00044891; F::meral ion binding; IEA.

R GO; GO:0006801; F::meral ion binding; IEA.

R DITERPO; PRO0142; F::meral ion binding; IEA.

R INTERPO; PRO0142; F::meral ion binding; IEA.

R PROSTEP: SOD CU-ZN; I.

P FroDom; PD0000469; SOD CU-ZN; I.

P R PROSTEF; PS00087; SOD CU-ZN; I.

R PROSTEF; PS00087; SOD CU-ZN; I.

R PROSTEF; PS00087; SOD CU-ZN; I.

P RODOM; PD00087; SOD CU-ZN; I.

R PROSTEF; PS00087; SOD CU-ZN; I.

R PROSTEF; PS00087; SOD CU-ZN; I.

R PROSTEF; PS00087; SOD CU-ZN; I.

R PROSTEF; PS00087; SOD CU-ZN; II.

R PROSTEF; PS00087; SOD CU-ZN; II.

R PROSTEF; PS00087; SOD CU-ZN; II.

R PROSTEF; PS00087; SOD CU-ZN; II.

R PROSTEF; PS00087; SOD CU-ZN; II.

R PROSTEF; PS00877; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROSTEF; PROST
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-!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
EMBL, AEO16813: AAC08341.1; -.
HSSP, P00446; 10AL.
GC; GC:0004785: F:copper, zinc superoxide dismutase activity; IEA.
GC; GC:0006801; F:metal ion binding; IEA.
GC; GC:0006801; F:superoxide metabolism; IEA.
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PROSTIE; PS00087; SOD_CU_ZN 1; UNKNOWN 1.
Complete proteome; Copper; M. Alal-binding; Oxidoreductase; Zinc. SEQUENCE 170 AA; 17985 WW; AABSDE3F11766977 CRC64;
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Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 47.6%; Pred. No. 1.1e-28;
Matches 81; Conservative 26; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLTVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.2%; Score 410; DB 2; 50.6%; Pred. No. 6.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR 2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26, Cu/Zn superoxide dismutase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OrderedLocusNames=VV21471;
Vibrio vulnificus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001424
Pfam; PF00080; Sod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Q8D454
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70 EHGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGP-LGNGHKGDLPRLVVKAD 128
                                                           60 LHGFHLHANGSCESSNKDGKVVLGGAAGGHYDPQNSGKHGYPWTEDNHLGDLPALFADAS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Yersinia pestis KIM.";
"Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).
-!- CATALYMIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 SVISEVHMIDDNGIKQSIGIVIFIDIDKGLQIKIDLKGLPAGEHGFHIHEGGSCGPAEHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=2213863; Bubbed=12142430;
MEDLINE=2213863; Bubbed=12142430;
MEDLINE=2213863; Bubbed=12142430;
Berna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Petherston J.D., Lindler D.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
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HSSP; P53636; 1EQW.
GO, GO:0004785; F:copper, zinc superoxide dismutase activity; 1EA.
GO; GO:0004881; F:metal ion binding; 1EA.
GO; GO:006801; P:superoxide metabolism; 1EA.
GO; GO:006801; P:superoxide metabolism; 1EA.
GO; GO:006801; P:superoxide metabolism; 1EA.
FILEPEYO; IPROM1424; SOD CU ZN.
Fram; PF00080; SOD CU ZN. 1.
FROSITE; PS00087; SOD CU ZN. 1.
FROSITE; PS00087; SOD CU ZN. 1; UNKNOWN 1.
FROSITE; PS00332; SOD CU ZN 2; 1.
COPPET; METAL-binding; Oxidoreductase; Zinc.
SEQUENCE 195 AA; Z0025 MW; E5D1605F3BE77950 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
EMBL; AE013684; AAM84402.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Yersinia.
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                                                                                                                                    129 GIAKETLLAPRLTVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
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Yersinia pestis
                                                                  AAS60586
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                                    AAS60586
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21470413; Pubmed=11586360; DOI=10.1038/35097083;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Peltwell T., Hamiln N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
Genome sequence of Exrainia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=91001 / Biovar Mediaevalis; Song Y., Fei D., Wang J., Zhou D. Song Y., Tong Z., Wang L., Han Y., Zhang J., Chen F., Qin H., Wang J., Li S., Guo Z., Yare C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 SVISEVHMIDDNGIKQSIGTVIFIDIDKGLQIKTDLKGLPAGEHGFHIHEGGSCGPAEHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Destroys radicals which are normally produced within cells and which are toxic to biological systems (By similarity)
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2) .
-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA. GO; GO:0046872; F:metal ion binding; IEA. GO; GO:0016491; F:oxidoreductase activity; IEA. GO; GO:0006801; P:oxidoreductase activity; IEA. IEA. IEA. GO; CO:0006801; P:superoxide metabolism; IEA. IEA.
                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
-!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
EMBL; A7414156; CAC92605.1; -.
EMBL; AED17128; AAS60586.1; -.
PIR; A10409; A10409.
HSSP; P53636; 1EQW.
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PROSITE; PS00087; SOD_CU_ZN 1; UNRNOWN_1.
COMPJITE; PS00033; SOD_CU_ZN_2; UNRNOWN_1.
COMPJETE PS00033; SOD_CU_ZN_2; Metal-binding; Oxidoreductase; Zinc. SEQUENCE 201 AA; 20675 MW; 75D25ABE48BF8DCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 201;
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                                                                                                                                     Last sequence update)
Last annotation update)
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54.2%; Pred. No. 2.6e-28;
ive 18; Mismatches 50
                                                                                              Name=sodC; OrderedLocusNames=YP0311; YP03375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 KGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
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                                                             201 AA
                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
0-92 / Biovar Orientalis;
                                                                                                                                                                                                                                                                                           Enterobacteriaceae; Yersinia.
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                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:523-527(2001)
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tes 83; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            Yersinia pestis.
                                                                                   Q8ZBN3; Q74XS8;
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CO-92
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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RESULT 27
Q8ZBN3
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RECORDENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-Tohana I / ATCC BAA-589 / NCTC 13251;

CSTRAIN-Tohana I / ATCC BAA-589 / NCTC 13251;

CSTRAIN-Tohana I / ATCC BAA-589 / NCTC 13251;

REDIAINS-22827954; PubMed=12910271; DOI=10.1038/ng1227;

RA Harris D.E., Holden M.TG., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Atkin R., Hample M., Cronin A., Davis P., Doggett J.,

RA Cerdeno-Tarraga A.-M., Hampin M., Houser H., Holroyd S., Jagels K.,

RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

RA Eather S., Moule S., Sanders M., Saunders D., Seeger K.,

RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

RA Diwin L., Whitehead S., Barrell B.G., Maskell D.J.;

RA Comparative analysis of the genome sequences of Bordetella pertussis,

R Bordetella parapertussis and Bordetella bronchiseptica.;

RC -i-FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 GKAVPALAAGGHLDPNKTGVHLGPYNDKGHLGDLPGLVVNADGTATYPVLAPRLKSLSEV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 SVISEVHMIDDNGIKQSIGTVIFIDIDKGLQIKTDLKGLPAGEHGFHIHEGGSCGPAEHD 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 GHLTAGLQAHGHYDPDKTGKHEGPLGN-GHKGDLPRLVVKADGIAKETLLAPRL-TVKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                     [1] SEQUENCE FROM N.A. STRAIN-91001 / Biovar Mediaevalis; STRAIN-91001 / Biovar Mediaevalis; STRAIN-91001 / Biovar Mediaevalis; Song Y., Tong Z., Wang L., Han Y., Zhang J., Chen F., Qin H., Wang J., Li S., Guo Z., Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z., Yang R., Wang J., Huang P., Yang R., Submitted (APR-2003) to the BMBL/GenBank/DDBJ databases. Submitted (APR-2003) To The EMBL/GenBank/DDBJ GATABASES.
                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
NCBI_TaxID=632;
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Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Alcaligemeceae, Bordetella.
NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.5%; Score 404; DB 2; Length 201; 54.2%; Pred. No. 2.6e-28; ive 18; Mismatches 50; Indels
                   AASGOS86;
24-MAR-2004 (TrEMBLrel. 27, Created)
24-WAR-2004 (TrEMBLrel. 27, Last sequence update)
04-MAY-2004 (TrEMBLrel. 27, Last annocation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative superoxide dismutase (EC 1.15.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 KGRIVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 KQHALMIHAGGDNYSDHPMPLGGGGARMACGVI 200
  201 AA
  PRT;
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les 83; Conservative
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PRELIMINARY;
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                                                                                                                            Superoxide dismutase.
SODC OR YP0311.
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 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-RB50 / ATCC BAA-588;

MEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;

RETAIN-RB50 / ATCC BAA-588;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Murgall K.L.,

A Cardeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

A Cardeno-Tarraga A.-M., Temple L., Basham D., Bason N., Cherevach I.,

A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

A Pathwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Samp S., Simmonds M., Skelton J., Squares S., Stevens K.,

Shamp S., Simmonds M., Skelton J., Squares S., Stevens K.,

A Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

R. Genet. 35:32-40(2003).

"In FUNCTION: Destroys radicals which are normally produced within the

Cells and which are toxic to biological systems (By similarity).

"Corphirytic ACTIVITY: 2 superoxide + 2 H++ = O(2) + H(2)O(2).

CORPACTOR: Binds I copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                         70 EHGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGPLG-NGHKGDLPRLVVKAD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 VHGFHLHDKPSCAMTKVDGKDMVGGGAGGHWDPDKTGAHKGPYDKTGHKGDLPAVYVAAD 119
                                                                                                                                                                                                                                                                                                                                                                      60
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                                                                                                                                                                                                                                                                                                                                                                                           10 SIVTISLLTSITSVVLACSVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKGLPAG
                                 c = 1. SIMILARITY: Belongs to the Cu-zn superoxide dismutase family.

EMBL; BK640417; EA242345.1; -...

EMBL; BK640417; EA242345.1; -...

R GO; GO:004085; F:copper. zinc superoxide dismutase activity; IEA.

GO; GO:0046812; F:metal ion binding; IEA.

GO; GO:0046812; F:metal ion binding; IEA.

GO; GO:006801; P:superoxide metabolism; IEA.

R GO; GO:006801; P:superoxide metabolism; IEA.

InterPro; IPR001424; SOD_CU_ZN.

R Pfam; PR00080; SOD_CU_ZN.

R PROSTIE; PS00080; SOD_CU_ZN; I.

R PROSTIE; PS00080; SOD_CU_ZN; I.

R ROSTIE; PS00080; SOD_CU_ZN; I.

R ROSTIE; PS00080; SOD_CU_ZN; I.

R ROSTIE; PS00080; SOD_CU_ZN; I.

R ROSTIE; PS00080; SOD_CU_ZN; I.

R ROSTIE; PS00080; SOD_CU_ZN; I.

R ROSTIE; PS00080; SOD_CU_ZN; I.

R ROSTIE; PS00080; SOD_CU_ZN; I.

R ROSTIE; PS00080; SOD_CU_ZN; I.

R ROSTIE; PS00080; SOD_CU_ZN; II.

R ROSTIE; PS00080; SOD_CU_ZN; II.

R ROSTIE; PS00080; SOD_CU_ZN; II.
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--- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
BEMBL; BR640447; CAB33849.11. -.
GO; GO:0004787; F:copper, zinc superoxide dismutase activity; IEA.
GO; GO:0046872; F:metal ion binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 GIAKETLLAPRLTVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
-1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2) -1- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OrderedLocusNumes=BB3357;
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                               42.0%; Score 399; DB 2; Length 170; 47.6%; Pred. No. 6e-28; Live 25; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative superoxide dismutase (EC 1.15.1.1).
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                                                                                                                                                                                                                                                                                                                                      81; Conservative
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70 EHGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGPLG-NGHKGDLPRLVVKAD 128
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SEQUENCE OF 23-173.
MEDLINE-83289129; PubMed=6884993;
Steffens G.J., Bannister W.H., Flohe D., Gunzler W.A., Kim S.-M.A., Ottling F.;
"The primary structure of Cu-zn superoxide dismutase from Photobacterium leiogonathi: evidence for a separate evolution of Cu-zn Superoxide dismutase in bacteria.";
Hoppe-Seyler's Z. Physiol. Chem. 364:675-690(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 SIVTISLLTSITSVVLACSVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKGLPAG
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Bannister J.V., Parker M.W.;
Bannister J.V., Parker M.W.;
"The presence of a copper/zinc superoxide dismutase in the bacterium Photobacterium leiopnathi: a likely case of gene transfer from eukaryotes to prokaryotes.";
Proc. Natl. Acad. Sci. U.S.A. 82:149-152(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leunissen J.A.M., de Jong W.W.; "Copper/zinc superoxide dismutase: how likely is gene transfer from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Bacteriocuprein superoxide dismutase of Photobacterium leiognathi.
Isolation and sequence of the gene and evidence for a precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIAKETLLAPRLTVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006801; P:superoxide metabolism; IEA.
InterPro; IRRO1424; SOD_CU_ZN.
Pfam; PF00080; Sod_Cu; 1.
ProDom; P0000469; SoD_CU_ZN; 1.
PROSITE; PS00087; SOD_CU_ZN; 1. UNKNOWN 1.
PROSITE; PS00332; SOD_CU_ZN 2: UNKNOWN 1.
Complete proceome; Copper; Metal-binding; Oxidoreductase; Sinc. SEQUENCE 170 AA; 17394 MW; DAEA2CCES0C4FASD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Photobacterium leiognathi.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae, Photobacterium.
                                                                                                                                                                                                                                                                                                                               similarity 47.1%; Score 391; DB 2; Length 170; Similarity 47.1%; Pred. No. 3.1e-27; Conservative 24; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISCUSSION OF POSSIBLE GENE TRANSFER FROM EUKARYOTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
01-RF-1988 (Rel. 07, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
01-OCT-2004 (Rel. 45, Last annotation (EC 1.15.1.1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ponyfish to Photobacterium leiognathi.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=87109348; PubMed=3805055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Evol. 23:250-258(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=658;
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similarity).
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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                    "Novel dimeric interface and electrostatic recognition in bacterial
     Bourne Y., Redford S.M., Steinman H.M., Lepock J.R., Tainer J.A., Getzoff B.D.;
                                                                                                                                                                                                                                                                                                      Pfam, PF00080; Sod_Cu_1.

Probom, PD000469; Sod_Cu_Zu_1.

PROSITE; PS00087; SOD_CU_ZN_1; 1.

PROSITE; PS00332; SOD_CU_ZN_2; 1.

3D-Structure, Antioxidant; Copper, Direct protein sequencing; Metal-binding; Oxidoreductase; Periplasmic; Signal; Zinc.

SIGNAL
                                                                                                                                                                                                                                                                                                                                                            Superoxide dismutase [Cu-Zn] Copper.
                                     Proc. Natl. Acad. Sci. U.S.A. 93:12774-12779 (1996)
                                                                                                                                                                                                                                                                                                                                                                                  Copper and zinc.
Zinc.
Zinc.
Zinc.
Copper.
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PDB: 1B5; X-ray; A=23-173.
PDB: 11BB; X-ray; A=23-173.
PDB: 11BB; X-ray; A=23-173.
PDB: 11BP; X-ray; A=23-173.
PDB: 11BF; X-ray; A=23-173.
PDB: 10AJ; X-ray; A=23-173.
PDB: 10AJ; X-ray; A=23-173.
PDB: 10AJ; X-ray; A=23-173.
PDB: 10AJ; X-ray; A=23-173.
PDB: 1AI; X-ray; A=23-173.
PDB: 1AI; X-ray; A=23-173.
PDB: 1AI; X-ray; A=23-173.
PDB: 1AI; X-ray; A=23-173.
PDB: 1AI; X-ray; A=23-173.
MEDLINE=97075068; PubMed=8917495;
                             Cu, Zn superoxide dismutase.";
                                                                                                                                                                                                                   EMBL; J02658; AAA25632.1; -.
                                                                                                                                                                                                                                                                                                                                                                                         A26689; DSFOCL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 GMHGFHIHQNGSCASSEXDGKVVLGGAAGGHYDPBHTNKHGFPWTDDNHKGDLPALFVSA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 GEHGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGP-LGNGHKGDLPRLVVKA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 SIVTISLLTSITSVVLACSVTSEVHMID-DNGIKQSIGTVTFTDTDKGLQIKTDLKGLPA 68
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-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-!- FUNCTION: May confer survival advantage by accelerating dismutation of superoxide of environmental origin to hydrogen peroxide, disruptive to the normal mucociliary clearance process in the host.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps.
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Kroll J.S., Langford P.R., Loynds B.M.;
"Copper-zinc superoxide dismutase of Haemophilus influenzae and H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBDNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Periplasmic (Potential).
-!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 DGIAKETLLAPRLTVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2) COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                           Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                 58; Indels
                                                                                                                                                                                                                                                                                                                        18109 MW; 5931576F1E2A8F47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1).
                                                                                                                                                                                                                                                                                                                                                                        41.2%; Score 391; DB 1;
47.4%; Pred. No. 3.2e-27;
ative 26; Mismatches 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 81; Conservative
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1122
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173 AA;
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STRAIN=12822 / ATCC BAA-587;

MEDLINE=2282754; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=2282754; PubMed=12910271; DOI=10.1038/ng1227;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R., Margall J. A. A. A. A. A. A. A. A. A. A. A. Baker S., Basham D., Bason N., Cherevach I., Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A., A. A. A. A. A. A. A. A. Hamin M., Hauser H., Holroyd S., Jagels K., A. Feltwell T., Goble A., Hamin N., Hauser H., Holroyd S., Jagels K., Peltwell T., Goble A., Morberczak H., O'Neil S., Ormond D., Price C., R. Babinowitsch E., Ruteer S., Sanders M., Saunders D., Seeger K., A. Babinowitsch E., Ruteer S., Sanders M., Saunders D., Seeger K., A. Shapp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., A. Dawin L., Whitehead S., Barrell B.G., Maskell D.J.;

Comparative analysis of the genome sequences of Bordetella pertussis, R. Comparative analysis of the genome sequences of Bordetella pertussis, R. Mat. Genet. 35:32-40(2003).

C. :- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).

C. :- COFACTOR: Binds I copper ion and I zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 GHLTAGLQAHGHYDPDKTGKHEGP-LGNGHKGDLPRLVVKADGIAKETLLAPRL-TVKEI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 GKLTSGLAAGGHWDPKGAKQHGYPWQDDAHLGDLPALTVLHDGTATNPVLAPRLKKLDEV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 SVISEVHMIDDNGIKQSIGTVIFIDIDKGLQIKTDLKGLPAGEHGFHIHEGGSCGPAEHD
                                            HSSP; P24702; ZARS.
InterPro; IPR001424; SOD_CU_ZN.
InterPro; IPR001424; SOD_CU_ZN.
Pfam; P700080; Sod_Cu; I.
PROSITE; PS00087; SOD_CU_ZN!; 1.
PROSITE; PS00033; SOD_CU_ZN[2; 1.
Antioxidant; Copper; Metal-binding; Oxidoreductase; Periplasmic; Signal; Zinc.
Signal; Zinc.
Signal; Zinc.
Signal; Zinc.
Signal; Zinc.
Signal; Zinc.
Signal; Zinc.
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Alcaligenaceae, Bordetella.
NCBI_TaxID=519;
                                                                                                                                                                                                                                           Superoxide dismutase [Cu-Zn].
Copper (By similarity).
Copper (By similarity).
Copper and zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
By similarity.
W, ACC3AG1EFAF201D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.2%; Score 391; DB 1; Length 187;
llarity 51.0%; Pred. No. 3.5e-27;
Conservative 22; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGRIVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 194 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              19510 MW;
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      EMBL; M84013; AAA24954.1;
PIR; B41654; B41654.
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es 78; Conserv
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114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 VHGFHLHAKPSCAMTKYDGKDMVGGGAGGHWDPDNTGAHKGPYDKTGHKGDLPAVYVTAD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).

-!- FUNCTION: Destroys radicals which are normally produced within the calls and which are toxic to biological systems (By similarity).

-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).

-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 SIVTISLLTSITSVVLACSVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKGLPAG
L. SIMILARITY;

-1 SIMILARITY;

REMBL; BX640428; CAE37052.1;

GO; GO:0004785; F:Copper, zinc superoxide dismutase family.

GO; GO:0016491; F:copper, zinc superoxide dismutase activity; IEA.

RE GO; GO:0016491; F:coxidoreductase activity; IEA.

RE GO; GO:0016491; F:coxidoreductase activity; IEA.

REMO; GO:0016491; F:coxidoreductase activity; IEA.

REMO; FPFO; IRROUL42, SOD_CU_ZN.

REMO; FPFO; IRROUL42, SOD_CU_ZN.

REMO; FPFO; REMO; SOD_CU_ZN.

REMO; FPFO; REMO; SOD_CU_ZN.

REMO; FPFO; REMO; SOD_CU_ZN.

REMO; FPFO; REMO; SOD_CU_ZN.

REMO; FPFO; REMO; SOD_CU_ZN.

REMO; FPFO; REMO; SOD_CU_ZN.

REMO; FPFO; REMO; SOD_CU_ZN.

REMO; FPFO; REMO; SOD_CU_ZN.

REMO; FPFO; REMO; SOD_CU_ZN.

REMO; FPFO; REMO; SOD_CU_ZN.

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REMO; FPFO; REMO; SOD_CU_ZN.

REMO; FPF
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MEDLINE-Sine Mile phase I / RSA 493;
MEDLINE-2260867; PubMed=12704232;
Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,
DeBoy R.T., Daugherty S.C., Brinkec L.M., Madupu R., Dodson R.J.,
Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
"Complete genome sequence of the Q-fever pathogen, Coxiella
burnetii.";
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GO; GO:0006801; P:superoxide metabolism; IEA.
InterPro; IPR001424; SOD_CU_ZN.
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-!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family EMBL; AE016965; AA091315.1; -.
HSSP; P55636; 1EQW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 GIAKETLLAPRLTVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Coxiellaceae; Coxiella.
NCBI_TaxID=777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 47.1%; Pred. No. 3.7e-27;
Matches 80; Conservative 24; Mismatches 62; Indels
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Name-sodC; OrderedLocusNames=CBU1822;
Coxiella burnetii.
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PRINTS; PR00068; CUZNDISMTASE.
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059623;
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                                                                                                                                                                                                                              Matches
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       KKW
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                                                                                                                                                                              68 AGE-HGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGPLG-NGHKGDLPRLVV 125
                                                                                                                                                                                                        65 PGRIHGFHIHVNPDCS-----NKGBAAGGHLDPANTGKHLGPYNPNGHLGDLPALTV 116
                                                                                                                               67
                                                                                                                                                         64
                                                                                                                                              14 ISLLTSIT-----SVVLACSVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=22491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
Kajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Destroys radicals which are normally produced within cells and which are toxic to biological systems (By similarity)
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).
-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                    126 KADGIAKETLLAPRLTVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                    ENGRATL PILAPRLYVKNLIGHSLMIHAGGDNYSDHPKELGGGGARIACGIV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
-!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
PROSTIE; PS00087; SOD_CU_ZN_1; UNRNOWN_1.
PROSITIE; PS00332; SOD_CU_ZN_2; UNRNOWN 1.
Complete proteome; Copper; Metal-binding; Oxidoreductase; Zinc. SEQUENCE 170 AA; 17871 MW; 5CB62830C4C2DE04 CRC64;
                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                       Length 170;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 45, Last annotation update)
Superoxide dismutase (Cu-Zn] precursor (EC 1.15.1.1).
Name=sodC; OrderedLocusNames=NMA1617;
                                                                                                  54;
                                                                      40.7%; Score 387; DB 2;
49.1%; Pred. No. 7.2e-27;
                                                                                    Pred. No. 7.2e
; Mismatches
                                                                                                                                                                                                                                                                                                                                     186 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     PRT;
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Pfam; PF00080; Sod Cu; 1.
Probom; PD000469; SOD CU ZN; 1.
PROSITE; PS00332; SOD CU ZN 1; 1.
PROSITE; PS00332; SOD CU ZN 1; 1.
                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL162756; CAB84845.1; -. PIR; E81855; E81855.
                                                                             Local Similaricy
nes 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitidis Z2491.";
Nature 404:502-506(2000),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                   NEIMA
                                                                                                                                                                                                                                                              117
                                                                      Query Match
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SODC_NEIMA
                                                                                             Matches
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66 LPAGEHGFHIHEGGSCGPAEHDGHLTAGLQAHGHYDPDKTGKHEGP-LGNGHKGDLPRLV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 VTSIVTISLLTS--ITSVVLACSVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIR=MCSB / Serogroup B;
STRAIR=MCSB / Serogroup B;
STRAIR=MCSB / Serogroup B;
STRAIR=MCSB / Serogroup B;
Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
Nelson K.J., Nelson W.C., Gwinn W.L., DeBoy R.T., Peterson J.D.,
Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
Qin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M.,
Graddi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKADGIAKETLLAPRIT-VKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=MCS8 / Serogroup B;
MEDLINE=88084476; PubMed=9423860;
MIDELINE=8808476; PubMed=9423860;
Wilst K.E., Dunn K.L., Farrant J.L., Reddin K.M., Gorringe A.R.,
Langford P.R., Kroll J.S.;
"Periplasmic superoxide dismutase in meningococcal pathogenicity.";
Infect. Immun. 66:213-217(1998).
                                                                                                     Copper (By similarity).
Copper (By similarity).
Copper and zinc (By similarity)
Zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
16-UTL-1999 (Rel. 45, Last annotation update)
01-OCT-2004 (Rel. 45, Last annotation update)
Superoxide dismunses (Cu-27) precursor (EC 1.15.1.1).
Name=sodC; Orderedocus/Names=NNB1398;
Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                    40.7%; Score 387; DB 1; Length 186; 45.1%; Pred. No. 8e-27;
                                                                              dismutase [Cu-Zn]
                                                                                                                                                                                                                                                                                                                                                                                                                            61; Indels
                                                                                                                                                                                                                                                                                           By similarity.
04C84AB87FC7522D CRC64;
                                                                                                                                                                                                                                                                     (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=MC58 / Serogroup B;
MEDLINE=96118708; PubMed=7496539;
Kroll J.S., Langford P.R., Wilks K.E., Keil A.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                            31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 AA
                                                                                                                                                                                                                                                                     Copper
                                                                                                                                                                                                                                                                                           182 B
19550 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                            Signal;
                                                                                                                                                    104
113
122
125
160
186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                            Periplasmic;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                       79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEIMB
                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
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Pasteurellaceae; Pasteurella
                                                                SEQUENCE FROM N.A.
                      NCBI_TaxID=747;
      8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interproj IRP001424; SOD_CU_ZN.

Pfam; PF00080; Sod_Cu; 1.

Probom; PD000469; SOD_CU_ZN, 1.

PROSITE; PS00037; SOD_CU_ZN_1.

PROSITE; PS00332; SOD_CU_ZN_2; 1.

Antioxidant; Complete proteome; Copper; Metal-binding; Oxidoreductase; Periplasmic; Signal; Zinc.

Periplasmic; Signal; Zinc.

Potential.

CHAIN

23 186 Superoxide dismutase [Cu-Zn].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 SVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKGLPAGEHGFHIHEGGSCGPAEHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 SIEVKVQQLDPVNGNKDVGTVTITESNYGLVFTPDLQGLSEGLHGFHIHENPSCEPKEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Bacterial [Cu,Zn]-superoxide dismutase: phylogenetically distinct from the eukaryotic enzyme, and not so rare after all!"; Microbiology 141:2271-2279(1995).
-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                        similarity).
-!- SUBUNT: Honodimer (By similarity).
-!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
-!- SUMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
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Superoxide dismutase [Cu-Zn].
Copper (By similarity).
Copper and zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.3%; Pred. No. 1.2e-26;
Matches 77; Conservative 22; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copper (By similarity).

By similarity.
6499049BFAC3427C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ001313; CAA04674.1; --
EMBL; AE002488; AAF41762.1; --
EMBL; X83126; CAA58207.1; --
EMPL; F81088; F81088.
HSSP; P24702; 2ABS.
TIGR; NMB1398;
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79 81
104 1
113 1
122 1
125 1
160 11
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DISULFID
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PASMU
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15-DEC-1998 (Rel. 37, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 44, Last annotation update)
Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1).
Name=sodC; OrderedLocusNames=PM1952;
Pasteurella multocida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

186 AA

STANDARD;

PASMU

SODC PA Q59689;

ID DAT DAT DAT OC OC OC

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RA XCOLINE=90118/U01, runomed=149053;

RRA XCOLI 0.2., Langford P.R., Wilks K.E., Keil A.D.;

Racterial [Uu,Zn]-superoxide dismutase: phylogenetically distinct

"Bacterial [Uu,Zn]-superoxide dismutase: phylogenetically distinct

RT from the eukaryotic enzyme, and not so rare after all!";

RI Microbiology 141:2271-2279 [1995].

EL Microbiology 141:2271-2279 [1995].

C. :- CAPATOTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).

C. :- CAPATATIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).

C. :- CAPATATIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).

C. :- CAPATATIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).

C. :- CAPATOTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).

C. :- SUBCELLULAR LOCATION: Periplasmic [By similarity).

C. :- SUBCELLULAR LOCATION: Periplasmic [By similarity).

C. :- SUBCELLULAR INCATION: Periplasmic [By similarity).

C. :- SUBCELLULAR INCATION: Periplasmic [By similarity).

C. :- SUBCELLULAR INCATION: Periplasmic [By similarity].

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EMSL; P24702; P24702; P24702; P24702; P24702; P24702; P24702; P24702; P24702; P24702; P260080; Sod Cu, 1...
Problem; P0008049; SoD Cu ZN, 1...
PROSITE; PS00087; SoD Cu ZN, 1.; PROSITE; PS00087; SoD Cu ZN, 2; 1...
PROSITE; PS00332; SoD Cu ZN, 2; 1...
PROSITE; PS00332; SoD Cu ZN, 2; 1...
PROSITE; PS00332; SoD Cu ZN, 2; 1...
PROSITE; PS00332; SoD Cu ZN, 2; 1...
PROSITE; PS00332; SoD Cu ZN, 2; 1...
PROSITE; PS00332; SoD Cu ZN, 2; 1...
PROSITE; PS00332; SoD Cu ZN, 2; 1...
PROSITE; PS00332; SoD Cu ZN, 2; 1...
PROSITE; PS00332; SoD Cu ZN, 2; 1...
PROSITE; PS00332; SoD Cu ZN, 2; 1...
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STRAIN=PMT0;
MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
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Copper (By similarity).
Copper and zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
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By similarity.

A -> V (in Ref. 2).
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Best Local Similarity 51.7%; Pred. No. 2.3e-26;
Matches 77; Conservative 17; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 VMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE006232; AAK04036.1; -.
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96118708; PubMed=7496539;
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186 AA;
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RESULT 39 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=20124004; PubMed=10656823,
POrest K.T., Landford P.R., Kroll J.S., Getzoff E.D.;
Cu, Zn superoxide dismutase structure from a microbial pathogen establishes a class with a conserved dimer interface.",
J. Mol. Biol. 296:145-153(2000).
I-FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
I-CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
I-COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit.
I-SUBUNIT: Homodaimer.
I-SUBUNIT: Belongs to the Cu-Zn superoxide dismutase family.
                                                                                                                                                                                       [1] -
SEQUENCE FROM N.A.
SIGUINCE FROM N.A.
STRAIN-Serotype III / Isolate 1421 (Nielsen);
MEDLINE=97101016; PubMed=8945543;
Langford P.R., Loynds B.M., Kroll J.S.;
"Cloning and molecular characterization of Cu, Zn superoxide dismutase from Actinobacillus pleuropneumoniae.";
Infect. Immun. 64:5035-5041(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 91-177 FROM N.A.

STAILN'SECTOYPE III / Isolate 1421 (Nielsen);

MEDLINE=56118708; PubMed=7496539;

Kroll J.S., Langford P.R., Wilks K.E., Keil A.D.;

Bacterial [Cu,Zn] -superoxide dismutase: phylogenetically distinct from the eukaryotic enzyme, and not so rare after all!";
                                                                                                                                 Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
Bacceria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Actinobacillus.
NCBI_TaxID=715;
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=S 4074 / Serotype 1;
Helie M.C., Sirois M., Ouellet C., Boissinot M.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                          01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1).
                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Serotype III / Isolate 1421 (Nielsen);
MEDLINE-921S8680; PubMed=1741300;
Medline-921S8680; PubMed=1741300;
"recF in Actinobacillus pleuropneumoniae.";
Nucleic Acids Res. 20:615-615(1992).
                                      190 AA
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EMBL; X83123; CAA58204.1; -...
PIR; 139650; 139650.
PDB; ZAPS; X-ray; A/B=29-190.
InterPro; IPR001424; SOD_CU_ZN.
Pfam; PF00080; Sod_Cu; 1.
                                              P24702; Q59135;

01-MAR-1992 (Rel. 21, Created)

01-NOV-1997 (Rel. 35, Last seq

01-OCT-2004 (Rel. 45, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X99396; CAA6771.1; -. EMBL; U51440; AAB02816.1; -.
                                     STANDARD;
                                   SODC ACTPL
                                                                                                                     Name=sodC;
        RESULT 38
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ProDom; PD000469; SOD CU ZN; 1.
PROSITE; PS00087; SOD CU ZN 1; 1.
PROSITE; PS00332; SOD CU ZN 2; 1.
3D-structure; Antioxidant; Copper; Metal-binding; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 190;
                                                                                                                               Superoxide dismutase [Cu-Zn]
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(in Ref. 2).
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Last annotation update)
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                                                                                                                                                                                      Copper and zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.6%; Score 376; DB 1, 51.7%; Pred. No. 8e-26; iive 18; Mismatches
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N -> D (in F
FVE -> TIA
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                                                                                Periplasmic; Signal; Zinc. SIGNAL 1 23
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Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 NLSSLPEGFRGFRGFRYHVNPSCD--TKDG--VIGGAAGGHYDPYQTNKHLGPYNINGHLGDL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRLVVKADGIAKETLLAPRL-TVKEIKGRTVMIHAGGDNYSDKPLPLGGGGARIACGVI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KIKLFFVTSIVTISLLTSITSVVLACSVTSEVHMIDDNGIKQSIGTVTFTDTDKGLQIKT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alsmark U.C.M., Frank A.C., Karlberg B.O., Legault B.-A., Ardell D.H., Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M., La Scola B., Holmberg M., Andersson S.C.B.;

La Scola B., Holmberg M., Andersson S.C.B.;

"The louse-borne human pathogen Bartonella quintana is a genomic derivative of the zoonotic agent Bartonella henselae.";

Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).

-! FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).

-! CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Langford P.R., Klohl J.S., "Distribution, cloning, characterisation and mutagenesis of sodC, "Distribution, cloning, characterisation and mutagenesis of sodC, gene encoding copper/zinc superoxide dismutase, a potential determinant of virulence, in Haemophilus ducreyi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).

-!-SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.

EMB1, BX897659; CAR27655.1; -.

InterPro; IPR001424; SOD_CU_ZN.

Pram; PF00080; Sod Cu; 1.

ProDom; PD000469; SOD_CU ZN; 1.

PROSITE; PS00087; SOD_CU ZN; 1.

PROSITE; PS00087; SOD_CU ZN 1; 1.

Complete proteome; Copper; Metal-binding; Oxidoreductase; Zinc.

SEQUENCE 175 AA; 18861 NW; 5CC83A4ADBF35DBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.4%; Score 374; DB 2; Length 175; 44.7%; Pred. No. 1.1e-25; ive 27; Mismatches 62; Indels 1
Name=sodC; OrderedLocusNames=BH08570;
Bartconella henselae (Rochalimea henselae).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bartonellaceae; Bartonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           059452; 059449; 059453; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Name=sodC; OrderedLocusNames=HD0848; Haemophilus ducreyi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 AA
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STRAIN=35000HP / ATCC 700724;
MEDLINE=97288949; PubMed=9143881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=35000HP / ATCC 700724;
MEDLINE=97149276; PubMed=8996084;
                                                                                                                        [1]
SEQUENCE FROM N.A.
STRAIN=AICC 49882 / Houston 1;
PubMed=15210978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 44.7%
nes 80; Conservative
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                                                                                             NCBI_TaxID=38323;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLOAHGHYDPDKTGKHEGPLG-NGHKGDLPRLVVKADGIAKETLLAPRL-TVKEIKGRTV 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X98737; CA67289.1; -.

EMBL; M47664; AAB4123.1; -.

EMBL; AAB1123.1; -.

EMBL; AR017153; AAP95739.1; -.

EMBL; A83125; CAA58206.1; -.

PIRSP; P24702; AAPS.

HSSP; P24702; AAPS.

HSSP; P24702; AAPS.

HSSP; P24702; AAPS.

HSSP; P24702; AAPS.

PROSITE; P6000469; SOD_CU_ZN, 1.

PROSITE; P600087; SOD_CU_ZN, 1.

PROSITE; P600332; SOD_CU_ZN, 2; 1.

Antioxidant; Complete proteome; Copper; Metal-binding; Oxidoreductase; Periplasmic; Signal; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 VHMIDDNGIKQSIGTVTFTDTDKGLQIKTDLKGLPAGEHGFHIHEGGSCGPAEHDGHLTA
                                                                                                                                                                                                                                                                                                                     Stevens M.K., Hassett D.J., Radolf J.D., Hansen E.J.; "Cloning and sequencing of the gene encoding the Cu, Zn-superoxide dismutase of Haemophilus ducreyi."; Gene 183:35-40(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Periplasmic.
-!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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Copper (By similarity).
Copper and zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
Zinc (By similarity).
Kopper (By similarity).
By similarity).
W, B41D3210AB2BCO6C CRC64;
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                                                                                                                                SEQUENCE FROM N.A.
STRAIN=35000HP / ATCC 700724;
Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur Johnson L., Nguyen D., Mang J., Forst C., Hood b.;
"The complete genome sequence of Haemophilus ducreyi.";
submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.4%; Score 374; DB 1;
52.7%; Pred. No. 1.3e-25;
iive 15; Mismatches 53;
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94 CC
1117 CC
135 211
136 211
138 CC
173 CC
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Matches 78; Conservative
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199 AA;
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Search completed: October 26, 2004, 09:44:55 Job time : 198 secs

OM protein - nucleic search, using frame_plus_p2n model

October 31, 2004, 00:05:50; Search time 92 Seconds (without alignments) 3878.435 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-009-823A-1 2586 1 WMGSLFIGATGMKTHSTGLG......NSKSVTTADTWLQKALELKR 502

BLOSUM62 Scoring table:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model - 120F=x1h
-MODEL=frame+ p2n.model - 120F=x1h
-O=/cgn2_1/USFTO_spool/US10009823/runat_26102004_100130_1634/app_query.fasta_1.647
-O=/cgn2_1/USFTO_spool/US10009823/runat_26102004_100130_1634/app_query.fasta_1.647
-O=/cgn2_1/USFTO_spool/US10009823/runat_SURFIX=xni - MINMATCH=0.1 - LOOPCL=0
-UONDEXT=0 - UNITS=bits - START=1 - END=-1 - MATKIX=blosum62 - TRANS=human40.cdi
-LIST-45 - DOCALIGN=200 - THR SCORE-pct - THR MAX=100 - THR MIN=0 - ALIGN=40
-USD=LOCAL - OUTFWT=pto - NORM=ext - HEAPSIZE=500 - MINLENE=0 - NAXLEN=200000000
-USDEXT=0 - OUTFWT=pto - NORM=ext - HEAPSIZE=500 - MINLENE=0 - NAXLEN=200000000
-USDEXT=0 - OUTFWT=PTO - NORM=CORE-0 - MINLENE=0 - NAXLENE=0 - ICPU=3
-UNO MMAAP - LARGEQUERY - NEG SCORES=0 - MAIT - DSPELOCK=100 - LONGLOG
-DEV TIMBOUT=120 - WARN TIMSOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7

Database :

lssued_Patents_NA:*
1: /cgn2_6/ptodatca1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodatca1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodatca1/ina/6B_COMB.seq:*
4: /cgn2_6/ptodatca1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodatca1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodatca1/ina/PcTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	. Score		Query Match Length DB	DB	ID	Description
	1 528.5		:	4	US-09-252-991A-2955	Sequence 2955, Ap
	2 528.5			4	US-09-252-991A-2728	Sequence 2728, Ap
•	3 475.5		1239	4	US-09-543-681A-4010	Sequence 4010, Ap
	4 414.5		6	4	US-09-790-988-1	Sequence 1, Appli
	5 303		810	4	US-09-252-991A-3144	Sequence 3144, Ap
υ	6 302	2 11.7		4	US-09-252-991A-2823	Sequence 2823, Ap
	7 286		798	4	US-09-543-681A-3938	Sequence 3938, Ap
	8 281.5			m	US-08-483-857-1	
	9 277.5			Н	US-08-436-748-1	Sequence 1, Appli
Ä	0 237.5			ო	US-08-483-857-3	
11				Н	US-08-436-748-4	Sequence 4, Appli
12				4	US-09-689-065B-2	'n

Sequence 13873, A	Sequence 13656, A	3047	68, 4	1, 1	1,	Sequence 1, Appli	ä	۲,	Sequence 1, Appli	1, Appl	99	'n	'n	Sequence 5, Appli	'n	'n	Š	'n	39,	H	N	N	• •	٠,	S	Ġ	'n	H	203,	198,	20	Sequence 44, Appl	-
-09-252-	-60	09-252-	09-206-942	US-08-038-682-1	302-832	US-08-530-198-1	US-08-469-880-1	7	US-08-617-697-1	US-08-719-641-1	19-206-942-	682-	832-	US-08-530-198-5	880-	470-	US-08-617-697-5	US-08-719-641-5	702B-3	US-09-252-991A-13774	-436	US-08-483-857-2	39-103-840A	- 1	US-09-206-942-64	US-09-206-942-62	-252	US-09-477-135A-117	-056-55	-072-596-1	US-09-072-967-203	US-09-206-942-44	
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176	176	~		•		173.5		173.5	173.5		173.5			173.5			173.5	173.5	165	160	155	155	151.5	151.5	149.5	149.5	145.5	4	144	144	144	142	
13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	78	29	30	31	32	33	34	9	36	37	38		40	41	42	43	44	45	
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ALIGNMENTS

Sequence 2955, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION: US/09252991A
Patent No. 6551795
GENERAL INFORMATION: US/09252991A
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AEROGAINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AEROGAINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PLILING DATE: 1998-02-18
PRIOR PLILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2955 TYPE: DNA ORGANISM: Pseudomonas aeruginosa US-09-252-991A-2955 US-09-252-991A-2955 LENGTH: 1416

Conservative: Mismatches: Indels: Length: Matches: 4.66e-47 528.50 45.84% 29.21% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match:

US-10-009-823A-1 (1-502) x US-09-252-991A-2955 (1-1416)

31 AGTITCAACATCGGCCTGAGCGGCATCCAGGCGGCCTCTAGCGGCCTGAACGTCACCGGC 90 4 SerLeuPheileGlyAlaThrGlyMetLySThrHisSerThrGlyLeuGlyThrValSer 23 ઠે

Db 1015 TCCACGCGTTCGCCCAGAGCAR	Oy 385 GlyAspLeuValAspValThrII 	Qy 405 SerGinValValAspPheTyrAs	Qy 425 ArgArgGluGlyAsnAsnHisTy ::	445	1243 GCGCCGCGCTCGGGCAC	Qy 465 AspMetSerArgGluWetValAs	Qy 485 LysSerValThrThrAlaAspTh	RESULT 2 US-09-252-991A-2728/c ; Sequence 2728, Application US/09252	GENERAL INFORMATION:	HAPLICANT: Marc J. Rubenfield et IITLE OF INVENTION: NUCLEIC ACID ITLE OF INVENTION: AERIGINOSA FO	FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/; CURRENT FILING DATE: 1999-02-107 PRIOR ADDITICATION NUMBER: US/09/	PRIOR FILING DATE: 1998-02-18 PRIOR PAPLICATION NUMBER: US 60/01 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEC 11 ANG. 23-10	; NOTES OF DEATH START ; SEQ ID NOS: 55142 ; LENGTH: 1512	; TYPE: DNA ; ORGANISM: Pseudomonas aeruginosa TR-09-252-09111-2728	Alignment Scores: 5.19e-47	Score: 528.50 Percent Similarity: 45.84% Best Local Similarity: 29.11%	6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	US-10-009-823A-1 (1-502) X US-09-252-6	150	Qy 24 ASDASNIleAlaASDAlaASDThr	Qy 44 LeuPheSerGlnAspLeuAlalle ::::::::::::::::::::::::::::::::::	Oy 64 MetGlyAlaGlnValGlySerVal	
24 AsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValValPheGlnAsp 43	44 LeupheserGlnAspLeuAlaileGlySerThrGlySerGlnGlyProAsnGlnAlaGly 63 ::::::::::::::::::::::::::::::::::::	GlnValGlySerValArgThrIlePheThrGlnGlyAlaPheGluProGly 83 :::	ThraspLeualaileGlyGlyLysGlyPhePheGlnValThrLeuGluAsp	256 AACAGCGTGCTGGACCTGGCCATCAACGGCTACTCTTCGTCACCAGCAACAACGGG 315 104 LysvalHisTvrThrArqalaGlvAsnPheArgPheThrGlnAsnGlvPheLeuAsnAsn 123		124 ProserdlyPheThrLeuMetGlySerArglleSerAsnAsnProAsnIleLysLysGlu 143		LysThrSerThrAlaLeuAsnAlaValValAsnLeuGlyAspSerThrAspLysThrGln		183 SerGluAlaAsnProTyrPheAlaLeuLeuGluSerTrpLysGlyAsnGlyThrProPro 202 	203 IleSerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsn 222 			676 ATTCCGGAGAACAGTGGACGATGAAAGTGCTGATCGACGGGGTCGATCGGTCGATCGG 735	254 GlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPhe 273 ::: 736 TCGAACAAGACGCCG	274 SerSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySer 290 		826 CCGGGCTTCAGCATCGACGGACCACCAGGTGATCCAGTTCAGTCCGGCC 876	305 AsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGlnProLeuThrLeu 324	325 AspPheGlylleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAlaSerAlaAlaAla 344	IleGlyThrAspIleGlyLysLeuProSerMetMetProlleGlnThrSerSerGlyAsn	98. AICTCCTTCGACATGCGGAAG	
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1383 GTCTACGCCGCCTCGGTGCTGGGTTCGGGCAGCAACCCGCAGGGC 133
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24 AsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValValPheGlnAsp 43
1503 AGTTTCAACATCGGCCTGAGCGGCATCCAGGCGGCCTCTAGCGGCCTGAACGTCACCGGC 144
4 SerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGlyThrValSer 23
-009-823A-1 (1-502) x US-09-252-991A-2728 (1-151
Scores: 5.19e-47 Length: 528.50 Matches: 65.84\$ Conservative: 5.11\$ Mismatches: 20.44\$ Indels: 4 Gaps:
DUBNCES RELATING TO THERAPEUTICS
485 LysSerValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeuLys 501
465 ASPMeCSerargGlumerValAanWet.lelleGlaArgGlyPheGluMetAanSer 484 :: :: :: :: 1303 GACATCTCCAACGAACTGGTGAACCTCATCGTCCACCAGGGCAACTACCAGGCCAATGCC 136
1243 GCGCCGCTCGGGCACCCTGGGGGCGTTGCAATCCGGCGCCCTGGAAGCGTCCAACGTG
445 LeuProGlyThrSerAsnTyrGlyJysLeuSerValAsnGlnLeuGluThrSerAsnVal
1183 ACGCCGATCGGCAAGACCTCCTGGGTGCAGTCCGGGGGGTGCGGGGGGGG
425 ArgArgGluGlyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyProGluPheGly
1123 GGCCAGTCCAAGGTGCAGGCCAGGTGGTGGTGGCGAACTTCGCCAACATCCAGGGCCTG 118
405 SerGinValValAspPheTyrAsnlleProLeuAlaArgpheThrSerGluAspGlyLeu 42
1063 GGTCAGCTGGCAGGCCTGGAAATCGACAGACACCGGGGGTGATCTTCGCCCGGTACACCAAT 112
385 GlyAspLeuValAspValThr11eThrSerGluGlyLysLeuGlnGlyLysTyrSerAsn 4
1015 TCCACGGGTTCGCCCAGAGCAACCGGATCCAGGACGGCTACACCACC

	Db 171 AAGACCATCCAGACGAGGATGACGGTGACGAGGATGACGGTGACGACGAGGATGACGAGCATGACGAGGATGACGAGGATGACGAGCATGACGACGAGGATGACGAGCATGACGAGCATGACACGAGCATGACACGAGCATGACACGAGCAGCAGCAGGAGAGACACACAC	Mignment Scores:	50 151 184 244 107 127
1338 AGCGGCGTGCTCCTCCGACGTCTCGCAGATGTTCAAGCAGGCAACATCGACTCGACC 1279 84 ASISETVAIThYASPLEUALAIIGGIYGIYLYSGIYPhEPHEGINVAITHYLEUGIUASP 103	### SECTION OF THE PROPERTY OF		325 AspPheGly1leLysSerGlnGlnAsnMetTrpAlaGlyAlaProalaSerAlaAlaAla 344
8 8 6 8 6 8 6 8	3 8 5 8 5 8 5 8 5	8 6 8 6 8 6 8 6 8	8 6 8 6 8 6 8 6 8 6

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MINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI HERAPEUTICS
LeuSerValAsnGlnLeuGluThrSerAsnVal 464
                                                        ||||
|TGCAATCCGGCGCGCTGGAAGCGTCCAACGTG 232
                                                                              ValValPheGlnAspLeuPheSerGlnAspLeu 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrGlnAspGlyPheleuAsnAspProSerGly 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asn...----AsnProAsnIleLysLys 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /alThrLeuGluAspLys-----ValHis 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :::
|||||||
\TT-----GAAGATAGTAACGGTGGCGTTTTC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaPheGluProGlyAsnSerValThrAspLeu 89
                                                                                                                       LeuGlnLysAlaLeuGluteuLys 501
                                                                                                                                                                                                                                                                                                                                                                                ength: 1239
atches: 136
onservative: 81
ismatches: 165
ndels: 157
aps: 159
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8 6 8 6 8

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5 B 5 B 5 B 5 B 5

	Oy 493 Metle pb 1210 ATCCT	RESULT 4 US-09-790-988-1 ; Sequence 1, Appli ; Parent No. 663293	GENERAL INFORMAI APPLICANT: SHIC APPLICANT: WAI APPLICANT: HAI	APPLICANT: SAKA TITLE OF INVENTI FILE REFERENCE: CURRENT APPLICAT	CURRENT FILING D PRIOR FILING DATE NUMBER OF SEQ ID		ORGANISM: Buchn US-09-790-988-1	Fred. No.: Soore: Percent Similarity: Best Local Similari	Query Match: DB:	US-10-009-823A-1 (1	Oy 4 Serber Db 372153 TCAAN	24.	Db 372213 AATAA	Cy 44 LeuPh. ::: Db 372273 ATGTT.	Oy 64 MetGly	84	Db 372372 GGACG	Qy 103 Asplys	123	::: Db 372492 AATATT	Qy 137 AsnPro	157	372594
358 ATGCGTATTACAGGTTATCCAGTACAAAACGTAGAAAAGGTAAAAAATGTAGTACAAAAAAAA	GluthrieuGlubrolleGlnLeuAspPheAsnAspProThrValAlaLySerProAla	163 LysThrSerThrAlaLeuAsnAlaValValAsnLeuGlyAspSerThrAsp 179	180 LysThrGlnSerGlualaAsnProTyrPheAlaLeuLeuGluSerTrpLysGlyAsnGly 199 ::: ::: :::	200 ThrProProlleSerThrSerasnTyrSerTyralaGlnProMetargValTyraspGln 219 556GATTCTTATAACTTTAGTACGTGACAACCTACGATAGC 597	220 GlnGlyAsnSerHisAsplleThrValTyrPheAspGlyAlaProSerSerThrGlySer 239	240 LysThrPheGluTyrLeuValalaMetAsnProSerGluAspGlySeralaalaSerGly 259 	260 ThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPheSerSerAsnGly 277		293 iysAspLeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuProGlnPheSerAla 312	789	313 AsnPheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGln 332 :::::: 790	AsnMetTrpAlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLysLeu	9	353 ProSerMetDeroileGinThrSerSerGiyAsnSerThrAlaArgAsnGiySerSer 372	373 SerThràzgargTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAspValThrile 392		GAGCCAGATGGTTCCATTATGGCGACCTACTCAAACCAACAAGCCAAGTGGTTGGT	413 IleProJeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyr 432	SerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGly	1030 TCTGAAACCAATGGTTCAGGCTCACCCATTGTTGGTGGGGAGGCTCTGGCGTTTGGT 1089	453 LysLeuSerValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMetValAsn 472	MetIlellelleGlnArgGlyPheGlnMetAsnSerLysSerValThrThrAlaAspThr	:::

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ATATGATAGCTATAAGTGGCTTACTAGCAAATAATGATTACATGGAAATTATATCC 372212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Snilealaarnalaarnthrileglytyrlysglnglnglnvalvalpheglnarp 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAAĞĞİATGTATCİAACTĞĞACTTAATACAİCİTGTTCAAAAAGTGATTTTAAİ 372551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------AGATCCAACTTAGAACCTATTAATTTA-----AAAAATTCTAAT 372593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oSerGlyPheThrLeuMetGlySerArgIleSer------Asn 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erValThrAspLeuAlaileGlyGlyLysGlyPhePheGln---ValThrLeuGlu 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sValHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsn 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oAsnIleLysLysGluThrLeuGluProlleGlnLeuAspPheAsnAspProThr 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .aLysSerProAlaLysThrSerThrAlaLeuAsnAlaValValAsnLeuGly--- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 euPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGlyThrValSer 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neSerGlnAspLeuAlaIleGlySerThrGlySerGlnGlyProAsnGlnAlaGly 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lyAlaGlnValGlySerValArgThrIlePheThrGlnGlyAlaPheGluProGly 83
                                                                                                              Upplication US/09790988
322935
WATION:
WATANABE, HIDEMI
HATTON: CASHITCA
SAKAKI, MASAHIRA
SAKAKI, CASHITCA
SATION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
ICCTION NUMBER: US/09/790, 988
MATION NUMBER: US/09/790, 988
MATION NUMBER: J02000-107160
i DATE: 2001-02-23
MATION NUMBER: J02000-107160
i DATE: 2000-04-07
i DATE: 2000-04-07
itentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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JeuGlnLysAlaLeuGluLeuLys 501
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; GENERAL INFORMATION:

Qy 176	JORGANDALION AREOLOGY, RUDENTIELD ET AL. APPLICANT: MACE J. RUDENTIELD ALD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AREQUINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252,991A
372714 ACTIATATAGG	; CURRENT FILING DATE: 1999-02-18 ; PRIOR APPLICATION NUMBER: US 60/074,788
210 TyrAlaGlnProMetArgValTyrAspGlnGlnAsnSerHisAspIleThrValTyr	; PRIOR APPLICATION NUMBER: US 60/094,190 ; PRIOR PILING DATE: 1998-07-27
DD 3/2/26	; NUMBER OF SEQ ID NOS: 33142 ; SEQ ID NO 3144 : LENGTH: R10
372768 TTTAATAAAAAGGAAACAATTAAATGGACAGTAAATGTGGAATCAAAT	TYPE: DNA ORGANISM: Ps
ProSerGluhspGlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGly 269	991A-3144 Scores:
372816	1.45e-23 Length: 307.00 Matches:
372852 GATTTAACGTTTAATGATGACGCGAATTAACTTCTGATAATGTTTTTAATATTACATCT	Percent Similarity: 30.74 CORSETVATIVE: 46 Best Local Similarity: 21.56* Mismatches: 93 Query Match: 11.87* Indels: 254
Oy 290 SerAlaThrLysAspLeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuProGln 309	4 Gaps:
Db 372912 AAAGATTCTAAAAAG 372926	-10-009-823A-1 (1-502) X US-09-252-991A-3144 (1-810)
310 PheSerAlaAsnPheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLys 329	Qy 1 MetMetGlySerLeuPheIleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20
SerGlnGlnAsnWetTrpAlaGlvAlaProAlaSerAlaAlaAlaIleGlvThrAspIle 349	Qy 21 ThrValSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnUalVal 40
	Db 85 ACCATTCCAACAACCTGGCCAACGTATCCACCACCGGCTTCAAGCGCGACCGCGGGGG 144
rGlyAsnSerThrAlaArgAsn 369	PheGlnAspLeuPheSerGlnAspLeuAlaIleGlySerThrGlySerGlnGlyProAsn
372951372974	145 TICCHGGACCIGCIGIACCAGCCGGCGGCCGGCCGGCCGGCCGGC
370 GlyserSerSerThrArgArgTyrSerGlnAspGlyTyrProGlnGlyAspLeuValAsp 389 372975 TCTRANGTWTCTRACARARAACAMCAAAAAAAAAAAAAAAAAAAAAAAA	Db 205 GAGCTGCCTTCGGGCTCCAACTGGGTGTGGCGTCGTCGGCGCCCCGGAAGAC 264
ValThrileThrSerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValValAsp	
373035 TTTGATATTGTTACTAATGGTGAAATTATTGGAACATATTGCAATGAAACAAAC	265 TTCACCCCGGGCAGCCTGCAGACCACCGAGCTGGACATGGCGGTCAACGGGCGC
PheTyrasnileProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsn	Oy 95 GlyPhePheGlnValThrLeuGluAspLysVaHHisTyrThrArgAlaGlyAsnPhe 113
_	Qy 114 ArgPheThrGlnAspQiyPheLeuAsnAspProSerGlyPheThrLeuMetGlySerArg 133
430 AshiisTyrSestAaThrLeuAspSestGlyProGluPheGlyLeuProGlyThr 448	Db 385 CACCTGAACTCCGACGGCAGATCGTCACCTCCAACGGCTTCGCCCTG 432
449 SerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMetSerArg 468	Qy 134 IleSerAsnAsnProAsnIleLysLysGluThrLeuGluProIleGlnLeuAspPheAsn 153
m	432
GluMetValAsnWetIleIleIleGlnArgGlyPheGlnMetAsnSerLysSerValThr	Oy 154 AspProThrValAlaLysSerProAlaLysThrSerThrAlaLeuAsnAlaValValAsn 173 1:: Db 433 GAGCCAGCGACT
373275 GAATTAATCAATATGATTATAGCACAACGTAATTATCAATCTAACGCTCAATCTTTAAA 373334	Qy 174 LeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGlu 193
489 InialaaspinimetteuGinLysalaleuGinLeulys 501 	Db 444 444
	Oy 194 SerTrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyrAlaGlnPro 213
5-09-252-991A-3144 Sequence 3144, Application US/09252991A	Db 444 444
atent No. 6551795	Qy 214 MetArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPheAspGlyAla 233

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HATCCACCACCGGTTCAAGCGCGACGCGGAG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sp---LysValHisTyrThrArgAlaGlyAsnPhe 113
                                                                                                                                                                                                                                                                                                                                                                                           snAspProSerglyPheThrieuMetGlySerArg 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCACCTCCAACGCTTCGCCCTG-----432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rolleSerThrSerAsnTyrSerTyrAlaGlnPro 213
                                                                                                                                                                                                                                                                                                 euAlalleGlySerThrGlySerGlnGlyProAsn 60
                                                                                                                                                                                                                                                                                                                                   GGCGCCAGCCGGCGACCCCAGGACAGC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGAGCAGCCGCTGGACATGGCGGTCAACGGGCGC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysGluThrLeuGluProIleGlnLeuAspPheAsn 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laLysThrSerThrAlaLeuAsnAlaValValAsn 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InserGluAlaAsnProTyrPheAlaLeuLeuGlu 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 MetArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPheAspGlyAla 233
                                                                                                                                                                                ||||||||:::
AGACCGGTCTGTCCGCCCAGGACATGAACCTGACC 84
                                                                                                                                                                                                                                                                                                                                                                 lyser---valargThrIlePheThrGlnGlyAla 79
                                                                                                                                                            lathrolyMetLysThrHisSerThrGlyLeuGly 20
                                                                                                                                                                                                                             laAsnThrIleGlyTyrLysGlnGlnGlnValVal 40
                                                                                                                                                                                                                                                                                                                                                                                                                                          ------AsphenalaileGlyGlyLys 94
 810
108
46
93
254
Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 SerAsnAsnProAsnIleLysLysGluThrLeuGluProIleGlnLeuAspPheAsnAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 ProThrValAlaLysSerProAlaLysThrSerThrAlaLeuAsnAlaValValAsnLeu 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerSerThrGlySerLysThrPheGluTyrLeuValAlaMetAsnProSerGluAspGly 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPheSer 274
                                                                                                                                                                                                                                                                                                                                                                                       GlnAspieuPheSerGlnAspLeuAlaIleGlySerThrGlySerGlnGlyProAsnGln 61
                                                                                                                                                                                                                                                                                                                                                96 PhePheGlnValThrLeuGluAsp---LysValHisTyrThrArgAlaGlyAsnPheArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMetGlySerArg1le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGluSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 ArgValTyrAspGlnGlnGlyAsnSerHisAspIleThrValTyrPheAspGlyAlaPro
                                                                                                                                                                                                                                                                    MetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGlyThr
                                                                                                                                                                                                                                                                                                                             22 ValSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AlaGlyMetGlyAlaGlnValGlySer---ValArgThrIlePheThrGlnGlyAlaPhe
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PRIOR FILING DATE: 1998-07-2
NUMBER OF SEQ ID NOS: 33142
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APPLICANT: MAKE J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERGINGOA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERGINGOA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190
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                                                                       --GTGGTGCCCAACGAG---
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; GENERAL INFORMATION:
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335 TrpAlaGlyAlaProAlaSerAlaAlaIleGlyThrAspIleGlyLysLeuProSer 354 1093 1093	
355 MetMetProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThr 374	196 AATGCGCCTTCTGGTTTACAAATTGGTACTGGTGTTCGCCCCAGTGGCGACAGACGTTTA 25
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5 IlelleGlnArgGlyPheGlnMetAsnSerLysSerValThrThrAlaAspThrMetLeu	194
846 ACCACCCAGCGCCTACGAGATGAACTCCAAGGTCATCTCCACGGCGACCAGATGTTG 787	Db 468 468
RESULT 7 US-09-543-681A-3938 ; Sequence 3938, Application US/09543681A	
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS	Db 508 CCTGCA 513
FILE REFERENCE: 2709.1002-001 CURRENT APPLICATION NUMBER: US/09/543,681A	Qy 254 GlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMetSerGlyThrMetThrPhe 273
CURRENT FILING DATE: 2000-04-05 PRIOR APPLICATION NUMBER: US 60/128,706	Db 513 513
ILING DATE: 1999-04-09 OF SEQ ID NOS: 8344	Qy 274 SerSerAsnGlyGluLeuLy8AsnMetThrAlaPheThrProThrGlySerAlaThrLys 293
SEQ ID NO 3938 . LENGTH: 798	Db 513 513
TYPE: DNA ORGANISM: Proteus mirabilis	Qy 294 AspLeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuProGlnPheSerAlaAsn 313
9	Db 514 519
Length:	Qy 314 PheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsn 333
ilarity: 30.57% Conservative:	Db 519 519
19.72% 11.06%	Cy 334 MetTrpAlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLySLeuPro 353
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	715 ATCCAAACTCAGGGGCTATGAAATTAATAGTAAAGGGGTTTCAACTGATCAGATG 774 494 Leuclintyshaleuciliueu 500 775 TTACAGAAACTCAGGCACTC 795 196 483-857-1 Sequence 1, Application US/08483857 Bergarence 1, Application US/08483857 Bergarence 1, Application US/08483857 BERGREAL INPORATION: APPLICANT: Chai, Von Loong APPLICANT: Chai, Von Loong APPLICANT: Chai, Von Loong APPLICANT: Chai, Wollie, Helena TITLE 0F INVENTION: BASAL BODY ROD PROTEIN GENES OF ADDRESSEE: Sim & McBurney STREET: Shife 701, 330 University Avenue TITLE 0F INVENTION: Charles 10 University Avenue STATE: One and ACCOUNTER FORM: WEBLING FEADABLE FORM: WEBLING STATE: Chaid Compatible STATE: One and ACCOUNTER FORM: WEBLING STATE: LANGE FORM: WEBLING SYSTEM: PC-DOG/MS-DOS CONFUTER FEADABLE FORM: WEBLING SYSTEM: PC-DOG/MS-DOS CONFUTER FEADABLE 18/08/483,857 TILLEG DATE: UNIVERSATION NUMBER: 18/08/483,857 TILLEG DATE: UNIVERSATION: THE SEGUENCE WICH STATES IN
	715 ATCCAAACTCAGGGCTCATAGAAATTAATAGTAAAGCGATTTCAACTTCTGATCAGTCGATCAGATCAGATCAGATCAGAACTCAGAACTCAGGCACTC 755 SULT 8 1
	115 ATCCAAACTCAGCGTGCTTATGAAATTAATAGTAAAGCGATTCAACTTCTGATCAGATG 494 LeuGlnLysAlaLeuGluLeu 500 175 TTAACGAAACTCACCAACTC 795 SULL 8 -08 + 481 S87-1 -18 -19 TTAACGAAACTCACCAACTC 795 SEGURACE 1. Application US/08483857 Batent No. 6020125 GENERAL INVOCATION: BASAL BODY ROD PROTEIN GENES OP TITLE OF INVENTION: CAMPYLOBACTER NUMBER OF SEQUENCES: 12 COMPRESSONDENCE ADDRESS: ADDRESSEE: Sin & McBurney CITY: TOCATIO STREET: Sin & McBurney CONTRY: Canada ZIP: McGarla ZIP: McG
	115 ATCCAAACTCAGCTGCTTATGAAATTAATAGTAAACTTCAACTTCTGATCAGATG 494 LeuGlnLysAlaLeuGluLeu 500 175 TTACGAAACTCACCACTC 795 18
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 101 ATGCAAA	547TITTATTAATGATAGCGGGTTAGAAAGTGTTGGGGAAAATCTGTACTTA
1 MetMetGl	414 ProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyrSer
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best Local Similarity Query Match: DB:	394 SerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValValAspPheTyrAsnIle 413
Score: Percent Similarity:	Db 535ACCCTCACC 543 P
Alignment Scores: Pred. No.:	Thr 393
	534
; NAME/KEY: CDS	Cy 354 SerMetDrolleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSerSer 373

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ATGGATATTATCAAGCAACTGGCGGAATGGTAACTCAGTTTAATAAACTTGAT 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||||||||:::
:GAAATTTTCAACTTGATGATGAGGTTATTTGGTAAATAAGCAAGGATACAAG 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| ||| ::
\tagaigaictaacccgiaftagagaftigaaaaactccaaigctaitcgccaa 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----IleLysLysGluThrLeuGluProlleGlnLeuAspPheAsn---- 153
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----AGAATGGTAGAAAATGTATGAAAAGTTATGACAGCTCATATGGATGAC 871
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                                                                                                                                                                                                                                                                                                   31ySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hrllePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAla
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PAGAAGCTATCAATAAGCTTGCAGCTGTTAAATAATTAAAATAAAAA
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                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                            502) x US-08-483-857-1 (1-1800)
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CDS
join(101..910, 942..1730)
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101 ATGCAAAATGGATATTATCAAGCAACTGGCGGAATGGTAACTCAGTTTAATAAACTTGAT 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 IleGlyGlyLysGlyPhePheGlnVal-----ThrLeuGluAspLysValHisTyrThr 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 ArgalaGlyasnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetMetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 ------PheGlnAspLeuPheSerGln-----53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 -----ThrGlySerGlnGlyProAsnGlnAlaGlyMetGly---AlaGlnValGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 AAAGATGGAAATTTTCAACTTGATGATGAGGGTTATTTGGTAAATAAGCAAGGATACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 ValArgThrIlePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1800
132
96
217
156
24
                                 CUMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,748
FILING DATE: 05-AUG-1995
CLASSIFICATION: 43<sup>G</sup>
ATTORNEY/Arever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-428 MIS
RELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(101..910, 942..1730)
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.12e-20
277.50
37.94%
21.96%
                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                              NY: Canada
M5G 1R7
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Query Match:
DB:
               STATE: Ontario
COUNTRY: Canad
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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------GTGGGTGTGGGTGTGCGTCCAACAGCGGTAACTAAAGTTTTTAC 1186
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1187 IGAAGGAAATITAAAATCAACAAGTACT----GATGGICITGATAIGGCTAITGCAGG 1240
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                                986 GCAAACACAAATTGATGTTACTTCAAATAACATGGCCAATGTTAATACAGCA-----GG 1039
                                                                                                     1040 TITTAAGAAAAGTCGCCAGAATTTGCTGATCTTATGTATCAAGTTATGAAGTATGCAGG 1099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 nSerThralaArgAsnGlySerSerSerThrArgArgTyrSerGlnAspGlyTyr---- 382
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                                                                                                                                         269 yThrMetThrPheSerSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGl 289
                                                                                                                                                                                                                                                                                   309 nPheSerAlaAsnPheValGlyAlaGlyIleGlnProLeuThrLeu------ 324
                                                                                                                                                                                                                                                                                                                                                                                                                             344 alleglyThrAspileGlyLysLeuProSerMetMetProlleGlnThrSerSerGlyAs 364
                                                                     ----MetSerGl 269
                                                                                                                                                                                                             yseralaThrLysaapLeuAsnalaTrpGlnProAlaProLeuValAsnGlyLeuProGl 309
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SerSerThrGly-SerLysThrPheGluTyrLeuValAlaMetAsnProSerGluAspGl
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APPLICANT: LOUIS, HELENA
TITLE OF INVENTION: BASAL BODY ROD PROTEIN GENES OF
TITLE OF INVENTION: CAMPYLOBACTER
                                                                     ySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeu-
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US-08-436-748-1
; Sequence 1, Application US/08436748
; Patent No. 5827654
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
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1 MetMetGlySerLeuPheIleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20
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                                                                                                                            1550 TGCGGGTATAGCAGGACAAGATGGGCTTGGAACAATAAGACATGGATTTATAGAACTTAG
                                                                                                                                                               rAsnValAspMetSerArgGluMetValAsnMetIleIleIleGlnArgGlyPheGlnMe
                                                     1490 GGGTCTTCATTCTATGGGTGATAATCTTTATCTTGAAACAGGAGCAAGTGGTGCACCTGT
                                                                                          442 uPheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSe
                                                                                                                                                                                                                                      482 tAsnSerLysSerValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeuLysAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08483857
Patent No. 6020125
GENERAL INFORMATION:
APPLICANT: Chan, Voon Loong
APPLICANT: Chan, Voon Loong
APPLICANT: Louie, Helena
TITLE OF INVENTION: BASAL BODY ROD FITLE OF INVENTION: CAMPYLOBACTER
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
STREET: Suite 701, 330 University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/483,857
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael 1.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1036
TELECHANTICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24,973
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
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237.50
27.45%
18.63%
9.18%
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LENGTH: 789 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC OPERATING SYSTEM:
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MSG 1R7
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Best Local Similarity:
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US-08-483-857-3
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------AATTCAGATGGTTATAGACTTTTACCTGAAATGACAATACCTGAAGGC-- 1379
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AGGATTAAAAATGATGAGATCACTTCATAC-----TGCTGCTACAGGAATGGTAGCGCA
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                                                                                                       -----IleLysGluThrLeuGluProIleGlnLeuAspPheAsn----
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Db 475 TCTGTAATGCTACCA	Oy 393 ThrSerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValValAsp ::: 	Qy 413 IleProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsn :::	Qy 433 SerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSer	Qy 453 LysLeuSerValAsnGlnLeuGluThrSerAsnValAspMetSerArgGlu ::	Qy 473 MetilellelleGlnArgGlyPheGlnMetAsnSerLysSerValThrThr ::::	Qy 493 McLeuGlnLysAlaLeuGluLeuLysArg 502	SULT 11	Joseph Application US/08436748 ; Patent No. 5877654 ; Patent No. 5877654	; GENERAL INFORMATION: ; APPLICANT: CHAN, VOON LOONG ; APPLICANT: LOUIS. HELENA	TITLE OF INVENTION: BASAL BODY ROD PROTEIN GENES OF TITLE OF INVENTION: CAMPYLOBACTER	; NUMBER OF SEQUENCES: 10 ; CORRESPONDENCE ADDRESSS: . ADDRESSEE: ALM & McBurnev	STREET: Suite 701, 330 University Avenue TY: Toronto CTATE: Ontario	; COUNTRY: Canada ; ZIP: MSG 1R7	ORM: ppy disk compatible	COPERATING SYSTEM: PC_DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30	; CUKRENI AFFILCATION DAIA: ; APPLICATION NUMBER: US/08/436,748 ; FILING DATE: 05-AUG-1995	; CLASSIFICATION: 435; ATTORNEY/AGENT INFORMATION:	, NAME: STEWART, MICHAEL I ; REGISTRATION NUMBER: 24,973 ; REFERENCE/DOCKET NUMBER: 1038-428 MIS	TION INFORMATION (416) 595-1155	를 돌 등	LENGTH: 789 ba TYPE: nucleic	; STRANDEDNESS: single ; TOPOLOGY: linear US-08-436-748-4	Alignment Scores: 1.4e-14 Length: 789	
AIGATGAGATCACTTCATACTGCTACAGGAATGGTAGCGCAGCAAAATTGAT ThrvalSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValVal ThrvalSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValVal	STTTTAAGAAAGTCGCGCAGAA erThrGlySerGlnGlyProAsn 	TTTGCTGATCTTATGTATCAAGTTATGAAGTATGCAGGAACTTCAACTTCAGCTACTGT GlnAlaGlyMetGlyAlaGlnValGlyserValargThrIle ::: :::			erGlyPheThrLeuMetGlySer	361 TTTACAAAAGATAATGAAGGTAATATTGTAAATTCAGATGGTTATAGACTT 411 133 ArgileSerAsnAsnProAsnIleLysLysGluThrLeuGluProIleGlnLeuAspPhe 152		153 ASnASPProThrValAlaLySSerProAlaLySThrSerThrAlaLeuAsnAlaVal. 172	173 AsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeu 192	411		411	411 411		411	411	273 PheSerSerAsnGlyGluLeuLysAsnMetThrAlaPheThrProThrGlySerAlaThr		293 LyBAspletastratingthrichtafromedvarhsidtyletricomedia. 412TTACCTGAA	313 AsnPheValGlyAlaGlyIleGlnP	421 478ACAATACCTGAAGC 438	, 333 AGIMETTEPALAGLYALAPFOALASERALAALAILEGLYTHKASFILEGLYLYSLEU 352	353 ProSerMetProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySerSer 372	
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luMetValAsn 472 |||||| |AAATGACAGAT 699 ThralaaspThr 492 |||:::||| ACAAGTGATGAT 759 Asnasnhistyr 432 :::||| ||| GATAATCTTTAT 579 -----GGCCAA 519 spvalThrile 392 spPheTyrAsn 412 erAsnTyrGly 452 ATGGGCTTGGA 639

438	Db 489	ANALITE DESTRUCTION OF THE CONTROLLY THE SELECT OF THE SEL	Cy '494 LeuGlnLysAlaLeuGluLeuLysArg 502	APPLICANT: Pfizer Products, Inc. TITLE OF INVENTION: LAWSONA INTRACELLULARIS PROTEINS AND RELATED METHODS AND TITLE OF INVENTION: MATRIALS FILE REFERENCE: 3153.00187/PC10589A CURRENT APPLICANTON NUMBER: US/09/689,065B CURRENT FILING DATE: 2000-10-12 PRIOR APPLICATION NUMBER: US Prov. 60/160,922 PRIOR APPLICATION NUMBER: US Prov. 60/163,858 PRIOR APPLICATION NUMBER: US Prov. 60/163,858 NUMBER OF SEQ ID NOS: 112 SRIOR PILING DATE: 1999-11-05 NUMBER OF SEQ ID NOS: 112 SOFTWARE: PatentIn Version 3.2 SEQ ID NO 2	i IBNGTH: 5445 i TYPE: DNA i OGGANISM: Lawsonia intracellularis US-09-689-065B-2 Alignment Scores: 6.45e-10 Length: 5445 Pred. No.: 193.00 Matches: 40 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 7.46% Indels: 0 DB: 4 Gaps: 0	US-10-009-823A-1 (1-502) x US-09-689-065B-2 (1-5445) Cy 463 AsnValAspMetSerArgGluMetValAsnMetIleIleIleGlnArgGlyPheGlnMet 482
Score Similarity 223.50	Db 61 GTTACT!CAATGACGCCAATGTTATACAGGGTTTTAAAAAAACGCGCAGAA 120 Qy 41 PheGlnAspLeuPheSerGlnAspLeuAlaileGlySerThrGlySerGlnGlyBroAsn 60 Db 121 TTTGCTGATCTTATGAAGTTATGAAGTATGCAGGAACTTCAACTTCAGCTACTACT 180 Qy 61 GlnAlaGlyMetGlyAlaGlnValGly	75 PheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaileGlyGly	325 134 349 154 361	Qy 174 LeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAlaLeuLeuGlu 193 Db 369	LSerGlyThrMetThrP :TTACCTGAAATGACAA OThrGlySerAlaThrL GAAGGC	Db 438 438 438 438 6

Db 2231 GCGGACGCCAACCATCATCATCACCGAIGGCAACGCCAACCGCAATTGGCCAGGTC 2172	acceccacceaceccataranary	2111	GTGGCCCCGGGGGCGCGGTGATC	Oy 249 AsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuWet 267	268		1901 ACGITCACCCCGGCACCCCGCTGGCCACCGTGATCAACGCCGTGGCCCAGGAC	Qy 287 ProThrGlySeralaThrLysAspLeuAsnAlaTrpGlnPro 300	Oy 301 AlaProLeuValAsn	Qy 313 AsnPheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGly 327	328 IlelysSerGlnGlnAsnMetTrpAlaGlyAlaProAlaSerAlaAlaAlaIleGlyThr	1664 GGCAAGTGGGCTTTCACGCCCGCCACGCCATGGCCAATGGCACG	Qy 348 AspileGlyLysLeuProSerMetProlleGlnThrSerSerGlyAsnSerThrAla 367	Qy 368 ArgAsnGlySerSerThrArgArgTyrSerGlnAspGlyTyrPrcGlnGlyAspLeu 387	388 ValaspValThr1leThrSerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnVal	Db 1529 ATCAATCCG	1505 ATCGCCGGTACCGCCGAGGCTGGTGCCACGGTGATCCTCACCGACGGCAAC	Qy 428 GlyasnasnHisTyrSerAlaThrLeuAspSerGlyGlyFroGluPheGlyLeuErocky 44,7	448 ThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMetSer	Db 1394 ACG 13/1 Db 1394 ACG 13/1	1370	Gy 488 ThrThralaAspThrMetLeuGlnLysAla 497	ACCACGG1GGAC1CGG1GGCGCCGGCCGC
DD 3 AACGTAGACATGAGCAGAGAATGGTTAATATTATTATTATTCAACGTGGTTTTCAGATG 62	Oy 483 ASDSELVSSELVAITHTHTALASPTHTMELEUGINLYSALALEUGIULYSALG 502	RESULT 13 US-09-252-991A-13873/c ; Sequence 13873, Application US/09252991A	d et al.	; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES KELATING TO PSEUDOMONAS; TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS; FILE REFERENCE: 107196.136 ; CHERENCE ADDITIONATION NUMBER: 18/09/252.991A	CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18	PRIOR APPLICATION NUMBER: US 60/094,190 FRIOR FILING DATE: 1999-07-27 NITMER OF SEO ID NOS: 33142	3873 129	; TYPE: DNA ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-13873	1.78e-08 Length: 176.00 Matches:	Mismatches: Indels: Gaps:	US-10-009-823A-1 (1-502) x US-09-252-991A-13873 (1-3129)		spleualaileGlySerThrGlySerGlnGly	Db 2585	2549	Db 2489CTCAACGGTACCGCCGGGCAGCAGCAGCTGACCTGAC	Qy 92 GlyGlyLysGlyPhePheGlnValThrLeuGluAspLysValHisTyrThrArgAlaGly 111	112 AsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMetGly	AGCTTCACGCCCGGCTCGCAACTACCCA 11eSeraanaanProaan11eLvsLvsG	2339 AGGAGGCGCGGGAATACCAGGGCTCCGCTACCAGGACGGTGGAT	PheAsnAspProThrValAlaLysSerProAlaLysThrSerThrAlaLeuAsnAlaVal	Db 2291 TCCTCGCTGCCGCTGCATCCCGCAGGTGGATCCGAGCAACGGTTCGGTGATCAGCGGCACC 2232 Qy 172 ValaenLeuGlyAspSerThraspLysThrGlnSerGluAlaAsnProTyrPheAlaLeu 191	

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                                    4456 GTGGTCAACGTGGTGGCGCGCAGCCCAAGCAATGTCGACAGTGCGCCGGCGGTGATCACT
                                                                                                                                                                        249 AsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeuMet---
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                                                                        230 PheAspGly---AlaProSerSerThrGlySerLysThrPheGluTyrLeuValAlaMet
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                                                                                                              1516 GIGGATGGCGTGGCCCCCGCGCGCGCGCG
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Patent No. 6551795
GENERAL INFORMATION:
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US-09-252-991A-3047
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                          US-09-252-991A-13656

Sequence 13656, Application US/09252991A

Patent No. 6551795

GENERAL INPORMATION:
TILLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TILLE OF INVENTION: ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TILLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

(CURRENT PAPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 13656

LENGTH: 9211
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4168 AACTGGAGCTTCACGCCCGGCTCGCAACTACCCAACGTCAACGTCAACGTGACCGCG 4227
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Matches:
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Mismatches:
Indels:
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ORGANISM: Pseudomonas aeruginosa
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176.00
33.21%
22.64%
6.81%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 SerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSer 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGln 320
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:038 ATCGATGCAAAAATGTAACAGTAAACAACAATATTACTTCTCACAAAGCAGTGAGCATC
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|251 GCTGTAAGCAATATTTCG----------
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Matches:
Conservative:
Mismatches:
Indels:
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              ; LENGTH: 3285
; TYPE: DNA
;; ORGANISM: Haemophilus influenzae
US-09-206-942-68
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Best Local Similarity:
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APPLICANT: MAXC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRESENT
FOR REPRESENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/4,788
PRIOR APPLICATION NUMBER: US/0074,788
PRIOR PLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Sequence 68, Application US/09206942

Sequence 68, Application US/09206942

Sequence 68, Application US/09206942

GENERAL INFORMATION:

APPLICANT: Loosmore. Sheena M.

APPLICANT: Yang, Yan-Ping

APPLICANT: Yang, Yan-Ping

TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High

TITLE OF INVENTION: Molecular Weight Proteins

FILE REFERENCE: 1038-861 MIS:jb

CURRENT APPLICATION NUMBER: US/09/206,942

CURRENT PILING DATE: 1998-12-08

BARLIER FILING DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 95

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 68
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43
64
64
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                          .046-09
174.00
50.00%
30.71%
6.73%
                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                   US-09-252-991A-3047
                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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DB:
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TELECOMMUNICATION INFORMATION: TELECOMMUNICATION FOR SEQ 10 NO: 1 TELEPHONE: (703) 415-0813	Oy 30 AsnThrIleGlyTyrLysGlnGlnValValPheGlnAspLeuPheSerGlnAspLeu 49	Db 3570GCCARAAAGTAACCTTT	129 LeuWetGlySerArglieSerAsnAsnProAsnilelysGluthrLeuGlubrolle 13) ATGATGCAAAAATGTAACAGTAAACAAATTTACTTCTCACAAAGCAGTGAGCACT 149 GlnLeuAspPheAsnAspProThrValAlaLySerProAlaLySThrSerThrAlaLeu 1371TCTGCGACAAGTGGAGAATTACCACTAAAACAGGTACAACCTT 169 AsnAlaValValAsnLeuGlyAspSerThrAspLySThrGlnSerGlualaAsnProTyr 169 AsnAlaValValAsnLeuGlyAspSerThrAspLySThrGlnSerGlualaAsnProTyr 189 PheAlaLeuLeuGluSerTrpLySGlyAsnGlyThr
Db 2515 GGTAATACGGTAAAT	Qy 407 ValValAspPheTyrAsnileProLeuAlaArgPheThrSerGluAspGlyLeuArgArg 426 Db 2809 GACGCTGAGCTAAATGGCGCAGCATTGGCTAACCACACAGTGGTAATGCAACCAAC	sy-	SQUENT 17 SQUENCE 1, Application US/08038682 SQUENCE 1, Application US/08038682 PRECIT NO. 5249897 APPLICANT: BARENKAMP, STEPHEN J APPLICANT: ST. GEME III, JOSEPH W APPLICANT: ST. GEME III, JOSEPH W APPLICANT: ST. GEME III, JOSEPH W APPLICANT: ST. GEME III, JOSEPH W APPLICANT: ST. GEME III, JOSEPH W APPLICANT: ST. GEME III, JOSEPH W ADDRESSES: SONORNESS: 8 CORRESPONDENCE STORESS: 8 CORRESPONDENCE ADDRESS: 8 APREST: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: 2202-0286 COUNTRY: U.S.A. ZIP: 22202-0286 COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/WS #1.0, Version #1.25 CURSING DATE: 16-WAR-1993 CLASSIFICATION: 424 ATTORNENT APPLICATION: 424 ATTORNENT APPLICATION: A24 REGISTRATION NUMBER: 22.651 REFERENCE/DOCKET NUMBER: 12.551

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FILING DATE: 16-SEP-1994
CLASSIFICATION: 435
FRUOR APPLICATION DATE:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAX-1992
FRIUNG DATE: 16-MAX-1992
APPLICATION NUMBER: US pct/us93/02166
FILING DATE: 16-MAX-1993
APPLICATION NUMBER: US pct/us93/02166
APPLICATION NUMBER: US pct/us93/02166
APPLICATION NUMBER: US pct/us93/02166
APPLICATION NUMBER: 1038-404
REFERENCE/DOCKET NUMBER: 1038-404
TELEPHONE: (703) 415-0810
TELEPHONE: (703) 415-0813
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5116 base pairs
TYPE : nucleic acid
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173.50
37.30$
22.18$
6.71$
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                       -----ATTAATGCGACAGAA 4262
                                                                                                                                                                                                                                                                                                                                  4482 GACGCTGAGCTAAATGGCGCAGCAİTİĞGGTAACCACÀCAGTGGTAAATGCAACCAACGCA 4541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMet 466
                                                                                                                                                                                                                                                                                                                                                                                      SerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGlnAsp 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 GlyTyrProGlnGlyAspLeu-----ValAspValThrIleThrSerGluGlyLysLeu 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerArgGluMetValAsnMetIleIleIleGlnArgGlyPheGlnMetAsnSerLysSer 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GlnglyLys-----TyrSerAsnSerGln 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 ValValAspPheTyrAsnIleProLeuAlaArgPheThrSerGluAspGlyLeuArgArg 426
                                                                                                                                                                                                        ProLeuThrLeuAspPheGlylleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAla 340
                              281 AsnMetThrAlaPheThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnPro 300
                                                                                                                 301 AlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGln 320
                                                                                                                                                                                                                                                                                               341 SerklaklahlaileGlyThrAspileGlyLysLeuProSerMetMetProlleGlnThr
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APPLICANT: Barenkamp, Stephen J
APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: ef No. 5603938-Typeable Haemophilus
TITLE OF INVENTION: ef No. 5603938-Typeable Haemophilus
TITLE OF INVENTION: ef No. 5603938-Typeable Haemophilus
NUMBER OF SEQUENCES: 8
CORRESPERS: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Didg. 1
CITY: Arlington
STATE: Virginia
CONFTRY: U.S.A.
ZIF: 2202-0286
COMPUTRY: LD.S.A.
ZIF: 2202-0286
COMPUTRY: IS PC Compatible
COMPUTRY: IS PC Compatible
COMPUTRY: BW PC Compatible
COMPUTRY: BW PC Compatible
COMPUTRY: BW PC Compatible
COMPUTRY: BW PC Compatible
COMPUTRY: US PATENTING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PREADMER: US/08/302,832
APPLICATION NUMBER: US/08/302,832
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                                                                                                                                                                                                                                                         4221 GATTTAACAGTTGGGAATGGCGCAGAA-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 18
US-08-302-812-1
'Sequence 1, Application US/08302832
'Patent No. 5603938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467
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------TCTGCGACAAGTGGAGAAATTACCACTAAAACAGGTACAATT 3815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 GlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThrAlaLeu 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 AsnAlaValValAsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyr 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 PheAlaLeuLeuGluSerTrpLysGlyAsnGlyThr--------ProProlle 203
                                                                                                                                                                                                                                                                                                                                                                                                                                              89 LeuklaileGlyGlyLysGlyPhePheGlnyalThrieuGluAsplysValHisTyrThr 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 ArgAlaçlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr 128
                                                                                                                                                                                                                                                                           68
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                                                                                                                                                                                                                  3570 ---GCCAAAAAGTAACCTTT------AACCAGGTTAAAGAT
                                                                                                                                                                                  30 AsnThrIleGlyTyrLysGlnGlnValValValPheGlnAspLeuPheSerGlnAspLeu
                                                                                                                                                                                                                                                                      50 AlaileglySerThrGlySer---GlnGlyProAsnGlnAlaGlyMetGlyAlaGlnVal
                                                                                                                                                                                                                                                                                                               3534 ACTATTGGTAACACCAATAGTGCTGATGGTACTAAT--------
                                                                                                                                                                                                                                                                                                                                                          69 GlySerValArgThrIlePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACGCAACCACTGGTAACGTGGAGATAACCGCTCAAACAGGTAGT----
5116
110
75
210
101
                      Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                US-10-009-823A-1 (1-502) x US-08-302-832-1 (1-5116)
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5116 base pairs
                                                                                                                                                                                                                                                                                                                                         (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173.50
37.30%
22.18%
6.71%
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
STREET: 2001 Jei
STREET: Bldg. 1
CITY: Arlington
                                                   Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                   STATE: Vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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                                                                                                      1128 GCAACAACAGGGGAGGCTAACGTAACAAGTGCAACAGGTACAATTGGTGGTACGATTTCC 4187
                                              1951 GITACIGITACTGCAAAI---AGCGGTGCATTAACCACTTTGGCAGGCTCTACAATTAAA 4007
                                                                                                                                                                             1068 GGCACAGTAGAGGTTAAAGCAACCGAAAGTTTAACCACTCAATTCAAAAATTAAA 4127
                                                                                                                                                                                                                                                                                                                     -----GTTACGGCAAACGCTGGC 4220
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                                                                                                                                                                                                                                                                                                                                                                                         -ATTAATGCGACAGAA 4262
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              224 HisAspIleThrValTyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGlu 243
                                                                                TyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAla 263
                                                                                                                                                                                                                                                                                   301 AlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGln 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4422 ACTACCGTGAAGGGTTCAAACATTAATGCAACCAGCGGTACCTTGGTTATTAACGCAAAA 4481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGlnAsp 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyTyrProGlnGlyAspLeu-----ValAspValThrIleThrSerGluGlyLysLeu 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TyrSerAsnSerGln 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446
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                                                                                                                                                 264 GlyLeuLeu------MetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4362 GGTAGCGTTGCAGGAAGTATTAATGCCGCCAATGTGACACTAAAATACTACAGGCACTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427 GluGlyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 ValValAspPheTyrAsnIleProLeuAlaArgPheThrSerGluAspGlyLeuArgArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08530198
Patent No. 5869065
GENERALINEOMATION:
APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEWE III, JOSEPH W
TILLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFAC
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
CORRESPONDENCES:
ADDRESSEE: Shoemaker and Mattare, Ltd
                                                                                                                                                                                                                                                                                                                                                                                      1221 GATTTAACAGTTGGGAATGGCGCAGAA----
                                                                                                                                                                                                                                                                                                                  4188 GGTAATACGGTAAAT-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128
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3711 ATCGATGCAAAAATGTAACGTAAACAACAATATTACTTCTCACAAAGCAGTGAGGATC
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                                                                                                                                                                                                                                                                                                               Version #1.25
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Matches:
Conservative:
Mismatches:
Indels:
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ZIP: 22202-0286

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,198
FILING DATE: 13-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERKEYRESSER, JERRY W
REGISTAATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: JWB-1186
TELECOMMUNICATION INFORMATION:
MEGISTAATION INFORMATION:
REFERENCE/DOCKET NUMBER: JWB-1186
TELECOMMUNICATION INFORMATION:
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189	PheAlaLeuLeuGluSerTrpLysGlyAsnGlyThr
3864	CTAGGTGGAATTGÁGTCCAGCTCTGGCTCTGTAACACTTACTGCAACCGAGGGCGCTCTT 3923
204	SerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSer 223
224	2 4
3951	0
244	TyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAla 263
4008	
264	GlyLeuLeuMetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys 280
4068	GGCACAGTAGAGGTTAAAGCAACCGAAAGTTTAACCACTCAATCCAAATTCAAAATTAAA 4127
281	AsnMetThrAlaPheThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnPro 300
4128	GCAACAACAGGCGAGGCTAACGTAACAGTGCAACAGGTACAATTGGTGGTACGATTTCC 4187
301	AlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGln 320
4188	GGTAATACGGTAAATGTTACGGCAAACGCTGGC 4220
321	ProLeuThrLeuAspPheGlylleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAla 340
4221	::: GATTTAACAGTTGGGAAATGGCGCAGAAATTAATGCGACAGAA 4262
341	SerAlaAlaAlaIleGlyThrAspIleGlyLysLeuProSerMetMetProIleGlnThr 360
4263	GGAGCTGCAACCTTAACTACATCGGGGAAATTA
361	SerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGlnAsp 380
4302	· Ë
381	GlyTyrProGlnGlyAspLeuValAspValThr1leThrSerGluGlyLysLeu 398
39	406
' '	CTACCGTGAAGGTTCAAACATTAATGCAACCAGGGTACCTTGGTTATTAACGCAAAA
407	ValValAspPheTyrAsnIleProLeuAlaArgPheThrSerGluAspGlyLeuArgArg 426
4482	
427	GluGlyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuPro 446
4542	
447	GlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMet 466
4593	GGGAATAICACATAAATGGATTAAATAICATT 4628
467	SerArgGluMetValAsnMetIleIleIleGlnArgGlyPheGlnMetAsnSerLysSer 486 ::: ::::: TCAAAAAACGGTATAAAACACCGTACTGTTAAAAGGGTTAAAATTGATGTGAAATAC 4685
487	ValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeuLysArg 502
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ZUZOZ-0266
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE DETAILS DOSS SOFTWAND TO THE SECONDATALING SYSTEM:
APPLICATION NUMBER: US/08/469,880
FILING DATE: 06-JUN-1995
CLASSIFICATION; 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1992
PRIOR APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
PRIOR RAPLICATION NUMBER: US 08/302,832
FILING DATE: 16-MAR-1993
PRIOR APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-MAR-1993
ATTORNEY/GENT INFORMATION:
MAME: BERKETCESSET, JOSTY W
REGISTRATION NUMBER: 103-516 MIS:vg
TELECOMMUNICATION NUMBER: 22,651
REFERENCE PLOCKET NUMBER: 1038-516 MIS:vg
TELECOMMUNICATION NUMBER: 24,651
REFERENCE PLOCKET NUMBER: 138-516 MIS:vg
TELECOMMUNICATION NUMBER: 25,651
REPERBONE: (703) 415-0813
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARRATERISTICS:
LENGTH: 5116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
TUDED CONTINE TYPE: DNA (Genomic)

APPLICANT: Barenkamp, Stephen J.

TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5876733-Typeable Haemophilus
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza

CITY: Arlington STATE: Virginia COUNTRY: U.S.A. ZIP: 22202-0286

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3534 ACTATTGGTAACACCAATAGTGCTGATGGTACTAAT------3569
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                                                                                                                                                                                                                                                                                                                                                                                  89 LeuAlaileGlyGlyLysGlyPhePheGlnValThrLeuGluAspLysValHisTyrThr 108
                                                                                                                                                                       30 AgnThrileGlyTyrLysGlnGlnGlnValValPheGlnAgpLeuPheSerGlnAgpLeu 49
                                                                                                                                                                                                                                                                                                             69 GlyserValArgThrIlePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAsp 88
                                                                                                                                                                                                                                          50 AlaileglySerThrGlySer---GlnGlyProAsnGlnAlaGlyMetGlyAlaGlnVal 68
              Length:
Matches:
Conservative:
Mismatches:
Indels:
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173.50
37.30%
22.18%
6.71%
                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores:
Pred. No.:
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RESULT 20
US-08-469-880-1
; Sequence 1, Application US/08469880
; Patent No. 5876733
; GENERAL INFORMATION:

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--AATATC---ATT 4628
                                                                                        4629 TCAAAAAACGGTATAAACACCGTACTGTTA---AAAGGCGTTAAAATTGATGTGAAATAC 4685
                                               467 SerArgGluMetValAsnMetIleIleIleGlnArgGlyPheGlnMetAsnSerLysSer
                                                                                                                                                                                                                                                 Sequence 1; Application US/08728470; Patent No. 5928651; GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: High Molecular Weight Surface Proteins TITLE OF INVENTION: High Molecular Weight Surface Proteins; TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus; NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: Stoemaker and Mattare, Ltd. STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: Bldg. 1 CITY: Artington STREET: Usigning STATE: Virginia
                                                                                                                                                              487 ValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeuLysArg
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/728,470

FILING DATE: US/08/728,470

FILING DATE: US/08/728,470

FILING DATE: US/08/728,470

FILING DATE: US/08/728,470

FILING DATE: US/08/728,470

FILING DATE: US/08/728,470

FILING DATE: US/08/728,470

FILING DATE: US/08/728,832

FILING DATE: US/08/193

PRIOR APPLICATION NUMBER: US/08/202166

FILING DATE: US/08/21/2020

APPLICATION NUMBER: US/08/21/2020

FILING DATE: US/08/21/2020

APPLICATION NUMBER: US/08/21/2020

FETERENCE/DOCKET NUMBER: 1038-633

TELECOMMUNICATION NUMBER: 1038-633

TELECOMMUNICATION NUMBER: 1038-633

TELECOMMUNICATION NUMBER: 1038-633

TELEPHONE: (703) 415-0813

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
         ---GATTTAATCACAATAAATGGATTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-009-823A-1 (1-502) x US-08-728-470-1 (1-5116)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5116 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173.50
37.30%
22.18%
6.71%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
      .593 GGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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3654 ACATCCGGTAGTAATAACAACACTGAAGATAGCAGTGACAATAAT---GCCGGCTTAACT 3710
                                                                                              iii atcgatgcaaaaatgtaacagtaaacaatattacttctcacaaagcagtgagcatc 3770
                                                                                                                                                                                  ... ICTGCGACAAGTGGAGAATTACCACTAAAACAGGTACATT 3815
                                                                                                                                                                                                                                                                            3816 AACGCAACCACTGGTAACGTGGAGATAACGCTCAAACAGGTAGT------ATC 3863
                                                                                                                                                                                                                                                                                                                                              ----GGCAACACC 3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3951 GTTACTGTTACTGCAAAT---AGCGGTGCATTAACCACTTTGGCAGGCTCTACAATTAAA 4007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4188 GGTAATACGGTAAAT------4220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4361
                                                                                                                                                                                                                                 AsnalavalvalAsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyr 188
                                                                                                                                                                                                                                                                                                                                                                                                             223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---ATTAATGCGACAGAA 4262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4421
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                                                                                                                                                  GlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThrAlaLeu 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1542 AATGGCTCCGGCAGCGTAATCGCGACAACCTCAAGC-----AGAGTGAACATCACT 4592
                                                               LeuMetGlySerArgIleSerAsnAsnProAsnIleLysLysGluThrLeuGluProIle 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 HisAspileThrValTyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGlu 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAla 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 AsnMetThralaPheThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnPro 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGln 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 ProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAla 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 SeralaalaalaIleGlyThrAspIleGlyLysLeuProSerMetMetProIleGlnThr 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGlnAsp 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                381 GlyTyrProGlnGlyAspLeu----ValAspValThrIleThrSerGluGlyLysLeu 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TyrSerAsnSerGln 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 GluGlyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuPro 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447 GlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMet 466
                                                                                                                                                                                                                                                                                                                     PheAlaLeuLeuGluSerTrpLysGlyAsnGlyThr-------ProProlle
                                                                                                                                                                                                                                                                                                                                                                                                      204 SerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 GlyLeuLeu------MetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GINGCGTTGCAGGAAGTATTAATGCCGCCAATGTGACACTAAATACTACAGGCACTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1422 ACTACCGTGAAGGTTCAAACATTAATGCAACCAGGGGTACCTTGGTTATTAACGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 ValValAspPheTyrAsnIleProLeuAlaArgPheThrSerGluAspGlyLeuArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1302 ACCGAAGCTAGTTCACACATTACTTCAGCCAAGGGTCAGGTAAATCTTTCAGCTCAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4221 GATTTAACAGTTGGGAATGGCGCAGAA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GlnGlyLys-------
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3924 GCTGTAAGCAATATTTCG-------
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30 AsnThrIleGlyTyrLysGlnGlnGlnValValPheGlnAspLeuPheSerGlnAspLeu 49

ą	3480 AATATTTCAGGTTTCAATAAAGCAGAGATTACAGCTAAAGATGGTAGTGATTTA	TTTA 3533
≵	50 AlaileGlySerThrGlySerGlnGlyProAsnGlnAlaGlyMetGlyAlaGlnVal	nyal 68
ď	3534 ACTATTGGTAACACCCAATAGTGCTGATGGTACTAAT	3569
≿ :	69 GlySerValArgThrIlePheThrGlnGlyAlaPheGluProGlyAenSerValThrAsp	88
q	3570GCCAAAAGTAACCITTAACCAGGTTX	AGAT 3602
*	89 LeuhlaileGlyGlyLysGlyPhePheGlnValThrLeuGluAspLysValHisTyrThr	108
ą	3603 TCAAAATCTCTGCTGACGGTCACAAGGTGACACTACACAGGAAAGTGGAA.	
<i>≿</i>	109 ArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr	
ą	3654 ACATCGGTAGTAATAACAĄCACTGAAGATAGCAGTGACAATAATGCCGGC	
Ä	129 LeuMetGlySerArglleSerAsnAsnProAsnIleLysLysGluThrLeuGluProlle	
q	3711 ATGGATGGAAAAATGTAACAGTAAACAACAATATTACTTCTCACAAAGGAGTG	SCATC 3770
⋩	149 GlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThrAlaLeu	168
ą,	3771TCTGCGACAAGTGGAGAAATTACCACTAAAACAGGTACA	CCATT 3815
<i>≿</i> ;	169 AsnalaValValAsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyr	
q	3816 AACGCAACCACTGGTAACGTGGAGATAACCGCTCAAACAGGTAGT	ATC 3863
<i>\</i>	189 PheAlaLeuLeuGluSerTrpLysGlyAsnGlyThrProProlle	
ąć	3864 CIAGGIGGAAIIGAGICCAGCICIGGCICIGIAACACITACIGCAACCGAGGGC	CTCTT 3923
λζ	204 SerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSer	snSer 223
qc	3924 GCTGTAAGCAATATTTCGGGC	ACACC 3950
à	224 HisaspileThrValTyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGlu	heGlu 243
ą	3951 GITACTGITACTGCAAATAGCGGTGCATTAACCACTTTGGCAGCTCTACA	TTAAA 4007
ć	244 TyrLeuValalaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAla	erAla 263
q	4008 GGAACCGAGAGTGTAACCACTICAAGTCAATCAGGGGATATCGGCGGTACGATTTCTGGT	cresr 4067
č	264 GlyLeuLeuMetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys	
qq	4068 GCACAGIAGAGGIIAAAGCAACCGAAAGIIITAACCACICAAICCAAIICAAAA	TTAAA 4127
δ	281 AsnMetThrAlaPheThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnPro	lnPro 300
qq	4128 GCAACAACGAGGCGAGGCTAACGTAACAAGTGCAACAGGTACAATTGGTGGTACG	TTTCC 4187
ò	301 AlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGln	leGln 320
qq	4188 GGTAATACGGTAAATGTTACGGCAAAC	CTGGC 4220
à	321 ProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAl	roAla 340
Dβ	4221 GATTTAACAGTTGGGAATGGCGCAGAAATTAATGCGACAGAA	CAGAA 4262
à	341 SeralaalaalaileGlyThrAspIleGlyLysLeuProSerMetMetProIleGlnThr	lnThr 360
d d	4263 GGAGCTGCAACCTTAACTACATCGGGCAAATTA	ACT 4301
ઠે	361 SerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGlnAsp	38
a a	4302 ACCGAAGCTAGTICACACATTACTTCAGCCAAGGGTCAGGTAAATCTTTCAGC	AĞĞAT 4361
č	381 GlyTyrProGlnGlyAspLeuValAspValThrIeThrSerGluGlyLyBleu	
Db	4362 GGTAGCGTTGCAĞĞAAGTATTAATGCCGCCAATGTĞACACTAAATACTACAĞĞC	CTŤŤÁ 4421

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Qy 487 ValThrThIAlaAspThIMetLeuGlnLysAlaLeuGluLeuLysArg 502 ::: :::	RESULT 22 US-08-617-697-1 Sequence 1, Application US/08617697 Patent No. 5977336 BENERAL INFORMATION: APPLICANT: Barenkamp, Stephen J TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: 6 No. 5977336-Typeable Haemophilus NUMBER OF SEQUENCES: 11 ANNERS OF SEQUENCES: 11	CONFURE READALES SINCHES SINCH STREET SO STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: Arlington STREET: Arlington STATE: Virginia COUNTRY: U.S.A. STREET: STREET STR	SOFTWARE: PARENTIN Release #1.0, Version #1.30 SOFTWARE: PARENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/617,697 FILING DATE: 01-APR-1996 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/302,832 FILING DATE: US -OCT-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US PCT/US93/02166	PILING DATE: 16-MAR-1993 ATTORNEY FAGENT INFORMATION: NAME: BERFERENCE JOETY W REGISTRATION NUMBER: 22,651 REPERENCE FOCKET NUMBER: 1038-557 TELECOMUNICATION INFORMATION: TELECHONE: (703) 415-0810 TELECHONE: (703) 415-0813 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 5116 base pairs TYPE: nucleic acid STRANDEDNESS: single TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid STRANDEDNESS: single MOLECULE TYPE: DNA (genomic) US-08-617-697-1

|||:: 4542 AATGGCTCCGGCAGAATCGCGACAACCTCAAGC-----AGAGTGAACATCACT 4592

8 6 8 6 8 6 8 6 8 6

427 GluglyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuPro 446

399 -----Glngiytys-----

-----TyrSerAsnSerGln 406

NAME: Berkstresser, Jerry W
REGISTRATION UMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-625
TELEPOMUNICATION INPORMATION:
TELEPAX: (703) 415-0810
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRRACTERISTICS:
LENGTH: 5116 base pairs
TYPE: nucleic acid
STRANDENESS: single
1009LGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-719-641-1

Alignment Scores: 7.39e-08 Length:
Pred. No.: 173.50 Matches:
Percent Similarity: 37.30% Conservative:
Best Local Similarity: 22.18% Mismatches:
Query Match: 6.71% Conservative:

US-10-009-823A-1 (1-502) x US-08-719-641-1 (1-5116)

3480 AATATTTCAGGTTTCAATAAAGCAGAGATTACAGCTAAAGAT-----GGTAGTGATTA 3533 3603 TCAAAAACTCTGCTGACGGT---CACAAGGTGACACTACACAGCAAAGTGGAA---- 3653 3654 ACATCCGGTAGTAATAACAACACTGAAGATAGCAGTGACAATAAT---GCCGGCTTAACT 3710 ::: 3711 ATCGATGCAAAAATGTAACAGTAAACAACAATATTACTTCTCACAAAGCAGTGAGCATC 3770 3771 ------TCTGCGACAAGTGGAGAAATTACCACTAAAACAGGTACAACTT 3815 3816 AACGCAACCACTGGTAACGTGGAGATAACCGCTCAAACAGGTAGT------ATC 3863 3924 GCTGTAAGCAATATTTCG------GGCAACACC 3950 3951 GITACIGITACIGCAAAI---AGCGGIGCAITAACCACTITIGGCAGGCICIACAAITAAA 4007 3570 ---GCCAAAAAGTAACCTTT-------3602 89 LeualaileGlyGlyLysGlyPhePheGlnValThrLeuGluAspLysValHisTyrThr 108 129 LeuMetGlySerArg1leSerAsnAsnProAsnIleLysLysGluThrLeuGluProIle 148 109 ArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr 128 149 GlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThrAlaLeu 168 169 AsnAlaValValAsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyr 188 189 PheAlaLeuLeuGluSerTrpLysGlyAsnGlyThr--------ProProIle 203 224 HisAspIleThrValTyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGlu 243 204 SerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSer 223 244 TyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAla 263 69 GlySerValArgThrIlePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAsp 88 30 AspThrIleGlyTyrLysGlnGlnGlnValValPheGlnAspLeuPheSerGlnAspLeu 49 50 AlaileGlySerThrGlySer -- GlnGlyProAsnGlnAlaGlyMetGlyAlaGlnVal 68 Ор à 셤 ò a g 셤 δ 요 δ g ઠે g ò ద 원 ò d ò ò ð ઠે

	GlyLeuLeuMetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys	280
Db 4068	GGCACAGTAGAGGTTAAAGCAACCGAAAGTTTAACCACTCAATTCCAATTCAAAAATTAAA	4127
Qy 281	AsnMetThrAlaPheThrProThrGlySerAlaThrLysAspieuAsnAlaTrpGlnPro	300
Db 4128	GCAACAACAGGCGAGGCTAACGTAACAAGTGCAACAGGTACAATTGGTGGTACGATTTCC	4187
Qy 301	AlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGln	320
Db 4188	GGTAATACGGTAAATGTTACGGCAAACGCTGGC	4220
Qy 321	ProLeuThrLeuAspPheGly11eLysSerGlnGlnAsnMetTrpAlaGlyAlaProAla	340
Db 4221	GATTTAACAGTTGGGAATGGCGCAGAAATTAATGCGACAGAA	4262
Oy 341	SeralaalaalaileGlyThraspIleGlyLysLeuProSerMetMetProlleGlnThr	360
Db 4263	GGAGCTGCAACCTTAACTACATCATCGGGCAAATTAACT	4301
Qy 361	SerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGlnAsp	380
Db 4302	ACCGAAGCTAGTTCACACATTACTTCAGCCAAGGGTCAGGTAAATCTTTCAGCTCAGGAT	4361
Qy 381	GlyTyrProGlnGlyAspLeuValAspValThr11eThrSerGluGlyLysLeu	398
Db 4362	GGTAGCGTTGCAGGAAGTATTAATGCCGCCAATGTGACACTAAATACTACAGGCACTTTA	4421
Oy 399	GlnGlyLysTyrSerAln	406
Db 4422	ACTACCGTGAAGGGTTCAAACATTAATGCAACCAGCGGTACCTTGGTTATTAACGCAAAA	4481
Qy 407	ValValAspPheTyrAsnIleProLeuAlaArgPheThrSerGluAspGlyLeuArgArg	426
Db 4482	GACGCTGAGCTAAATGGCGCAGCATTGGGTAACCACAGTGGTAAATGCAACGCA	4541
Qy 427	GluglyAsnAsnHisTyrSerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuPro	446
Db 4542	AATGGCTCCGGCAGCGTAATCGCGACAACCTCAAGCAGAGTGAACATCACT	4592
Qy 447	GlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMet	466
Db 4593	GGGGATTTAATCACAATAAATGGATTAAATATCATT	4628
Qy 467	SerArgGluMetValAsnMetIleIleIleGlnArgGlyPheGlnMetAsnSerLysSer	486
Db 4629	TCAAAAAACGGTATAAACACCGTACTGTTAAAAGGCGTTAAAATTGATGTGAAATAC	4685
Qy 487		
Db 4686	ATTCAACCGGGTATAGCAAGCGTAGATGAAGTAATTGAAGCGAAACGC 4733	
RESULT 24 US-09-206-942-66 ; Sequence 66, A ; Patent No. 643 ; Patent No. 643 ; APPLICANT: Ya ; APPLICANT: YA ; TITLE OF INVE ; TITLE OF INVE		

US-09-206-942-66

Sequence 66, Application US/09206942

Sequence 66, Application US/09206942

Sequence 66, Application US/09206942

GENERAL NO. 643269

GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Lasin, Michell H.
TITLE OF INVENTION: Protective Recombinant Haemophilus:
TITLE OF INVENTION: Protective Recombinant Haemophilus:
TITLE OF INVENTION: Molecular Weight Proteins
TITLE OF INVENTION: Molecular Weight Proteins
TITLE OF INVENTION: Wolceular Weight Proteins
CURRENT APPLICATION NUMBER: US/09/26,942

CURRENT FILING DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 95

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 66

LENGTH: 516

TYPE DNA

TYPE DNA

ORGANISM: Haemophilus influenzae

1008 GGAACCGAGAGTGTAACCACTİCAAGTCAATCAGGGGATATCGGCGGİACGATTİCİGGT 4067

us-10-009-823a-1.rni

		4422 ACTACCGTGAAGGTTCAAACATTAATGCAACCAGGGTACCTTGGTTATTAAGGCGAAAA 407 ValValAspPheTyrAsnIleProLeualaArgPheThrSerGluAspGlyLeuArgArg ::: 4482 GACGCTGAGCTAAATGGCGCAGCATTGGTAAACCCACAGTGGTAAATGCAACCGCA	427 GludlyAshAshAshHisTyrSarlaThkTeuAspSerGlyGluPheGlyLeuPro 446	Qy 467 SerArgGluMetValAsnMetIleileileileGlnArgGlyPheGlnMetAsnSerLysSer 486	RESULT 25 US-08-038-682-5 US-08-038-682-5 Sequence 5, Application US/08038682 Patent No. 5548897 GENERAL INFORMATION: APPLICANT: BARENKAMP, STEPHEN J APPLICANT: ST. GEME III, JOSEPH W TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS	WYENTION: OF NON-TYPEABLE HAEMOP SEQUENCES: 8 SEQUENCES: 8 3: Shoemaker and Mattare, Ltd 2001 Jefferson Davis Hwy., 1203 Bldg. 1 Clington firginia	M: y disk ompatible PC-DOS/MS-DC Release #1.	### APPLICATION WUMBER: US/08/038,682 FILING DATE: 16-MAR-1993
7.39e-08 Length: 173.50 Matches: 37.30% Conservativ Y: 22.18% Mismatches: 6.71% Gaps:		3534 69 3570	OY 89 LeualaileGlyGlyLysGlyPhePheGlnValThrLeuGluAspLysValHisTyrThr 108	LeumetGlySerArglleSerAsnAsnProAsnIleLysLysGluThrLeuGluProlle ::: ATCGATGCAAAAAATGTAAACAACAATATTACTTCTCACAAAGCAGTGAGCATC GlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThrAlaLeu	Oy 169 AsnalaValValAsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyr 188	QY 204 SerThrSerAsnTyrSerTyralaGlnProWetArgValTyrAspGlnGlnGlyAsnSer 223 Db :::	Oy 244 TyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAla 263	OY 281 ASIMETTALAIAPHETHYPTOTHIGINSERAIATHILYSASPLEUASBALAITIFGINPERO 300

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4078 GCAACAACAGGCGAGGCTAACGTAACAAGTGCAACAGGTACAATTGGTGGTACGATTTCC 4137
                                                                       4138 GGTAATACGGTAAAT-------
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FILING DATE: 16-SEP-1994
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7 Sequence 5. Application US/08302832
Patent No. 5603938
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
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                                                                                                                                                                           Length:
Matches:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9171 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear Genomic)
                                                                                                                                                          1.92e-07
173.50
37.30$
22.18$
6.71$
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Best Local Similarity:
Query Match:
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1171 GATTTAACAGTTGGGAATGGCGCAGAA----------ATTAATGCGACAGAA 4212
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                                                                                                                         321 ProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAla 340
301 AlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGln 320
                                                                                                                                                                                                                                                                                                                                                                               361 SerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGlnAsp 380
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: Of No. 5603938-Typeable Haemophilus
INVER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Lington
STREET: Virginia
CITY: Arlington
STREET: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DAIR:
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4017

4251

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380

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4491

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4018 GGCACAGTAGAGGTTAAAGCAACCGAAAGTTTAACCACTCCAATCCAATTCAAAATTAAA 4077
                                                                                                                                                                                                                               [078] GCAACAĄCAGGCGAGGCTAACGTAACAAGTGCAACAAGGTACAATTGGTGGTACGATTTCC 4137
             9901 GTTACTGTTACTGCAAAT---AGCGGTGCATTAACCACTTTGGCAGGCTCTACAATTAAA 3957
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                                                 244 TyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAla
                                                                                                                       264 GlyLeuLeu------MetSerGlyThrMetThrPheSerSerAsnGlyGluLeuLys
                                                                                     3958 GGAACCGAGAGTGTAACCACTICAAGTCAATCAGGCGATATCGGCGGTACGATTTCTGGT
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4171 GATTTAACAGTTGGGAATGGCGCAGAA-----
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Patent No. 5869065
GENERAL INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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                   FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US pct/us93/02166
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :::
1874 GCTGTAAGCAATATTTCG-------
                                                                                                               NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-404
TELECOMMUNICATION INFORMATION:
     GB 9205704.1
                                                                                                                                                                                 TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
INPORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9171 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-302-832-5
APPLICATION NUMBER: GB 92
FILING DATE: 16-MAR-1992
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173.50
37.30%
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Best Local Similarity:
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4579 TCAAAAACGGTATAAACACCGTACTGTTA---AAAGGCGTTAAAATTGATGTGAAATAC 4635 466 467 SerArgGluMetValAsnMetIleIleIleGlnArgGlyPheGlnMetAsnSerLysSer 486 447 GlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMet APPLICANT: BARENTAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Shoemaker and Mattare, Ltd
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Azlington

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4492 AATGGCTCCGGCAGCGTAATCGCGACAACCTCAAGC-----AGAGTGAACATCACT 4542
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------GGCAACACC 3900
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| 1213 GGAGCTGCAACCTTAACTACATCATCGGGCAAATTA--------ACT 4251
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204 SerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSer 223
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                                                                                                224 HisaspileThrvalTyrPheaspGlyalaProSerSerThrGlySerLysThrPheGlu
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IIILE OF INVENTION: High Molecular Weight Surface Proteins
IIILE OF INVENTION: of No. 5876733-Typeable Haemophilus
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                                4138 GGTAATACGĠŤÄÄÄŤ-~------
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                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ELING DATE: 13-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESER, JERRY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: JWB-1186
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0813
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) US-08-530-198-5
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37.30%
22.18%
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EDNESS: single
                ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
Query Match:
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CLASSIFICATION:
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                                                                              149 GlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThrAlaLeu 168
                                                                                                                                                                                                                                      189 PheAlaLeuLeuGluSerTrpLysGlyAsnGlyThr--------ProProIle 203
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      LeuMetGlySerArglleSerAsnAsnProAsnIleLysLysGluThrLeuGluProIle 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 TyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAla 263
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                                           3661 ATCGATGCAAAAATGTAACAGTAAACAACAATATTACTTCTCACAAAGCAGTGAGCATC
                                                                                                                                                             169 AsnAlaValValAsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyr
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                      MUNESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                 COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,880
FILING DATE: 06-UN-1995
CLASSIFICATION BATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser. Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-516 MIS:V9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-009-823A-1 (1-502) x US-08-469-880-5 (1-9171)
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TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
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173.50
37.30%
22.18%
6.71%
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TYPE: nucleic acid
STRANDEDNESS: single
NUMBER OF SEQUENCES:
                                                                    STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
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Best Local Similarity:
Query Match:
DB:
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467 SerArgGluMetValAsnMetIleIleIleGlnArgGlyPheGlnMetAsnSerLysSer 486

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3604 ACATCCGGTAGTAATAACAACACTGAAGATAGCAGTGACAATAAT---GCCGGCTTAACT 3660
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                                                              69 GlySerValArgThr1lePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAsp
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:36 ATTCAACCGGGTATAGAGCGTAGATGAAGTGAAGTGAAACGC 4683
                                                        487 ValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeuLysArg 502
                                                                                                                                                                            Sequence 5, Application US/08728470
Patent No. 5928651
GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUT TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFWANARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATORNEY/AGENT INFORMATION:
NAME: BETKETESSEY, JG:TY
REGISTRATION NUMBER: 12,651
REFERENCE/DOCKET NUMBER: 1038-633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPAX: (703) 415-0810
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9171 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
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173.50
37.30%
22.18%
6.71%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                            08-728-470-5
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Percent Similarity: 37.30% Conservative: 75 Best Local Similarity: 22.16% Mismatches: 210 Query Match: 6.71% Indels: 24 DB: 24 US-10-009-823A-1 (1-502) x US-08-617-697-5 (1-9171) QY 30 ASHTHILEGLYTYLYSGINGINDALVAIPHEGINASpleuvheSerGlnAspleuv 49	3520GCCAAAAAGTAACCTTTAACCAGGTTAAAGAT 89 LeuAlaileGlyGlyLyGlyPhePheGlnValThrLeuGluAspLysValHisTyrThr	Oy 129 LeuMetGlySerArglleSerAsnAsnProAsnIleLysLysGluThrLeuGluProIle 148 3661 ATGGATGCAAAAATGTAACAACAACAATATTACTTCTCACAAGCAGTGAGCATC 3720 Qy 149 GlnLeuAspPheAsnAspProThrValAlaLysSerProAlaLysThrSerThrAlaLeu 168 Db 3721	169 ASRALAVAlVALASENLEUGLYASPSETTHTASPLYSTHTGLUSETGLUALAASRPTOTYT 3766 AACGCAACCACTGGTAACGTGGAGATAACCGCTCAAACAGGTAGTATC 189 PheAlaLeuLeuGluSetTrpLyGCTYABGGTYThrProProIle 181 SHAH CTAGGTGGAATTGAGTCTCTGGCTCTGTAACACTTACTGCAACCGAGGGCGCTCTT	Qy 204 SerThrSerAsnTyrSerTyrAlaGlnProMetArgValTyrAspGlnGlnGlyAsnSer 223 1:::	Oy 244 TyrLeuValAlaMetAsnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAla 263		Db 4171 GATTTÄÄCÄGTTGGGAATGGCGCAGAAATTAATGCGACAGAA 4212 Qy 341 Seralaalaala1leGlyThräspileGlyLysLeuProSerWetMetProIleGlnThr 360 :::
Db 4372 ACTACCGTGAAGGGTTCAAACATTAATGCAACCAGGGGTACCTTGGTTATTAACGCAAAA 4431 Oy 407 ValValAspPheTyrAsnileProLeualaArgPheThrSerGluAspGlyLeuArgArg 426 1	487 ValThrThralaAspThrMetLeuGlnLysAlaLeuGluLeuLysArg 502 ::: 4636 ATTCAACCGGGTATAGCAAGCGTAGAAGTAATTGAAGCGAAACGC 4683 SULT 30 -08-617-697-5 Sequence 5, Application US/08617697	GENERAL INFORMATION: APPLICANT: Barenkamp, Stephen J TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS: ADDRESSEE: Shoemaker and Mattare, Ltd. STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza	STREET: Bldg. 1 CITY: Arlington STATE: Virginia COUNTRY: U.S.A. TE: 22202-0286 COMPUTER READALE: FORM: MEDIUM TYPE: Flopy disk COMPUTER: IBM PC compatible	CURRENT APPLICATION DATA: SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/617,697 FILING DATE: 01-APR-1996 CLASSIFICATION: 4.24 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/302,832	FILING DATE: 05-OCT-1994 PRIOR APPLICATION DATA: PRIOR APPLICATION UNMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993 ATTORNEY/AGBUT INFORMATION: NAME: Berkstresser, Jerry W REGISTRATION NUMBER: 22.651 REFERENCE/DOCKET NUMBER: 1038-557	TELEPHONE: (703) 415-0810 TELEPHONE: (703) 415-0810 TELEFAX: (703) 415-0813 FINEORMATION FOR SEQ ID NO: 5: SEQUENCE FRARACTERISTICS: TYPE: nucleic acid STRANDENNESS: single MOLECULE TYPE: DNA (genomic) US-08-617-697-5	Alignment Scores: 1.92e-07 Length: 9171 Pred. No.: 173.50 Matches: 110

	9 () - 3 () - 3 ()
TATION INFORMATION: (703) 415-0810 PR SEQ ID NO: 5: ARACTERISTICS: 117 Dase pairs 110 Lose pairs 110 Lose 1 Linear PE: DNA (Genomic) 1 1.92e-07 Matci 1 1.92e-07 Matci 1 1.92e-18 Mism Arity: 22.18 Mism Arity: 22.18	00
SerThrargargTyrSerGlnAsp CAGGTAAATCTTTCAGGAT Thr II = 1	4492 AATGGCTGGGGGGGGGTAATGGCGGAACTCAAGCAGAGTGAACACCCT 4542 447 GLYTHSERABITYTGLYLAYEUSETAATAAGGGTTAAAATGGCTTAAATGGATTAAATGGCTTAAATGGATTAAATGGCTTAAATGGATTAAATGGCTTAAAATGGATTAAATGGCTTAAAATGGATTAAATGGCTTAAAATGGATTAAATGGCTTAAAATGGATGAATAC 4635 447 GLYTHSERABAACGGTAAAAAAGGGTAGATGAATGAATGGATGAATAC 4635 4579 TCAAAAAAACGGTATAAACACGGTAGATGAATGAATGGATGAAAATGGATGAATAC 4635 4579 TCAAAAAAACGGTATAAACACGGTAGATGAATGAATGGAATAC 4635 4579 TCAAAAAAACGGTATAAACACGGTAGATGAATAAATTGAAGCGAAACGC 4683 REBUIT 31 US 08-719-64-5 105 08-719-64-5 105 08-719-64-5 106 08-719-64-5 107 108-719-64-5 10

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13429 GATCAAACCATCAGCGGGGGGGGGGCCGCCGCCGCTGGCGATACGGTCACCGTGACG 13488
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189
236
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Mismatches:
Indels:
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                                                                                                                 NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REGISTRATION INMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEPAX: (608) 251-9166
APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
PLING DATE: 03-Dec-1999
CLASSIFICATION: «Unknown»
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                              NO: 39:
                                                                      APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   TYPE: nucleic acid

STRANDEDNESS: double

DOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID IUS-09-453-7028-39
                                                                                                                                                                                           TELEFAX: (608) 251-9
INFORMATION FOR SEQ ID NO: 399
SEQUENCE CHARACTERISTICS:
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165.00
33.70%
22.62%
6.38%
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                                           GCAACAÁCÁGGCGAGGCTAACGTAACAÁGTGCÁACAGGTACAATTGGTGGTACGATTTCC 4137
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              AsnMetThrAlaPheThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnPro 300
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                                                                                                                                                                                                                                                                                                            GlyTyrProGlnGlyAspLeu-----ValAspValThrIleThrSerGluGlyLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                4372 ACTACCGTGAAGGGTTCAAACATTAATGCAACCAGGGGTACCTTGGTTATTAACGCAAAA
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Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E.
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: I South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.44Mb
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|171 GATTTAACAGTTGGGAATGGCGCAGAA-------
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MEDIUM TYPE: Diskette, 3.50 inch.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Blattner, Frederick R.
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Patent No. 6365723
GENERAL INFORMATION:
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                                                                                                   GGTAATACGCTAAAT-----
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STATE: WI
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13018 GGAAACAGCGGCAGCGCTACCCATCAGGTGACGGTCAATACCGGGCTGCCGACCATTACC 13077
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8 GlyAlaThrGlyMetLysThrHis------SerThrGlyLeuGlyThrValSer
                                                                                                                                                                                        -- AsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGln
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                                                                                                                                                                                                                                                                                                                                                                   38 GlnValValPheGlnAspLeuPheSerGlnAspLeuAlaIle-----GlySerThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 ValHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 SerGlyPheThrLeuMetGlySerArglleSerAsnAsnProAsnIleLysLysGluThr
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37

13248

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104

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164

PSEUDOMONAS

us-10-009-823a-1.rni

Mon Nov

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151.50
31.12%
20.24%
5.86%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4403765
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Pred. No.:
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                                                                            ArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr 128
                                                                                                                                        ::: ||||||||||||::: ||||||||| 361 AAAGATGGAAGGTTATTTGGTAATAAGCAAGGATACAAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetMetGlySerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 IleGlyGlyLysGlyPhePheGlnVal-----ThrLeuGluAspLysValHisTyrThr
71 ValargihrilePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAla
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                               APPLICANT: Chan, Voon Loong
APPLICANT: Chan, Voon Loong
APPLICANT: Louie, Halena
TITLE OF INVENTION: BASAL BODY ROD PROTEIN GE
TITLE OF INVENTION: CAMPYLOBACTER
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBURNEY
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-009-823A-1 (1-502) x US-08-483-857-2 (1-810)
                                                                                                                                                                                                    GTATTAAGTAGTGATTATTTTAATAATCCT 450
                                                                                                                                                                                LeuMetGlySerArgIleSerAsnAsnPro 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPE
COMPACE: PATENTIN SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,857
FILING DATE: 07-JUN-1995
CLASSIFFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART MICHAEL I.
                                                                                                                                                                                                                                           RESULT 35
US-08-483-857-2
; Sequence 2, Application US/08483857
; Patent No. 6020125
; GENERAL INFORMATION:
APPLICANT: Chan, Voon Loong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEBRAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 810 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155.00
49.33%
30.67%
5.99%
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STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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368334 AACTCGGGCACCGGCAACGTCGGAAACACCGCGAACCTCGGCATCGCA 368275
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                                                                                                                                                                                                                                                                                                                                                                                           109 ArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThr 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::: ||||||||||:::
361 AAAGATGGAAATTTTCAACTTGATGATGAGGGTTATTTGGTAAATAAGCAAGGATACAAG 420
                                                                                      91 IleGlyGlyLysGlyPhePheGlnVal-----ThrLeuGluAspLysValHisTyrThr 108
61 GTGATTACTAATAATCTTGCCAATATCAATACAAGTGGATATAAAAGAGATGATGTGGTT 120
                                                                                                                                                                                                                                                                                       URBOULD 3-840A-2/C

Sequence 2, Application US/09103840A

Sequence 2, Application US/09103840A

Patent No. 6294328

GRNERAL INFORMATION:

APPLICANT: FRASER, Owen R.

APPLICANT: FRASER, Chair M.

APPLICANT: FRASER, Chair M.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

TITLE OF INVENTION: DNA SEQUENCES

TITLE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SEQ ID NO S: 2.1

SEQ ID NO S. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDC 1551 "n" bases at various positions throughout the sequence represent a, t, c or \ensuremath{\mathbf{g}}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GlySerLeuPheileGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGlyThrVal 22
                                                41 ------phedlnAspLeuPheSerGln-----AspLeuAlaileGlySer--- 53
                                                                                                                                                  54 -----ThrGlySerGlnGlyProAsnGlnAlaGlyMetGly---AlaGlnValGlySer 70
                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                      71 ValargihrilepheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAla
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Mismatches:
Indels:
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Matches:
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ORGANISM: Mycobacterium tuberculosis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at
OTHER INFORMATION: represent a,
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के ह		Oy 306 GlyLeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGlnProLeu 322
કે દેં દ		Qy 323 ThrLeuAspPheGlyIleLysSerGlnGlnAsnWetTrpAlaGlyAlaProAlaSerAla 342
g &	388217 AACICGGGCAGCITCAACACCGGGCAGCAGCAGCACCACACGC 368167 76 ThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeuAlaIleGlyGlyLys 94	Oy 343 AlaalaIleGlyThrAspIleGlyLysLeuProSerMetMetProIleGlnThrSerSer 362 Dh 367194
유 6 6	368166GGCTGTTCAACCCGGGCAACGTCAACACCGGCGTCGGCAACAACGGAAC 368113	363 GlyanSerThrAlaArgAsnGlySerSerThrArgArgArgTyr377
2 A	GCAGCACCAATACCGGCAGCTTC	367152 decearichaecragecardedeaccraeccaecarcraarriceaceaegearcaacarc 36
à à	108	Oy 378SerGlnAspGlyTyrProGlnGlyAspLeuValAspValihr11eThr8erGlu 395 Db 367092 GGCGGTAACAACGAATCGCCAACACCGGGATCTTCGATATCGGCTTGGCGAACCTG 367033
g & .	109 ArgalaGlyAsnPheArgPhe	Oy 396 GlyLysLeuGlnGlyLysTyrSerAsnSerGlnValAspPhe 410
dg ·	367992 AACGCGGGGTGACTACACACGGGTGTGGCCAACGCGCCAACGTCAACACGCGGCGTTC 367933	411TyrkanileProLeualaArgPheThrSerGluAgo
රු දි	11617hrGlnAspGlyPhe	366972 GGCAGC
3 &	125	423GlyLeuArgArgGluGlyAsnAsnHisTyrSer
op Op	367872 CTITCCACAAGGATCACCATTCCGGAAATCCCCTACGCTAGGACTTGAGTGTTCCAATC 367813	366912 GGCAGCTACAACATCGGGTTTCGCGAATACCGGTAACAACAACATCGGCGTCGGGCTCACC 36
λ̈́o	126 GlyPheThrLeuMetGlySerArgIleSerAsnAsnProAsn 139	OY 434
дg	367812 GACATACCCATCACCGGCACCGTCGTCGCCACCACGCCAAACAGTTTCACCATTCCCGGT 367753	446ProGlyThrSerAsnTyrGly 452
& A	140	
ें	Ala	RESULT 38 US-09-206-942-64
: 음	:::	; Sequence 64, Application US/09206942 ; Patter No. 6432669;
<u>ک</u>	- ro 	; GENERAL INCRMATION: ; APPLICANT: Loosmore, Sheena M. ; APPLICANT: Yang, Yan-Ping
요 :	ATGGTTGGCACCGGCTTCGGCCCCGATCCCCATCGGCATCGGTACGGTACCCCG	; APPLICANT: Klein, Michel H. ; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
g G	100 IYIPHANJALBULEUG-LUSETITDLYSGLYABRG-PINTEYOPIOLIESEKIRINESEKABR 20/) TILE OF INVENTY. MOLECULAR WEIGHT PROCESTINS ; FILE REFERENCE: 1018-861 MIS.jb ; CURRENT APPLICATION NUMBER: US/09/206,942
à	TyrSer	; CUREENT FILING DATE: 1998-12-08 ; EARLIER APPLICATION NUMBER: 09/167,568 ; EARLIER FILING DATE: 1998-10-07
g G	367554ACCGGCCCGTCGGGTTTCTTCCACAGGCGGCCGGCCATGTATCGGGC 367504	; NUMBER OF SEQ ID NOS: 95
o o	228 ValtyrPheAspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeuValAla 247 367503 TTCGGGAACTTCGGCGCCGGGAACATGTCGGGGAACTTC36759	64 3543 A
δ	MetasnProSerGluAspGlySerAlaAlaSerGlyThrAspSerAlaGlyLeuLeu 266	; ORGANISM: Haemophilus influenzae US-09-206-942-64
g	367458	Scores:
Š	285	. No.: 1.5/e-U5 3: 149.50 37.09%
අ (cal Similarity: 20.55% Mismatches: atch: 5.78% Indels:
à	286 ThrProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnProAlaProLeuValAsn 305	DB: 4 Gaps: 21

QUENCES RELATING TO PSEUDOMONAS THERAPEUTICS ValAspValThrileThrSe 394 ThrSerAsnTyrGlyLysLe 454 SerargglumetValAsnme 473 ::: ATTCAACCGGGTATAGCAAG 3312 ValaspheTyrasnilePr 414
:::
GCAAACAGCGCCACCTTGGT 3075 |||||||::: GGTAACCATACAGTAGTGAA 3135 3GCAAATTA----- 2905 :::::: GCTAATAACCAGGTAAACCT 2955 31yLysLeuProSerMetMe 356 3lySerSerSerThrArgAr 376 ValThrThrAlaAspThrMe 493 SerGlnGlnAsnMetTrpAl 336 3lyAsnAsnHisTyrSerAl 434 1284 103 57 149 154 18

Oy Op	2 MetGlySerLeuPheIleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGly 20 :::	346
oy B	21 ThrvalSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyr 34	332 297
oy Ob	35 LysglnglnglnValValPheglnAspLeuPheSerGlnAspLeuAlaIleGlySerThr 54 ::: :::	345 238
S d	55 GlySerGlnGlyProAsnGlnAlaGlyMetGlyAlaGlnValGlySerValArgThr11e 74	Qy 365 erTh
È	LeuAla	
q a (GAGGACCAGAGTTGGCGCGCGCTACGAGCCGAACCATCCGCCGCGGGAT	0y 405 er 4
상 옵	91 ILEGIYGIYLY8GIYPhePheGinValThrLeuGluAspLy8ValHisTyrThrArgAla 110 895 895	3 25 88 CC
8	111 GlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSerGlyPheThrLeuMet 130	Search completed: Job time : 4833 se
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දු පු	131 GlySerArgileSerAsnAsnProAgnileLysLysGluThrLeuGluProIleGlnLeu 150 	
ò		
qo	828 AGCCGTCCCTTCCAGACCAACGCGGAAATGATGATGATACCGCCAAACAGATGATGATGAGAAG 769	
yo da	171 ValValAsnLeuGlyAspSerThrAspLysThrGlnSerGluAlaAsnProTyrPheAla 190	
& i	LeuLeuGluSerTrpLysGlyAsnGlyThrProProlleSerThrSerAsnTyrSerTyr	
g n	/1/700	
SS qa	211 AlaGInProMetArgValTyrAspGlnGlyAsnSerHisAspIleThrValTyrPhe 230 699GTC 688	
95 25	231 AspGlyAlaProSerSerThrGlySerLysThrPheGluTyrLeuValAlaMetAsnPro 250	
ò á	251 SerGluAspGlySerAlaAlaSerGlyThrAspSerAlaGly 264	
ł à	LeuLeumetSerGlyThrMetThrPheSerSerAsnGlyGluLeu	
qq	ATCGCCCAACTGGCC	
දු දු	280	
<u>ک</u> ک	287 othrGlySerAlaThrLysAspLeu	
5	DG 1 D Pro 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2	
2 8		
δλ	312 laAsnPheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGlnG 332	-

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arch completed: October 31, 2004, 19:48:46
b time : 4833 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

October 26, 2004, 09:09:07; Search time 132 Seconds (without alignments) 1231.264 Million cell updates/sec

US-10-009-823A-1 2586 1 MMGSLFIGATGMKTHSTGLG......NSKSVTTADTMLQKALELKR 502

Title: Perfect score:

Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

1364641 segs, 323758627 residues Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1, Appli	Sequence 48141, A	Sequence 101, App	Sequence 50763, A	Sequence 4820, Ap	Sequence 7, Appli	Sequence 8, Appli	Seguence 10, Appl	Sequence 9, Appli	Seguence 4818, Ap	Sequence 4763, Ap	Sequence 4764, Ap	Sequence 4765, Ap	
DI	US-10-009-823A-1	US-10-282-122A-48141	US-10-127-032-101	US-10-282-122A-50763	US-10-335-977-4820	US-10-009-823A-7	US-10-009-823A-8	US-10-009-823A-10	US-10-009-823A-9	US-10-335-977-4818	US-10-335-977-4763	US-10-335-977-4764	US-10-335-977-4765	
1	141	72	14	15	15	14	14	14	14	15	15	15	12	
% Query Match Length DB	502	414	462	413	718	477	462	400	401	221	262	271	279	
% Query Match	100.0	20.5	20.4	19.6	18.8	13.7	13.6	13.1	12.9	11.4	11.1	11.1	11.1	
Score	2586	529.5	527.5	506.5	485	355.5	351	337.5	333	296	288	288	288	
Result No.		7	M	4	Ŋ	y	7	ω	o	10	11	12	13	

11,	Sequence 12, Appl	484(4	H	4	ż	Seguence 65, Appl	Sequence 2, Appli	Seguence 63, Appl	Sequence 77944, A	Seguence 4817, Ap	Seguence 4, Appli	Sequence 66335, A	Sequence 4839, Ap	Sequence 4819, Ap	Sequence 4, Appli	Sequence 150, App	Sequence 58893, A	Sequence 49147, A	Sequence 13825, A	Sequence 4779, Ap	Sequence 64364, A	Sequence 61, Appl	Sequence 59, Appl		٠,	٠,	4.	٠.	٠.	_
US-10-009-823A-11	US-10-009-823A-12	US-10-335-977-4840	US-10-335-977-4844	US-10-009-823A-13	US-10-369-493-4713	US-10-369-493-7473	US-10-193-764-65	US-10-092-880-2	US-10-193-76	US-10-282-12	US-10-335-977-4817	US-10-246-33				US-10-147-299A-4	US-09-881-752A-150	US-10-282-122A-58893	US-10-282-122A-49147	US-10-369-493-13825	US-10-335-977-4779	US-10-282-122A-64364	US-10-193-764-61	US-10-193-764-59	S US-10-335-977-4780	US-10-369-493-18460	US-10-316-175-12	US-10-282-122A-47930	US-10-316-175-15	US-10-369-493-5176	US-10-369-493-5177
14	14	15	15	74	14	14	14	13	14	15	15	14	15	15	15	15	σ	15	15	14	15	15	14	14	15	14	14	15	14	14	14
480	360	152	464	370	655	655	1095	1536	1536	3705	91	2468	2468	124	343	1954	1230	1230	3073	679	269	2204	1180	1188	273	1649	486	1331	529	1797	1805
10.9	9.0	7.8	7.3	7.2	7.0	7.0	6.7	6.7	6.7	6.7	6.4	6.4	6.4	6.4	6.3	6.3	6.2	6.2	6.1	5.9	5.9	5.9	5.8	5.8	5.7	5.7	5.7	5.5	5.4	5.4	5.4
282	233	201.5	189.5	186	180.5	180.5	173.5	173.5	173.5	172.5	166	166	166	165.5	164	162	160	160	156.5	153.5	151.5	151.5	149.5	149.5	148.5	147	146.5	143	140.5	139.5	139.5
14	15	16	17	18	19	20	21	22	23	24	. 52	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ORGANISM: Lawsonia intracellularis US-10-009-823A-1

Gaps ö Query Match

100.0%; Score 2586; DB 14; Length 502;
Best Local Similarity, 100.0%; Pred. No. 1.6e-202;
Matches 502; Conservative 0; Mismatches 0; Indels 0;

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Sequence 101, Application US/10127032
Sequence 101, Application US/10127032
Sequence 101, Application No. US20030113742A1
Sequence 101, Application No. US20030113742A1
SEQUENCE INFORMATION:
APPLICANT: Whiteley, Marvin
APPLICANT: Greathery, Stephen
APPLICANT: Greathery, ENFERT BIFFILM FORMATION
TITLE OF INVENTION: BIFFILM FORMATION
TITLE OF INVENTION: BIFFILM FORMATION
FILE REFERENCE: UIZ-070CP
CURRENT APPLICATION NUMBER: US/10/127,032
CURRENT FILING DATE: 2002-04-19
FRICK APPLICATION NUMBER: US 60/285,190
FRICK FILING DATE: 2001-04-20
FRICK FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 101
LENGTH: 462
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Matches 149; Conservative
                                                                                                                                                                                                                                                        Similarity
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APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Vanamoto, Robert
APPLICANT: You, H.
TITLE OF INVANION: Identification of Essential Genes in Microorganisms
TITLE OF INVANION: Identification of Essential Genes in Microorganisms
TITLE OF INVANION: Identification of Essential Genes in Microorganisms
TITLE OF INVANION: Identification of Essential Genes in Microorganisms
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/203,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PRIOR DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/233,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLING DATE: 2001-02-09
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QAGMGAQVGSVRIIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGF 120
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                                                                                         LNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDK 180
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Sequence 48141, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: AZMUNIO, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, Sobert
APPLICANT: Prasylok, Robert
APPLICANT: Porsylh, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 -;-----WLAYAGVÇĞTPTNLGTVTFDASGRISSTTS-AATG------QPTP--- 250
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PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 48141
LENGTH: 414
                                                                                                                                                                                                                                                      DB 15; Length 414;
                                                                                                                                                                                                                                                      20.5%; Score 529.5; DB 15;
29.8%; Pred. No. 1.4e-34;
tive 72; Mismatches 182;
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US-10-282-122A-50763
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US-10-335-977-4820
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APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Raselbeck, Rabert
APPLICANT: Haselbeck, Rabert
APPLICANT: APPLICANT: Dailel
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, Schort
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yu, H.
APPLICANT: Yu, H.
APPLICANT: Yu, H.
APPLICANT: Soloy, R.
APPLICANT: APPLICATION NUMBER: 05/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-28
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                                                                                                                                   169 PTVTPF------DPSDAATYNSSSSLGIYDSQGNSHTWSQFFIKNEPDPNATPP 216
                                                                                                                                                                                                                                                                                                                                                                                                    ---GSKITEFYLV-AMNPSEDGSAASGIDSAGLLMSGIMIFSSNGELKNMIAFIPIGS--- 290
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                                                                                                                  4 SLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAG
                                                                                                                               64 MGAQVGSVRIIFTQGAFEPGNSVIDLAIGGKGFFQVTLEDKVHYTRAGNFRFIQDGFLND
                                                                                Gaps
                                                                                93;
                                              Length 462;
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                                           , Score 527.5; DB 14; Length
, Pred. No. 2.4e-34;
84; Mismatches 199; Indels
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ORGANISM: Pseudomonas aeruginosa
                                             20.4%;
Best Local Similarity 28.5%;
Matches 150; Conservative 84
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               US-10-127-032-101
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PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-03
PRIOR PELING DATE: 2000-110-23
PRIOR FILING DATE: 2000-112-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PELING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-03-04
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NOS: 76614
SOFTWARE: PALENTIN Version 3.1
LENGTH: 413
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Best Local Similarity 27.2%; Pred. No. 1e-32;
Matches 137; Conservative 81; Mismatches 180; Indels 105;
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGFOMNSKSVTTADIMLOKALEL 500
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	440 GPEFGLPGTSNYGKLSVNQLETSNYDMSREMVMIIIQRGFQMNSKSVTTADTWLQKALE 49 450 GPEFGLPGTSNYGKLSVNQLETSNYDMSREMVMIIIQRGFQMNSKSVTTADTWLQKALE 49 500 LKR 502 500 LKR 502 116 LKQ 718	US-10-009-823A-7 Sequence 7, Application US/10009823A Publication No. US20030157120A1 Sequence 7, Application No. US20030157120A1 APPLICANT: Panaccio, Michael APPLICANT: Sinistaj, Merit APPLICANT: Sinistaj, Merit APPLICANT: Barson, Jim APPLICANT: Ankenbauer, Robert G. TITE OF INVENTION: LAWSONIA DERIVED GENE AND PROTEINS AND THEIR USES FILE REFERENCE: DAVI150.001APC CURRENT APPLICATION NUMBER: US/10/009,823A	CURKENT FILING DATE: 2002-08-13 PRIOR FILING DATE: 2000-05-11 PRIOR FILING DATE: 2000-05-13 PRIOR FILING DATE: 1999-05-13 NUMBER OF SEQ ID NOS: 13 OF Windows Version 4.0 SEQ ID NO 7 LENGTH: 477 TYPE: PRIOR Treponema phagedenis US-10-009-823A-7	Query Match 13.7%; Score 355.5; DB 14; Length 477; Best Local Similarity 23.7%; Pred. No. 2.8e-20; Matches 142; Conservative 68; Mismatches 171; Indels 217; Gaps 21; QY I MMGSLFIGATGMXTH	TIGYKQQQ
CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street CITY: Boston STRYE: Nassachusetts COUNTRY: USA ZIP: 02109-1875 COMPUTER READABLE FORM: MEDIUM TYPE: CD/ROM ISO9660 COMPUTER: IBM PC Compatible CORPUTER: UNIX CURRENTING SYSTEM: Windows NT 4.0 SOFTWARE: UNIX APPLICATION DATA: MADDICATION NUMBER: US/10/335,977	FILING DATE: 30-Dec-2002 PRIOR APPLICATION NUMBER: 08/93,002 PRIOR APPLICATION NUMBER: 08/93,002 FILING DATE: 17-DEC-1997 ATTORNEY/AGENT INFORMATION: MAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207 REFERENCE/DOCKET NUMBER: GTN-018 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 742-4214	INFORMATION FOR SEQ ID NO: 4820: SEQUENCE CHARACTERISTICS: LENGTH: 718 amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: protein HYPOTHETICAL: YES ORGANISM: Helicobacter pylori FRATURE: NAME/CES: LOCATION: (B) LÖCATION 1718 SEQUENCE DESCRIPTION: SEQ ID NO: 4820: US-10-335-977-4820	Query Match	QY 113 FRFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAK 163	Qy 216 VYDQQGNSHDITVYFDGA

206AKATIDVAYTWAIDFNVYDTFGEQHKLQMVFSRVPGTNNQWLAI 249	
NGELKUMT	245 LVAMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKNWTAFTPTGSATKDLNAW
Db 250 VVTDTAGNVTAPNVDPENQAGTETRVGIGTTDGAGQVLVQATENTFIVSFDNYGHLAS 307	EAA
CY 284 AFTFTGSATKDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAP 339 Db 308SYNVVGANPDEGGAPTRHTFNINDQSGIITGVY 340	QY 299 QPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNWAGAPASAAIG 346
OY 340 ASAAAIGTDIGKLPSMMPIQTSSGNSTARNGSSSTRRYSODGYPQ 384 :	Qy 347pdigklesmpiqtssgnstarngssstrrygdgvpgdlvdvtitseg 396
OY 385 GDLVDVTITSECKLQGKYSNSQVVDFYNIPLARFTSEDGLRREGNNHYSATLDSGGPEFG 444	QY 397 KLQGKYSNSQVVDFYNIPLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSV 456 :
445 LPGTSNYGKLSVNQLETSNYDMSREMVNMIIIQRGFQMNSKSVTTA :	Qy 457 NQLETSNYDMSREMVNMIIIQRGFQMNSKSVTTADTMLQKALELKR 502
RESULT 7 US-10-009-823A-8 US-10-009-823A-8 Sequence 8, Application US/10009823A Publication No. US20030157120A1 GENERAL INPORMATION: APPLICANT: Panaccio, Michael APPLICANT: Rosey, Everett Lee APPLICANT: Rosey, Detlef APPLICANT: Paraccio, Meri APPLICANT: Paraccio, Meri APPLICANT: Hasse, Detlef APPLICANT: Ankenbauer, Jam APPLICANT: Ankenbauer, Jam APPLICANT: Ankenbauer, Jam APPLICANT: Ankenbauer, Uscobert G. TITLE OF INVENTION: LAWSONIA DERIVED GENE AND PROTEINS AND THEIR USES TITLE OF INVENTION: POLYPEPTIDES, PEPTIDES AND PROTEINS AND THEIR USES TITLE OF INVENTION: POLYPEPTIDES, PEPTIDES AND PROTEINS AND THEIR USES TITLE OF INVENTION NUMBER: POLYO00/00437 PRIOR PELICATION NUMBER: POLYO00/00437 PRIOR PELICATION NUMBER: POLYO00/00437 PRIOR PELICATION NUMBER: POLYO00/00437 PRIOR APPLICATION NUMBER: POLYO00/00437 PRIOR APPLICATION NUMBER: POLYO00/00437 PRIOR APPLICATION NUMBER: POLYO00/00437 PRIOR PELING DATE: 1999-05-13 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 8 LENGTH: 462 TYPE: PRI ORGANISM: Treponema pallidum US-10-009-823A-8	RESULT 8 US-10-009-823A-10 US-10-009-823A-10 Sequence 10, Application US/10009823A Publication No. US20030157120A1 SEQUENCE 10, Application US/10009823A Publication No. US20030157120A1 APPLICANT: Paraccio, Michael APPLICANT: Ansery Everett Lee APPLICANT: Ansery Dellef APPLICANT: Anserbauer, Nobert G. TITLE OF INVENTION: LAWSONIA DERIVED GENE AND RELATED FLGE TITLE OF INVENTION: LAWSONIA DERIVED GENE AND PROTEINS AND THEIR USES TITLE OF INVENTION: POLYPEPTIDES, PEPTIDES AND PROTEINS AND THEIR USES TITLE OF INVENTION: DAVISO.001APC CURRENT APPLICATION NUMBER: US/10/009, 823A CURRENT APPLICATION NUMBER: PCI/AU00/00437 PRIOR FILING DATE: 2000-05-11 PRIOR FILING DATE: 1999-05-13 NUMBER OF SEQ ID NOS: 13 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 400 LENGTH: AUGUST AND AUGUST AUGU
Query Match Best Local Similarity 23.0%; Pred. No. 6.2e-20; Matches 135; Conservative 67; Mismatches 176; Indels 208; Gaps 17;	COMPANIA (1)(400) COTHER INFORMATION: Xaa = Any Amino Acid US-10-009-823A-10
QY 1 MMGSLFIGATGMKTHSTGLGTVSNNIANANIJGYKQQQVVFQDLF 45	Query Match 13.1%; Score 337.5; DB 14; Length 400; Best Local Similarity 25.1%; Pred. No. 6.4e-19; Matches 128; Conservative 69; Mismatches 165; Indels 147; Gaps 21;
Qy 46 SQDLAIGSTGSQGPNQAGMGAQVGSVRTIFTQGAFEBGNSVTDLAI 91	OY 11 GMKTHSTGLGTVSNNIANANTIGYKQQQVVPQDLFSQDLAIGSTGSGGPNQAGMGAQVGS 70
Qy 92GGKGFFQVTLEDKVHYTRAGNFRFTQDGFLNDFSGFT 128 : : : : : Db 89 ARPNEEVGQGSGFFVLKSGEKTFFTRAGAFGVDNAGTLVNPANGACNLDKRLMRVQGWMA 148	QY 71 VRTIFTQGAFEPGNSVTDLAIGGKGFFQ-VTLEDKVHYTRAGNFRFTQDGFLN 122
QY 129IMGSRISNNPNIKKETLEP-IQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSE 184 149 QDDVAGERLINSSAQPELAADANEADVRKSTQDLVIPIGQKIDAQQT- 195	OY 123DPSGFTLMGSRISNNPNIKKETLEPIQLDFNDFTVAKSPAKTSTALNAVVNL 174
QY 185 ANPYFALLESWKGNGTPPISTSNYSYAQPMKVYDQQGNSHDITVYFDGAPSSTGSKTFEY 244	QY 175 GDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAP 234

203 297 251 357 254 413 445	REGULT 10 REGULT 10 REGULT 10 REGULT 10 REGULT 10 RELATING TO HISTORY OF SEQUENCES PUBLICORATE PULCAL FOR THE ADDRESS SHIP et al. TILE OF INVENTION: NULLEC CATD AND ANINO ACID SEQUENCES RELATING TO HISTORY TO HISTORY PULCAL FOR A THERAPEUTICS NUMBER OF SEQUENCES: 1003 CORRESSED THE SESSED THAT THE SEGUENCES TO AND THERAPEUTICS COUNTYER TO SECUENCES TO AND THERAPEUTICS COUNTYER TO SECUENCES TO AND THERAPEUTICS COUNTYER TO SECUENCES TO AND THERAPEUTICS COUNTYER TO SECUENCES TO AND THERAPEUTICS COUNTYER TO SECUENCES TO AND THE ADDRESS TO AND THE	Os-10-355-9//-4818 Query Match Best Local Similarity 33.2%; Pred. No. 6.6e-16; Matches 78; Conservative 37; Mismatches 98; Indels 22; Gaps 3;
	131	OY 187 PYFALLESWKNGTPP1STSYSYSYAQNENHULYYFDGAFSS 236 DD 156 SYNKPAPITIPNTLMAAKSTTTASMKGTVTVXDSQGNAHDMNVYFVK 202 CY 237 TGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATKDLN 296

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414 PLARFISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNYDMSREMVNM 473
                                                                                                                                                        114 RFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVN 173
                                                                                                                                                                                        121 KLDEQGNLVTSEGYLLI------PQI---TL-------PEDTTQ-----VN 150
                                                                                                                                                                                                                                          174 LGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGA 233
                                                                                                                                                                                                                                                                                      ----VDGT 156
                                                                                                                                                                                                                                                                                                                                   234 PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKNWTAFTPTGSATK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 SMMPIQISSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNI 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 DINAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP 353
61 -----QAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLED-KVHYTRAGNF
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS INTER et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
COPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 ITAQRAYEANSKSIQTADAMLQTVNSLKR 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 IIIORGFOMNSKSVTTADTMLOKALELKR 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DCCKET NUMBER: GTN-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 10031
CORRESPONDENCE PUDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 17-DEC-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
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SEQUENCE CHARACTERISTICS
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151 IG-----
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US-10-335-977-4764
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                                                                                                                  332 ONMWAGAPASAAAIGTDIGKLPSMMPIQTSSGNS----TARNGSSSTRRYSQDGYPQGDL 387
                                                                                                                                                            -----GADA------PORINLAFGSSGSFDGLTSVDKISETYAIEQNGYQAGDL
                                                                                                                                                                                                      388 VDVTIISEGKLQGKYSNSQVVDFYNIPLARFISEDGLRREGNNHYSATLDSGGPEFGLPG 447
                                                                      5 SYRSEGAEWNFRVIVPEPGELVGGSAARPNVFEGGRLHFNNDGSLAGMNPPLLQFDPKN- 63
                                                                                                                                                                                                                                                                                             TSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMNSKSVTTADTMLQKALELKR 502
                                                                                                                                                                                                                                                                                                                       167 TGRRGSISGSKLESSNVDLSRSLTNLIVVQRGFQANSKAVTTSDQILNTLLNLKQ 221
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                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-10-335-977-4763
i Sequence 4763, Application US/10335977
; Sequence 4763, Application US/2004005279941
; Publication No. US2004005279941
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES
; TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES
; DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/ACBNT INFORMATION:
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ), NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...262; SEQUENCE DESCRIPTION: SEQ ID NO: 4763: US-10-335-977-4763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617)227-7400
TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 4763:
SEQUENCE CHARACTERISTICS:
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: YEORIGINAL SOURCE:
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1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPN 60

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138 KLDEQGNLVTSEGYLLI ------PQI---TL-------PEDITQ----VN 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 RFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 TLANEVNPAGLHSWGDNLFSITNASGDAIVGNPDSQGLGKLRQGFLELSNVRLVEEMTDL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 PLARFISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNOLETSNVDMSREMVNM 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 -----QAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLED-KVHYTRAGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 DLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 SMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 MLRSLYSATSGMLAQQTHIDTTSNNIANVNTTGFKKSRADFNDLFYQAMQYAGTNTSNTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.1%; Score 288; DB 15; Length 279; Best Local Similarity 21.0%; Pred. No. 4.2e-15; Matches 107; Conservative 39; Mismatches 109; Indels 254; Gaps
                                     SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAWE/KEY: misc_feature

COCATION: (B) LOCATION 1...279

SEQUENCE DESCRIPTION: SEQ ID NO: 4765:
U8-10-335-977-4765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIIORGFOMNSKSVTTADIMLOKALELKR 502
COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                       NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 279 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                     TELEFAX: (617)742-421.
INFORMATION FOR SEQ ID NO: 4765.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PEDTTQ-----VN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .-----VDGT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 DLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 PLARFISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNM 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 TLANFVNPAGLHSMGDNLFSITNASGDAIVGNPDSQGLGKTRQGFLELSNVRLVBEMTDL 242
                                                                                                                                                                                                                                                                                                                                                                                               69
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ----QAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLED-KVHYTRAGNF
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                                                                                                                                                                                                                                                                  Query Match 11.1%; Score 288; DB 15; Length 271;
Best Local Similarity 21.0%; Pred. No. 4e-15;
Matches 107; Conservative 39; Mismatches 109; Indels 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-10-335-977-4765
US-10-335-977-4765
Sequence 4.765, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: PORALICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 KLDEQGNLVTSEGYLLI-----PQI---TL----
                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...271
SEQUENCE DESCRIPTION: SEQ ID NO: 4764:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474 IIIORGFOMNSKSVTTADTMLOKALELKR 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Helicobacter pylori
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
  LENGTH: 271 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCI
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: Massachusetts
                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 -----
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                                                     APPLICANT: Panaccio, Michael
APPLICANT: Rosey, Everett Lee
APPLICANT: Rosey, Everett Lee
APPLICANT: Rosey, Everett Lee
APPLICANT: Asinistaj, Meri
APPLICANT: Hasse, Detlef
APPLICANT: Ankenbauer, Robert G.
APPLICANT: Ankenbauer, Robert G.
TITLE OF INVENTION: LAWSONIA DERIVED GENE AND PROTEINS AND THEIR USES
FILE REFERENCE: DAVISO. OLAPPC
CURRENT APPLICATION NUMBER: US/10/009,823A
CURRENT PILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US 60/133,973
PRIOR APPLICATION NUMBER: US 60/133,973
PRIOR PILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
SOFTWARE: Fastesey for Windows Version 4.0
SEQ ID NOS: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 -DIGKLPSMMPIQTSSGNST-----ARNGSSSTR-RYSQDG----YPQGDLVDV-- 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANPYFALLESWKGN----- 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --PINLDERAPILYVQGFKVNPVTGEVT--GTQIDQTTTPFNP----LDSFTYNYLEDIR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATKDLNAWQPAPLVNGLPQFSAN--FVGAGIQPLTLDFGIKSQQNMWAGAPASAAIGT- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TQKVWTIGSFKQTEITTDLAIPIFQDMVSQVVVG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MMGSLFIGATGM-----KTHSTGLGTV-----SINIANANTIGYKQQQVVFQDL 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.9%; Score 282; DB 14; Length 480; 22.9%; Pred. No. 2.9e-14; tive 73; Mismatches 160; Indels 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 TITSEGKLQGKYSNSQVVDFYNIPLARFISEDGLRREGNNHYSATLDSGG
Sequence 11, Application US/10009823A Publication No. US20030157120A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 22.9
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-009-823A-1
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RESULT

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APPLICANT: Sinistaj, Meri
APPLICANT: Sinistaj, Meri
APPLICANT: Hasse, Detlef
APPLICANT: Hasse, Detlef
APPLICANT: Hasse, Detlef
TITLE OF INVENTION: LAWSONIA DERIVED GENE AND RELATED FLGE
TITLE OF INVENTION: DOLVEPTIDES, PEPTIDES AND PROTEINS AND THEIR USES
TITLE OF INVENTION: DOLVEPTIDES, PEPTIDES AND PROTEINS AND THEIR USES
FILE REFERENCE: DOAY 150.001APC
CURRENT APPLICATION NUMBER: US/10/009,823A
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US 60/133,973
PRIOR PLLING DATE: 2000-05-11
PRIOR PLLING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 DLVDVTITSECKLQCKYSNSQVVDFYNIPLARFISEDGLRREGNNHYSATLDSGCPEFGL 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- WTOSFSSCAPIMGV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 SHTVTQYFTKTADNAWEVNVPTGSFNQVDGGKT--PVVSTIPVTFNKDGTLAAAFPAAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : |: :| |: || : || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 GWKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHDITVYF ---- DGA----- PSST-----GSKTFFYLVAMNP---SEDGSAASGTDSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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9.0%; Score 233; DB 14; I
Best Local Similarity 22.0%; Pred. No. 1.9e-10;
Matches 110; Conservative 59; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 GVEVASTELNTISHHIANASTYGFK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 360
; TYPE: PRT
TYPE: PRT
ORGANISM: Vibrio parahaemoliticus
US-10-009-823A-12
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61 QAGMGAQVGSVRTIFTQ-GAFEPGNSVTDLAIGGKGFFQV-------TLEDK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 NFLTRAGNFARDADGYLVTPEGYYVYGIDLKKIKDGTINSTARDEDIEKLHGNTLSPLQ1 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 VHYTRAGNFRFTQDGFLNDPSGFTLMG------SRISNNPNIKK---ETLEPIQL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPN 60
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US-10-009-823A-13
Sequence 13, Application US/10009823A
Sequence 13, Application No. US20030157120A1
SENERAL INFORMATION:
APPLICANT: Panaccio, Michael
APPLICANT: Sinistaj Meri
APPLICANT: Bassey, Betlef
APPLICANT: Parsons Jim
APPLICANT: Parsons Jim
APPLICANT: ARRENDAUER, ROBERT G.
TITLE OF INVENTION: POLYPEPTIDES, PEPTIDES AND PROTEINS AND THEIR USES
TITLE OF INVENTION: POLYPEPTIDES, PEPTIDES AND PROTEINS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.3%; Score 189.5; DB 1
Best Local Similarity 28.9%; Pred. No. 9.9e-07;
Matches 59; Conservative 29; Mismatches 81
                                                                                                                                                                                                                                           SOFTWARE: UNIX
CURRENT APPLICATION UNBER: US/10/335,977
APPLICATION NUMBER: US/10/335,977
PILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...464
SEQUENCE DESCRIPTION: SEQ ID NO: 4844:
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM 1809660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTOREY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 DFNDPTVAKSPAKTSTALNAVVNL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 464 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 4844:
SEQUENCE CHARACTERISTICS:
                                                                          STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59; Conservative
                                                                                                    COUNTRY: USA
ZIP: 02109-1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 SQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFISEDGLRREGNNHY---SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15; Length 152;
  APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4844, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
ODERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
PRIOR APPLICATION NUMBER: 08/993,002
PILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
7.8%; Score 201.5; DB
Best Local Similarity 34.6%; Pred. No. 2e-08;
Matches 47; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...152
SEQUENCE DESCRIPTION: SEQ ID NO: 4840:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAWE: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REPERENCE/DOCKET NUMBER: GTN-018
TELECOWGUNICATION INFORMATION:
TELEFAK: (617)227-400
TELEFAK: (617)742-4214
                                                                                                    NUMBER OF SEQUENCES: 10031
CORRESPONDENCE PUBRESS:
ADDRESSEE: LAHIVUE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECTLE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 152 amino acids TYPE: amino acid
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         487 VITADIMLQKALELKR 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-335-977-4840
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Sequence 7473, Application US/10369493

publication No. US2003023367SA1

general invervation

GENERAL INPORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Alater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

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APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: ALING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 7473

LENGTH: 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 TGDTSELSVOYLG-----QAGANPAATPONLPDSKIDGGTLGGLLAFRSQTLDPGEAQL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 GLLM--SGTWTFSSNGELKNWT---AFTPTGSATKDLNAWQPAPLVNGLPQFSANFVGAG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 IQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSNMPI-----QTSSGNSTARNGS-- 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460 AGYIMPINSTITLSYDGTGLSGFPAGSTVTVAGTPPTTYTIASAATVVPYSSATGATLTIN 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATQPITGDYTLAYNGTTYTLTDNSTGTVVGSAT---NLSQP---INGL----NFSTTG
                                                                                                                                                                                                                  178;
                                                                                                                                      DB 14; Length 655;
                                                                                                                             Query Match 7.0%; Score 180.5; DB 14; Length Best Local Similarity 22.4%; Pred. No. 8.9e-06; Matches 138; Conservative 75; Mismatches 225; Indels
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        ORGANISM: Burkholderia fungorum
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; Sequence 4713, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Chor, Yongwei
; APPLICANT: Blater, Steven C.
; APPLICANT: Glann, Barry S.
; APPLICANT: Chor, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10 (52052) B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR APPLICATION NUMBER: US 60/360,039
; RIGH OF SECTION OF AT374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             th 7.2%; Score 186; DB 14; Length 370; Similarity 21.9%; Pred. No. 1.4e-06; 98; Conservative 57; Mismatches 143; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 SQDLAIGSTGSQGPNQAGMGAQVGSVRTIFTQGAFEPGNSVTDLAI----
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CURRENT APPLICATION NUMBER: US/10/009,823A
CURRENT FILING DATE: 2002-08-13
FRIOR APPLICATION NUMBER: PCT/AU00/00437
FRIOR FILING DATE: 2000-05-11
FRIOR FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
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ORGANISM: Borrelia burgdorferi
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LENGTH: 655
TYPE: PRT
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Best Local S
Matches 98
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                                                                                                                                                                                                                                                                                                                                                            EANPYFALLESWKGNGT-----PPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSSTG 238
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Publication No. US20020164354A1
GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS OF NON-TYPEABLE
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 MKTHSTGLGTVSNNIANAN-TIGYKOOOVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVGS 70
                                                                                                                                             DLTIGNINSADGINAKKVIFNOVKDSKISADG-HKVILHSKVE--ISGSNNNIEDSSDNN
                                                                                                                 12 MKTHSTGLGTVSNNIANAN-TIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 MPIQTSSGNSTARNGSSSTRRYSQDGYPQGDL--VDVTITSEGKL---QGK-----
                                    6.7%; Score 173.5; DB 14; Length 1095; 22.8%; Pred. No. 7.1e-05; ive 80; Mismatches 222; Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13; Length 1536;
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6.7%; Score 173.5; DB 13;
Best Local Similarity 22.8%; Pred. No. 0.00012;
Matches 119; Conservative 80; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/092,880
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 09/155,614
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 08/617,697
PRIOR FILING DATE: 1996-04-01
PRIOR PILING DATE: 1996-04-01
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                                  Query Match
Best Local Similarity 22.8%
Matches 119; Conservative
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SEQ ID NO 2
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US-10-193-764-65
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US-10-092-880-2
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; ORGANISM: Ha
US-10-092-880-2
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                                                                                                                                                                                                                                                                                                      DKVHYTRAGNFRFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPA 162
                                                                                                                                                                                                                                                                                                                                                                                                                            247 TGDTSELSVQYLG-----QAGANPAATPQNLPDSKIDGGTLGGLLAFRSQTLDPGEAQL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATOPTTGDYTLAYNGTTYTLTDNSTGTVVGSAT---NLSOP---INGL-----NFSTTG 403
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                                                                                                                                                                   1 MMGSLFIG-ATGMKTHSTGLGTVSNN---IANANTIGYKQQQVVFQ-----DLFSQD
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APPLICANT: Xang, Xan-Fing
APPLICANT: Xlein, Michel H.
TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
TITLE OF INVENTION: MOLECTIAR WEIGHT PROTEINS
FILE REFERENCE: 1038-1239MIS
CURRENT APPLICATION NUMBER: US/10/193,764
CURRENT FILING DATE: 2002-07-12
PRIOR FILING DATE: 1998-10-07
                                                                                                       Gaps
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                                                                                                    178;
                                                            DB 14; Length 655;
                                                          7.0%; Score 180.5; DB 14; Length 22.4%; Pred. No. 8.9e-06; tive .75; Mismatches 225; Indels
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Burkholderia cepacia
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                                                            Query Match 7.0%
Best Local Similarity 22.4%
Matches 138; Conservative
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SOFTWARE: PatentIn Ver. 3
SEQ ID NO 65
LENGTH: 1095
  , ORGANISM: Burk
US-10-369-493-7473
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APPLICAMT: Xu, H.

TITLE OF INVENITON: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PLILORION NUMBER: 60/191,078
PRIOR PLILORION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PLILNG DATE: 2000-05-26
PRIOR PLILNG DATE: 2000-05-66
PRIOR PLILNG DATE: 2000-05-66
PRIOR PLILNG DATE: 2000-05-69
PRIOR PLILNG DATE: 2000-05-69
PRIOR PLILNG DATE: 2000-01-23
PRIOR PLILNG DATE: 2000-10-23
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PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2003-04
PRIOR PLING DATE: 2003-04
PRIOR PLING DATE: 2003-04
PRIOR P
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1117 -AGLTIDAKNVTVANNITSHKAVSI-----SATSGEITTKTGTTINATTGNVEITAQTGS 1170
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Xang, Yan-Ping
APPLICANT: Xang, Yan-Ping
APPLICANT: Xiein, Michel H.
TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
FILE REFERENCE: 1028-1239MIS
CURRENT APPLICATION NUMBER: US/10/193,764
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: 09/167,568
PRIOR FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 63
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US-10-193-764-63
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400 GKYSNSQVVDFYNIPLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQL 459
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APPLICANT: Wah, Thien-Fah
TITLE OF INVENTION: BIOFILM-SPECIFIC ANTIBIOTIC RESISTANCE;
FILE REPERENCE: 14537-002001
CURRENT APPLICATION NUMBER: US/10/246,330
CURRENT APPLICATION NUMBER: US 60/323,241
PRICR APPLICATION NUMBER: US 60/323,241
PRICR APPLICATION NUMBER: US 60/323,241
PRICR APPLICATION NUMBER: US 60/323,241
SPICR PILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 6.4%; Score 166; DB 15; Best Local Similarity 38.4%; Pred. No. 7.6e-06; Matches 33; Conservative 20; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             )

NAME/KEY: misc_feature
)

SEQUENCE DESCRIPTION: SEQ ID NO: 4817:
US-10-335-977-4817
                                        APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 ETSNVDMSREMVNMIIIQRGFQMNSK 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Helicobacter pylori
                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
  FILING DATE: 30-Dec-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                    E: (617)227-7400 (617)742-4214
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                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4817:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          LENGTH: 91 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 YSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPL----ARFT---SEDGLRREG
                                                                                      Query Match 6.7%; Score 172.5; DB 15; Length 3705; Best Local Similarity 21.7%; Pred. No. 0.00051; Matches 119; Conservative 58; Mismatches 180; Indels 191; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 25
US-10-335-977-4817
US-10-335-977-4817
Sequence 4817, Application US/10335977
Sublication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES
HITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 AFTPTGSATKDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLD
                                                                                                                                                                                                         2404 GNGGELTSTDTLINTGMINVTDGILNLENGGASSISGGL
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APPLICATION NUMBER: US/10/335,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 10031
CORRESPONDENCE PUBBESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
TYPE: PRT
ORGANISM: Yersinia pestis
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                                                                                      Query Match
Best Local Similarity
                                           US-10-282-122A-77944
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1718 GTABAGATVILTDGNGNPIGO-----VTADG--SGNWSFTPGTPLSNGTVVNAVAQDA-- 1718
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                                                                                                                                                                                                                                                                 1298 GTVVNAVA--------ODPA-GNTGPOGSTTVDAVAPNTPVVNPSNGNL 1337
                                                                                                                                                                                                                                                                                                                                                  | : : | || : : : | | | 144 TADGSGNWSFTPGIPLPDGTVVNVVARSPSNVDSAPAVITVDGVAPAAP-----VI 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 RNGSSSTRRYSQD--GYPQGDLVDVIITSEGKLQGKYSNSQVVDFYNIPLARFISEDGLR 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 LESWKGNG--TPPISTSNYSYAQPMRVYDQQGNSHDITVYFDG-APSSTGSKTFEYLVAM 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SGTMTFS----SNGELKNMTAFT 286
                                                                                                                                                                                                                                                                                                                                                                                                                  132 SRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANPYFAL 191
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                                                                                                                                                                                                                                                                                                                    72 RIIFIQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGFLNDPSGFTLMG
                                                                                                                                                                                                                         20 GTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQG------PNQAGMGAQVGSV
                                                                                                                           Query Match
6.4%; Score 166; DB 15; Length 2468;
Best Local Similarity 21.9%; Pred. No. 0.00095;
Matches 112; Conservative 67; Mismatches 197; Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1719 -AGNTSGPVSTTVDAVAPATPVIDPSNGVELS 1749
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APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0 SOFTWARE: UNIX
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 NPSEDGSAASGTDSAGLLM-----
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Publication No. US20040052799A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 IKSQQNWWAGAPASAAAIGTDIGKL-
                    LENGTH: 2468
; TYPE: PR: Pr
; CYPE: PR: Pr
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66335
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COUNTRY: USA
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SEQ ID NO 66335
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  SRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANPYFAL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                      1444 TADGSGNWSFTPGIPLPDGTVVNVVARSPSNVDSAPAVITVDGVAPAAP-----VI
                                                                                             192 LESWKGNG--TPPISTSNYSYAQPMRVYDQQGNSHDITVYFDG-APSSTGSKTFEYLVAM
                                                                                                                                                                                           NPSEDGSAASGTDSAGLLM-----SGTMTFS----SGTMTFS
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SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -AGNTSGPVSTTVDAVAPATPVIDPSNGVELS 1749
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CUCKENT PILING DATE:

PRIOR PEPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR PELING DATE: 2000-03-21

PRIOR PELING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

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PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                      328 IKSQQNMWAGAPASAAAIGTDIGKL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto, Robert
Forsyth, R.
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86 VTDLAIGGKGFFQVTLEDKV--HYTRAGNFRF---TQDGFLNDPSGFTLM-----GSRI 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 SSAKTPSDGINPVYDSGTNLAHVPENMGSLYNEDGDALLLIENHGIWVSYKSAKAVKDIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 PSAENSTLELMGVKISFTNDSAVSRTSSLVAAKNAINAVKSOTGIEAYLDGKOLRLENTN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---STGSKTFEYLVAMNPSEDGSAASG----TDSAGLLMSGTM 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 IGYKQQQVVFQDLFSQDLAIGS----TGSQGPN--QAGMGAQVGSVRTIFTQGAFEPGNS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LGFKYSRASFVDMLSQVKLIATDPYKNGLAGONDFSVGLGVGVDATTKIFSQGNIQNTDV 62
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APPLICANT: RO, ALBERT I.
APPLICANT: RO, ALBERT I.
APPLICANT: REIS, MITERAAYER GALVAO
APPLICANT: REIS, MITERAAYER GALVAO
APPLICANT: REIS, MITERAAYER GALVAO
APPLICANT: RIGH, JULIO HERRIQUE ROSA
APPLICANT: SIQUEIRA, ISADORA CRISTINA
APPLICANT: RILEY, LEE W.
APPLICANT: RILEY, LEE W.
TITLE OF INVENTION: DOMAINS WITH REPETITIVE BACTERIAL-IG-LIKE (BIG)
TITLE OF INVENTION: DOMAINS PRESENT IN LEPTOSPIRA SPECIES
TITLE OF INVENTION: DOMAINS PRESENT IN LEPTOSPIRA SPECIES
CURRENT APPLICATION NUMBER: US/10/147,299A
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NOS: 33
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 ESWK--GNGTPPISTSNYSYAQPWR----VYDQQGN-----SHDITVYFDGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.3%; Score 164; DB 15; Length 3
Best Local Similarity 24.5%; Pred. No. 7.7e-05;
Matches 82; Conservative 52; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 ELDGDEKLKNIVVTQAGTGAFANFLDGDKDVTAFK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 TFSSNGELKNMT-----AFTPTGSATKDLNAWQ 299
                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...343
SEQUENCE DESCRIPTION: SEQ ID NO: 4819:
                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10147299A Publication No. US20040058323A1 GENERAL INFORMATION:
                                                                                                                             LENGTH: 343 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                  TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 4819:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Leptospira kirschneri
                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                     FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            443 FGL--PGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMNSKSVTTADTMLQKALEL 500
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
6.4%; Score 165.5; DB 1
Best Local Similarity 32.0%; Pred. No. 1.3e-05;
Matches 39; Conservative 24; Mismatches 48
                   FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36, 207
REFERENCE/DOCKET NUMBER: 36, 207
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 722-7400
TELEPHONE: (617) 742-4214
INFORMATION FOR SEQ ID NO: 4839:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISOS660

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Windows NT 4.0

SOFTWARE: UNIX

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/335,977

FILING DATE: 30-Dec-2002

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature;
;
; LOCATION: (B) LOCATION 1...124
;
US-10-335-977-4839
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
APPLICATION NUMBER: 08/993,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

**RAPLICATION WINBER: 08/993,002 FILING DATE: 17-D5C-1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4819, Application US/10335977 Publication No. US20040052799A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:
123 KK 124
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US-10-335-977-4819
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852 AQKI--ANIIASSGNNKGVENGLKQFFEALKONSSSLSNLCGNGSSGSSGTTCSGWLINL 909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 DINAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP 353
                                                                                                                                                                                                                                     GITINIQAKSNAPKLKAMVVVNNEEEAKTANLAQSSGITIQSPNSTVMGA----LNTVL- 596
                                                                                                                                                                                                                                                                                                      77 QCAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRFT-QDGFLNDPSGFTLMGSRIS 135
                                                                                                                                                                                                                                                                                                                                                               ---ONVSNFQQSIQNAFQNQESNIQAWANAIY 625
                                                                                                                                                                                                                                                                                                                                                                                                                 136 NNPNIKKETLEP-----IQLDFNDPTVAKS-PAKTSTALNAVVNLGDSTDKTQSBANP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 YFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSSTGSKTFEYLVA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   686 NNACASGMSG-----SNGNWCYQQ------WSDSKAYYSGLQSALGYQT---- 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----YSSSSGSNNGYTPCNST--NGSNKTSGNNCYEPNKQONATTATATTTDSNLQKVYND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQVVDFYNI PLARFTS---EDGLRR--EGNNHYSATLDS--GGPEFGLPGTSNYGKL--S
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                                                                                                                                                                                           GTVSNNIANANTIGYKQQQVV--FQDLFSQDLAIGS-TGSQGPNQAGMGAQVGSVRTIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456 VNQLETSNVDMSREMVNMI---IIQRGF-QMNSKSVTTADTMLQKAL 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : : | : | : ::|:: | | | | | | | :| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                                                                                Length 1230;
                                                                                Query Match 6.2%; Score 160; DB 9; Lu Best Local Similarity 21.6%; Pred. No. 0.0011; Matches 114; Conservative 71; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 58893, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-38
PRIOR PLING DATE: 2000-05-28
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR FILING DATE: 2000-05-06
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Oblsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
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Yamamoto, Robert
Forsyth, R.
Xu, H.
, ORGANISM: Helicobacter pylori
US-09-881-752A-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 32
US-10-282-122A-58893
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Sequence 150, Application US/09881752A
Sequence 150, Application US/09881752A
Septent No. US20020115078A1
GENERAL INFORMATION:
APPLICANT: Al-Garawi, Amal
APPLICANT: Aniler, Charles
APPLICANT: Tomb, Jaan-Francois
APPLICANT: Occomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
APPLICANT: Occomen, Raymond P.
TITLE OF INVENTION: Encoding No. US20020115078A1e1 Helicobacter Polypeptides in the
FILE REFERENCE: 66132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT PILING DATE: 2001-66-15
PRIOR FILING DATE: 1997-04-01
                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 PIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPNIAKGLNODFVATGYYTDGSSRDLTTQVTWNSSNTSTATISNANGTQGRMAAVDTGST 967
                                                                                                                                                                                                             469
                                                                                                                                                                                                                                                                                                                                                                              90 AIGGKGFFQVTLEDKVHYTRAG-NFRFTQDGFLNDPSGFTLMGSRISNNPNIKKETL--- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                523 SVNAATLVSIEVSPTNPSVSSGLTVPFTATGVYTDGSNQNLTSQVTWNSSNTNRATISNA 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              583 NGTQGIALGSSVGİTNISATLGAVTİSATTLTTVTNAVLNSITITPSLPSVAVGRSLNLTA 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        703 FTVSAAVLDSİQVILEDSPIAKGISİ--RAİAIGVFSDGSNLNISDQVIWDSSQINVIQL 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVANGLTQ---NFTATGV-----YSDGSNQNLTDSVTWASSNPAVATISNASGTNGKAT 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------GNNHYSATLDSGGPEFGLPGTSNYGKL 454
                                                                                                                                                    49
                                                                                                                                                                                                                                                                  83
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                                                                                                                                                                                                          110 VGSTNITAAIGGVDITVSLNVTNATLESIQVVSDSHSIARGTSTFVQAIGVYSDGSSQNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---EPIQLDFNDPT-----VAKSPAKTSTALNAVVN------LGDSTDKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLLMSG----IMTFSSNGELKNMTAFTPTGSAT-----KDLNAWQPA-----
                                                                                                                                                                                                                                                                  ---AIGSTGSOGPNOAGMGAQVGSVRTIFTQGAFEPGNSVTDL
                                                                                                                                                                                                                                                                                                                     470 SDQVAWNSSNSSILQISNLNAVPKREIQSPSSGGLG-----TARITATLEAISSYTDI
                                                                                                                                                       7 IGATGMKTHSTGLG-TVSNNIANA-------NTIGYKQQQVVFQDLFSQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----QSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSH-------
                                                                                                  Gaps
                                         6.3%; Score 162; DB 15; Length 1954;
19.3%; Pred. No. 0.0014;
.ive 80; Mismatches 241; Indels 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVN-----QLETSNVDMSREMVNMIIIQRGFQMNSKSVTTADTML 494
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 150
IENUTH: 1230
TYPE: PRT
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                                                                                                     125; Conservative
                                                                          Similarity
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us-10-009-823a-1.rapb

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APPLICANT: randwalled, Roller,
APPLICANT: Applicant: Another,
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms:
FILE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITEA, 0.34A
CURRENT APPLICATION NUMBER: 0/191,078
PRIOR APPLICATION NUMBER: 0/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/203,335
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR PLING DATE: 2001-11-27
PRIOR PLING DATE: 2001-11-27
PRIOR PLING DATE: 2001-11-27
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-06
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PRIOR FILING DATE: 2001-02-06
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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                     Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity
Matches 139; Conserv
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LENGTH: 3073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 MNPSEDGSAASGTDSAGLLMSGT--MTFSSNGELK------NMTAFTPTGSATK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 DLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP 353
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PRIOR FILING DATE: 2000-09-09
PRIOR PELING DATE: 2000-10-09
PRIOR PELING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PELING DATE: 2001-02-16
NUMBER FO SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 GTVSNNIANANTIGYKQQQVV--FQDLFSQDLAIGS-TGSQGPNQAGMGAQVGSVRTIFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.2%; Score 160; DB 15; Length 1230;
Best Local Similarity 21.6%; Pred. No. 0.0011;
Matches 114; Conservative 71; Mismatches 182; Indels 160; Gaps
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Masone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Chisen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-282-122A-58893
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2328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---AASGTD----SAGLL-----MSGTMTFSSNGELKNMTAFTP--TGSATKDLNAWQ 299
                                                                                                                                                                                                                                                             53 S---TGSQGPNQAGMGAQVGSVR-TIFTQGAFEPGNSVTDLAIG----GKGFFQVTLEDK
                                                                                                                                                                                                                                                                                                                                                                                           105 VHYTRAGNFRFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFN---DPTVAKSP
                                                                                                                             4 SLFIGAT-----GMKTHSTGLGTVS-NNIANANTIGYKQQQVVFQDLFSQD----LAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2275 ASATSAGSIAIGYGAFLN-PSATNSMALGL----NSSVSAANAVAIGYNAVADRANAVS-
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   DB 15; Length 3073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 -FVGAGIQPLTLDFGIKS-----QNWWAGAPASAAAIGTD-----
6.1%; Score 156.5; DB 15; ilarity 22.2%; Pred. No. 0.0079; Conservative 73; Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 PAPLVN--GLPQFSAN------
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Db 387 TTTPPPVIDGFTIALNGGALSAGDTFKVTPTRNAASSIGTVLTDPKK 433 Qy 352 LPSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQG-KYSNS 405	RESULT 35 US-10-335-977-4779 US-10-335-977-4779 Sequence 4779, Application US/10335977 Publication No. US20040052799A1 GENERAL INFORMATION: TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI RELATING TO HELICOBACTER PYLORI RELATING TO HELICOBACTER PYLORI STATE ADDRESSE: CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street CITY: Boston STATE: Masachusetts COUNTRY: USA ZIP: 02109-1875 COMPUTER: IBM PC COMPATISE: EMPCOMPATISE: IBM PC COMPATISE: IBM PC COMPATISE: UNIX CURRENT APPLICATION DATA:	APPLICATION NUMBER: US/10/335,977 PRICR ADDICATION NUMBER: US/10/335,977 PRICR APPLICATION DATA: APPLICATION NUMBER: 08/993,002 FILING DATE: 17-DEC-1997 ATTORNEY/AGENT INFORMATION: NAME: MANDER: Amy E. REFERENCE/DOCKET NUMBER: 36,207 REFERENCE/DOCKET NUMBER: 36,207 REFERENCE/DOCKET NUMBER: 36,207 REFERENCE/DOCKET NUMBER: 36,207 REFERENCE/DOCKET NUMBER: 36,207 REFERENCE/DOCKET NUMBER: 36,207 TELEPHONE: (617) 227-7400 TELEPHONE: (617) 742-4214 INFORMATION FOR SEQ ID NO: 4779: SEQUENCE CHARACTERISTICS: LENGTH: 269 amino acids TOPOLOGY: 1 inear NOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE: ORGANISM: Helicobacter pylori FEATURE DECRIPTION: SEQ ID NO: 4779: US-10-335-977-4779:	Query Match Best Local Similarity 25.9%; Pred. No. 0.00057; Matches 58; Conservative 39; Mismatches 90; Indels 37; Gaps 8; Qy 6 FIGATG-MKTHSTGLGTVSNNIANANTIGYKQQQVVFQD
Db 2555 GANGAERQIINVANATNSTDAVNLSQLQAMGANVNSSGVVTNAFVAYDDSTKGKVTLGGV 2614 Qy 353 PSYMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQG 400 Db 2615 GSSMPYLLANVAEGVYTSKQALNGSQLYGTANSVASALGGTSSVGSNGNVTARSLDG 2674 QY 401 KYSKSQVVDFYNI PLARFYSEDGLRREGNNHYSATLDSGGPERGLPGTSN 450 Db 2675 KTYNSVATTMDALNAKIAT-GSTDGVVYDTSAHNKLTLGGVNATTPVTVANVAAATSD 2731 QY 451 YGKLSVNQLETSNVDMSREMVNMI 475 DD 2732 DQAVNLAQLKAAGLNVDTSGNVTNSFV 2758	RESULT 34 US-10-369-493-13825 Sequence 13825, Application US/10369493 Publication No. USZ0030233675A1 SERVERAL INFORMATION: APPLICANT: Cao, Yongwei APPLICANT: Goldman, Barry S. APPLICANT: Goldman, Barry S. TITLE OF INVENTION: ELARESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES TITLE OF INVENTION: ELARESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION UNBER: US/10/369,493 CURRENT APPLICATION NUMBER: US 60/360,039 PRIOR PILING DATE: 2003-02-28 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 13825 LENGTH: 679 TYPE: PRT CRANISM: Pseudomonas fluorescens US-10-369-493-13825	Query Match 5.9%; Score 153.5; DB 14; Length 679; Best Local Similarity 20.3%; Pred. No. 0.0015; Matches 127; Conservative 69; Mismatches 208; Indels 221; Gaps 30; Qy 5 LFIGATGMXTHSTGLGTVSNNIANNTIGYKQQVVFQDLFSQDLAIGSTGSQGPNQA-62 Db 2 LNIGMSGLAASSSLAVTGNNIANNTIGYKQQVVFQDLFSQDLAIGSTGSQGPNQA-62 Db 46 YGNVPIGTTLADVRRVINSYLESQLRTATSLNSEAAARGAQATALDGGTKSIQ 45 Qy 63GGTKSTIADVRRVINSYLESQLRTATSLNSEAAARGAQATALDGSLSD 98 Qy 116 TQDGFLNDPSGF-TLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALN 169 Db 99 TNTGLTGVLQKFFTSMQGVSTSATDDTSRQSVLTGAQALTSRFNALAKQMNDQNATLN 156 Qy 170 AVVNLGDSTDKTQSEANPYPALLESWKGNGTPPISTSNVSYAQPMRVYD	267 MTGGEIGGLITYRKEVLDPALNELGRVALVVADQINRQQAQGIDKNGDFGAAIFNINSA 265LLMSGTMTFSSNGELKOMTAFTPTGSATKDLNAWQ- 267 ALISQRSIAQSGNLDVTIKDTGKLTTSDYQVTFTSATNYTVKREGTDMGSFST 300PAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNWWAGAPASAAAIGTDIGK :::

1516 NGGSFNTGLG-NTGSTNTGLFNPGNVNTGVGNTGSINTGSINTGSFNTGSTNTGSF 157 100 TLED	Db 1691 ITIDVNQVIAIDSFIQOTISMVGTGGFGPIPIGISIGGTPGFGNST 1736 Oy 208 YSYAQPKRVYDQGASHDITVYFDGAESTGSKTFEYLVAMTPSEDGSAAGG-TDSAGLL 266 1737TGPSSGFFHTGAGHVSGFGNFGAGNNSGSGNFGAGNSGFFNAGGLG 1782 OY 267 MSGTMTFSS-NGELKAMTAFTPTGSATKDLNAWQPAPLVNGLPQFSANFVGAGIQPL 322	Application US/101. No. US20030133943A1 No. US20030133943A1 Loosmore, Shena M. Loosmore, Shena M. Klah, Mchel H. VENTION: PROTECTIVE VVENTION: PROTECTIVE VVENTION: MOLECULAR NOE: 1038-1239MS. ING DATE: 1998-10-07- CATION NUMBER: 09/14 G DATE: 1998-10-07- EQ ID NOS: 91 Vatentin Ver. 2.1 80 Haemophilus influenz 61	Best Local Similarity
Qy 52 GSTGSQGPNQAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKG-FFQVTLEDKVHYTRA 110 Db 65 AKVLNRNLNRVPILSEIYTDRSLGAFEGTNNPLDFALTSPNLYFAIQTNEGVAYTRD 121 Qy 111 GNFRFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPA 162 Db 122 GHFSVDRDGFLVTLMGFRVL-SRSGLNEKGGIMLMPNABIEVDQNGGITFRDNEA 175 Qy 163 KTSTALANAVNLGDSTDKTQSEANPYFALLESWKGNGTPPISTS 206 176 Q1QAGALALVSFSEPKNLKKIGQNLYTYQGEGVHQVSDS 214	RESULT 36 US-10-282-122A-64364 Sequence 64364, Application US/10282122A Sequence 64364, Application US/10282122A Sequence 64364, Application US/10282122A Septence No. US20040029129A1 GENERAL INFORMATION: APPLICANT: Wallone, Cheryl APPLICANT: Haselbeck, Robert APPLICANT: Wall, Daniel APPLICANT: Trawick, John APPLICANT: Trawick, John APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT APPLICATION NUMBER: US/10/282,122A	PRIOR FILING DATE: 2000-03-21 PRIOR FILING DATE: 2000-05-32 PRIOR FILING DATE: 2000-05-32 PRIOR PILING DATE: 2000-05-23 PRIOR PILING DATE: 2000-05-23 PRIOR PILING DATE: 2000-05-26 PRIOR PILING DATE: 2000-09-09 PRIOR PILING DATE: 2000-09-09 PRIOR PILING DATE: 2000-09-09 PRIOR PILING DATE: 2000-09-09 PRIOR PILING DATE: 2000-10-23 PRIOR PILING DATE: 2000-10-23 PRIOR PILING DATE: 2000-11-27 PRIOR PILING DATE: 2000-11-27 PRIOR PILING DATE: 2000-10-2-3 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-16 PRIOR PILING DATE: 2001-02-17 PRIOR PILING DATE: 2001-02-17 PRIOR PILING DATE: 2001-02-17 PRIOR PILING DATE: 2001-02-17 PRIOR PILING DATE: 2001-02-17	CRGANISM: Mycobacterium tuberculosis US-10-282-122A-64364 Query Match Query Match Best Local Similarity 20.2%; Préd. No. 0.012; Matches 119; Conservative 64; Mismatches 220; Indels 185; Gaps 24; Qy 3 GSLPIGATGMKTHSTGLGTVSNNIANANTIGYKQQOVFQDLFSQDLAIGSTG 55 Db 1458 GNIGIGLTGTGQIGFGSFNSGSHNIGLFNSGDGNVGFFNSGTGNVGIGNTGTRNFGIA 1515 Qy 56 SQGPNQAQMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQV 99 1

-NAWQPAPLVN 305

-----SHDITVYFDGAPSSTGSKTFEYLVAMNPSEDGSAASG-

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366 TARNGSSSTRRYSQDGYPQGDL--VDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSEDG 423
                                                                                                                      GLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTSSGNS 365
868 STITGTESVTTSSQSGNIGGMISGGKVEVSATKDLITKSGSEIKATAGEVNVTSATGTID 927
                                                                                                                                                           928 GIISGNIVNVTANTGDLIVEDAAK-----IDAIGGAATLIAISGKL-----TIKASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 39
10-335-977-4780
US-10-335-977-4780
US-10-335-977-4780

| Sequence 4780, Application US/10335977
| Publication No. US20040052799A1
| GENERAL INFORMATION:
| APPLICANT: DOUGLAS SMITH et al APPLICANT: DOUGLAS SMITH et al IIILE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES IIILE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES IIILE OF INVENTION: DIAGRAPHING TO HELICOBACTER PYLORI FOR DIAGRAPHICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION WUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...273
SEQUENCE DESCRIPTION: SEQ ID NO: 4780:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0 SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Mandragouras, Amy E.
REGISTATION UNDBR: 35,207
REFERENCE/DOCKET NUMBER: GIN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                       265 LLMSGIMTFSSNGELKNMTAFTPTG-
                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 4780:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                     483 NSKSVITADIMLOKALELKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIGGKGFFQVTLEDKVHYTRAGNFRFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQ 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .---- QSGNIGGKISG 810
                                                                                                                                                                                                                                                                                                                                                                        424 LRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVD-MSREMVNMIIIQRGFQM 482
   222
                         264
                                                                                                      803 KTVNVKATNSLTTQADSKIBATEG---BANVTSKTSIIGGTISGGTVEVTATEGLTTQAG 859
                                                                                                                                                 265 LLMSGTMTFSSNGELKNWTAFTPTG----SATKOL-------NAWQPAPLVN 305
                                                                                                                                                                               860 STITGTESVTTSSQSGNIGGMISGGKVEVSATKDLITKSGSEIKATAGEVNVTSATGTID 919
                                                                                                                                                                                                                      GLEQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTSSGNS 365
                                                                                                                                                                                                                                                  366 TARNGSSSTRRYSQDGYPQGDL--VDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSEDG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 NTIGYKOOOVVFODLFSQDLAIGSTGSQGPNOAGMGAQVGSVRTIFTQGAFEPGNSVTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.8%; Score 149.5; DB 14; Length 1188; Best Local Similarity 20.2%; Pred. No. 0.0073; Matches 113; Conservative 88; Mismatches 212; Indels 147; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LOCSMORE, Sheena M. APPLICANT: Yang, Yan-Ping APPLICANT: Yang, Yan-Ping APPLICANT: Yang, Yan-Ping APPLICANT: Yang, Yan-Ping TITLE OF INVENTION: MICHEL H. TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS FILE REPERBNES: 1038-1239MIS CURRENT APPLICATION NUMBER: US/10/193,764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GTPPISTSNYSYAQPMRVYDQQGN-
   -GIPPISTSNYSYAQPMRVYDQQGN-
                                                                            ----SHDITVYFDGAPSSTGSKTFEYLVAMNPSEDGSAASG
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PRIOR FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVKYIQPGIASVDEVIEAKR 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 59, Application US/10193764; Publication No. US20030133943A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     483 NSKSVTTADTMLOKALELKR 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-193-764-59
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Search completed: October 26, 2004, 09:20:50 Job time : 140 secs
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Greer, Greven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 18460
LENGTH: 1649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1049 ------YPNATLSTPYVQTS----GLINLSD-LDLSTNKGNLF-----WKPIGNPPTSI 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .092 SNTYNGA----YWGTQAAFPILT--FNGGDTSTKSG-----AVNISPNN--FSGVDSAK 1137
                                                                                                                                                                                                                              69 AKYLNRNLNRVPILSEIYTDRSL---GAFEGTNNPIDPALTSPNLYFAIQTNBGVAYTKD 125
                                                                                                                                                                                                                                                                                                                     52 GSTGSQGPNQAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKG-FFQVTLEDKVHYTRA 110
                                                                                                                                                                                                                                                                                           111 GNFRFTQDGFLNDPSGFTLMGSRISNN------PNIKKETLEPIQLDFNDPTVAKSPA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 GTTISGTITSGESSDNLTDAIAVANNKSAITLGNSTSHNDIT---INGSLINFNSAEIT 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 DKVHYTRAGNFR-----FTQDGF----LNDPSGFTLMGSRISNNPNIKKETL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 EPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANPYFALLESWKGNGTPPIST 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263
                                                                                                                                                   -----STGSQGPNQAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGK--GFFQVTLE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 GLIMSGTWIFSSNGELKNWI------AFTPTGSAIKDLNAWO---PAPLVNGLPQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SN-YSYAQPMRVYDQQGNSHDITVYFDGAPSSTGSKTFEYLVAMNPSEDGSAASGTDSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 5.7%; Score 147; DB 14; Length 1649;
Best Local Similarity 22.4%; Pred. No. 0.019;
Matches 124; Conservative 76; Mismatches 215; Indels 138; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GSLFIG---ATGMKTHSTGLGTVSNNI-ANANTIG--YKQQQVVFQ---DLFSQDLAIG-
                                          DB 15; Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                        : :: | : : | | : | CIQAGALALVSFSEPKNLKKIGQNLY----TYQGEGVHQVSDS 218
                                                                                                                                                                                                                                                                                                                                                                           163 KTSTALNAVVNLGDSTDKTQSEANPYFALLESWKGNGTPPISTS 206
                                     5.7%; Score 148.5; DB 15;
ilarity 25.4%; Pred. No. 0.001;
Conservative 40; Mismatches 90;
                                                                                                                        6 FIGATG-MKTHSTGLGTVSNNIANANTIGYKOOOVVFQD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18460, Application US/10369493
Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Lactococcus lactis
US-10-369-493-18460
                                     Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-369-493-18460
US-10-335-977-4780
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1138 NYAFLGDYTMSSLSTPSNPTWIGYVVPGQVRVYNTTGDA--DSGNWQHHLKSNVTTGNPV 1195
                                                                                                                                                                                                                                                                                      1232 SFTAKAPYY-----IKSRTATAFDGKVINNYPSTN------PNFDVNAGTTGAT 1274
                                                                                                                                                                                                                                                                                                                                                                                                                           310 FSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTSSGNSTARN 369
                                                                                                                                             -----QTMQAWA---SVASDTDASSI-KVMYVMGYSDSTTAPF
                                                                                                                                                                                                                         370 GSSSTRRYSQDGYPQGDLVDVTITS-EGKLQGKYSNSQVVDFYNIPLARFTSEDGLRREG
                                                                                                                                                                                                                                                                                                                                                                          429 NNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQNNSKSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1334 QA--QLÓKIVGLK 1344
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

protein search, using sw model OM protein - October 26, 2004, 09:04:15; Search time 197 Seconds (without alignments) 1466.183 Million cell updates/sec Run on:

US-10-009-823A-1 2586 1 MMGSLFIGATGMKTHSTGLG......NSKSVTTADTMLQKALELKR 502 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

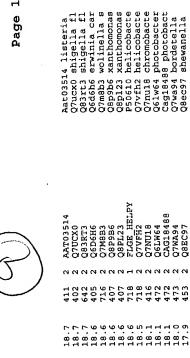
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

	Description	i e	Aas94790 desulfovi		Aas95921 desulfovi	Q74g30 geobacter s	Aar33751 geobacter	Q9rqb6 treponema d	Aas13285 treponema	Q6mhy9 bdellovibri	Cae78193 bdellovib	Q56326 treponema p	Q8zfb5 yersinia pe	Aas61825 yersinia	Q72t33 leptospira	Q8f2c6 leptospira	a					•		Q8fiq4 escherichia		Q7af93 escherichia) listeria (Q7ap22 listeria in
SUMMARIES		Q72FA7	AAS94790	Q72C41	AAS95921	Q74G30	AAR33751	Q9RQB6	AAS13285	6 XHW9Ö	CAE78193	FLGE TREPH	Q8ZFB5	AAS61825	·Q72T33	Q8F2C6	AAS69795	FLGE TREPA	Q82XG9	Q8R9Z7	Q914P9	FLGE BORBU	Q8XSX2	Q8FIQ4	FLGE SALTY	Q7AF93	QBX8L1	FLGE ECOLI	FLGE HELPJ	Q92DV7	Q722K0	Q7AP22
	DB	6	7	7	~1	~	N	N	N	C)	N	-	~	N	~	7	~	-	Ŋ	7	N	7	N	N	Н	ď	~	н	Н	N	N	71
	₽	498	498	564	564	419	419	463	463	427	427	463	428	428	464	464	464	463	410	41	46	442	401	401	402	401	401	401	718	411	411	411
,	강성	47.8	47.8			26.8							21.	21.		21.	21.	20.	20	20	20	19	19	19	19	19	19	19	18			18.7
		1235	1235	961	961	693.5	693.5	595.5	595.5	579.5	579.5	567.5	U)	ഗ	550	550	550	534.5	533	528.5	527.5	509	502	498	498	493	493	491.5	485	484.5	484.5	484.5
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ALIGNMENTS

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172FA7 PRELIMINARY; 72FA7; 5-UUL-2004 (TrEMBLrel. 27, C 5-UUL-2004 (TrEMBLrel. 27, L 1agella basel body rod domai rederedicousNames=DVU0307; esulfovibrio vulgaris (strai 303). seulfovibrio vulgaris (strai acteria, Proteobacteria; Del esulfovibrionaceae; Desulfov CBI_TaxID=882; ubMed=15077118; DOI=10.1038/ ubMed=15077118; DOI=10.1038/ ubMed=15077118; DOI=10.1038/ clearson J.F., Seehadri R., olonay J.F., Eisen J.A., War augherty S.C., DeBoy R.T., Delach W.T., Sullivan S.A., F eterson J.D., Davidsen T.M., imitrov G., Hance M., Tran & eldblyum T.V., Wall J.D., Vo The genome sequence of the a cenlfovibrio vulgaris Hilden at. Biotechnol. 22:554-559(2 MBL; AE0177110; AAS94790.1; -TGR; DVU0307; -TGR; DVU0307; -TGR; DVU0307; -TGR; PRO01444; Flag_bb -TGR; -TGRI; PS00588; FLAGELLA_B -TRAGELLA_B -TRAGELLA_B -TRAGELLA_B -TRAGELLA_B -TRAGELLA_B -TRAGELLA_B -TRAGELLA_B -TRAGELLA_B -TRAGELLA_B -TRAGELLA_B -TRAGELLA_B -TRAGELLA_B	atch cal Similarity 49.6%; Pred. No. 5.1e-67; 253; Conservative 74; Mismatches 163; Indels 20; Gaps	1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGFN 60	61 QAGMGAQVGSVRIJFTQGAFBPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGF 120 	121 INDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDFTVAKSPAKTSTALNAVVN 173	LGDSTDATQSBANFIFALDBSARGIGIFFISISIAISIAN 15KGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
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                                                                                                        234 PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATK
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Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolebberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Melson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D., Davidsen T.M., Zafar N., Zhou L., Radune D., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.; "The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough.";
Mat. Biotechnol. 22:554-559 (2004).
TIGR. DVIJ443.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Flagellar hook protein Fl93
Name=fl98; OrderediccusNames=DVU1443;
Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 /
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Best Local Similarity 39.0%; Pred. No. 2.9e-50;
Matches 223; Conservative 85; Mismatches 184; Indels
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Pfam, PF00460; F1g bb rod; 1.
PROSITE; PS00588; F1AGELIA BB ROD; 1.
COMPLETE protecme; F1AGellum.
SEQUENCE 564 AA; 60542 MW; 50DC084F6D7A4DBE CRC64;
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Interpro; IPR001444; Flag_bb_rod.
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                                                                                                     349 GGATTPKLAATSTTAYKGSSSSTYMKQDGYAEGVLMNLEVATDGIVSGKYSNGQSQSLPR
                                                                             PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATK
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Nat. Biotechnol. 22:554-559(2004).
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Bacteria, Proteobacteria, Deltaproteobacteria, Desulfovibrionales,
Desulfovibrionaceae; Desulfovibrio.
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27-APR-2004 (TrEMBLrel. 27, Last sequence update)
11-WAY-2004 (TrEMBLrel. 27, Last annotation update)
Flagella basal body rod domain protein.
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Matches 253; Conservative
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                                                                                                                                                                                                                                                                                 357 LPMNVANFSGLIDSSVVGSPIAONFLMELDLGLRSTNATIPWISTP-NAARIGIDASLLD 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 GLTSSQRQPSATISYAGSSSTQFQKQDGYTFGFLQNITVDRDGIMQGKYSNGVTLDLYQV 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 476 TLVDFISKQNLRREGGNLFSGTRDSGDP---LPGPANSNGLGAISSNSLEQSNVDLAREF 532
                                                                                                                        164 TSTALNAVVNLGDSTDKTQSEANPYFALLESWKG----NGT-PPISTSNYSYAQPNRVYD 218
                                                                                                                                                                                                                                                219 QQGNSHDITVYFDGA-PSS-----TGSKTFEYLVAMNPSED-----GSAASGTDSAGLLM 267
                                                                                                                                                                                                                                                                                                                                                                           SGTMTFSSNGELXNMTAFTFTGSAT-------KDLNAWQPAFL-VNG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                297 TGTLTFDTTGQLVDQTAFTPFGQYTDTTPPWNEPTPNPGPPVTTPADLVNWQPTQMSSNG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 LPQFSANFVG------AGIQPLTLDFGIKSQQ--NWWAGAPASAAIGTDIGKLP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 SMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNI 413
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-----IKKETLEPIQLDFNDPTVAKSPAK 163
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Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
Rolonay J.F., Eisen J.A., Ward N., Methe B.A., Brinkac L.M.,
Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
Feldblyum T.V., Wall J.D., Voordoww G., Fraser C.M.,
The genome sequence of the anaerobic, sulfate-reducing bacterium
Desulfovibrio vulgaris Hildenborough.",
TIGR: DVU1443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Deltaproteobacteria, Desulfovibrionales,
Desulfovibrionaceae, Desulfovibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     564 AA; 60542 MW; 50DC0B4F6D7A4DBE CRC64;
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27-APR-2004 (TrEMBLrel. 27, Last sequence update)
11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Flagellar hook protein FlgE.
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119 GFLNDPSGFTLMGSRISNNPN---
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AAS95921;
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                                                                            GFLNDPSGFTLMGSRISNNPN------IKKETLEPIQLDFNDPTVAKSPAK 163
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STRAIR-ECA / ATCC 51573;

PubMed=14671304; DOI=10.1126/science.1088727;

Methe B.A., Nelson K.E., Elsen J.A., Paulsen I.T., Nelson W.C.,

Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,

Madugu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,

Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,

Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,

Weidman J.E., Enveley D.R., Fraser C.M.;

"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                     59 QVGRGVSIGAIFGDYSQGAFQTTNESTDLAIQGRGFFSVKPKGTEDTYYTRAGNFRFDAD
                                                                                                                                                                                                  177 QNITLNVNLDSNPGNDKSSSTTNPYFSLFETWNGQNPLTGTQPALAQSAFAYQSTIKVYD
                                                                                                                                                                                                                                                                                                                                                 164 TSTALNAVVNLGDSTDKTQSEANPYFALLESWKG----NGT-PPISTSNYSYAQPMRVYD.
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QAGMGAQVGSVRIIFIQGAFEPGNSVIDLAIGGKGFFQVTLE--DKVHYTRAGNFRFTQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Flagellar hock protein Flgs.
Name-flgs; ORTNames-GSU0419;
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InterPro; IPRO11491; Flag.
InterPro; IPRO11444; Flag.bb rod.
InterPro; IPRO02371; Flag.bb rod.
Pfam; PF06429; DUF1078; 1.
Pfam; PF07559; Flag.bb_rod; 1.
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05-JUL-2004
61
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EMBL; AE017208; AAR33751.1;
TIGR; GSU0419; -.
                                       419 AA;
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SEQUENCE FROM N.A.
STRAIN-ATCC 35405;
                           Flagella.
SEQUENCE
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                                                                                                     4 SLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAG
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                                                                                                                                                                                                                                                                                          244 YLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATKDLNAWQPAPL
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PubMed-14671304;
Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
Madugu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
Gwinn M.L., Kolomay J.F., Sullivan S.A., Haft D.H., Selengut J.S.,
Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
Weidman J., Khouri H.M., Feldblyum T.V., Utterback T.R.,
Van Aken S.E., Lovley D.R., Fraber C.M.,
"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                  Gaps
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Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
                                                                                  91;
                                                          Score 693.5; DB 2; Length 419;
Pred. No. 3.7e-34;
0; Mismatches 166; Indels 91;
                                                                                                                                                                                                                                                                                                                                                              -----TFAG-GVTAPOPIFFDLGV------TFAG-GVTAPOPIFFDLGV------
                                  419 AA; 44051 MW; 3148770150C5C6EF CRC64;
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Last annotation update)
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PRINTS; PR01005; FLGHOOKAP1.
PROSITE; PS00588; FLAGELLA_BB_ROD; 1.
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                                             26.8%; Scu.
34.9%; Pred
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Science 302:1967-1969(2003).
                                                                                Matches 175; Conservative
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                                                     Query Match
Best Local Similarity
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                       Flagellum.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 EANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSSTGSKTFE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 LA-----R-DPANPVATSNYSTS--LSVYDSQGNAHTATVYF----RKTADNAWD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 YLVAMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKNWTAFTPTGSATKDLNAWQPAPL 303
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                                                                                                                                                                                                                                                 28
                                                                                                                                                                                4 SLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAG
                                                                                                                                                                                                                       6 ALYTGISGINANGEAMSVIGNNISNVNTIGFKQGRMLFSDVLSSTISGGS-----QIG
                                                                                                                                                                                                                                                                                                         64 MGAQVGSVRIIFIQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGFLND
                                                                                                                                                                                                                                                                                                                                                59 RGVQIQTVENQFTQGSFESTESGTDLAIQGDSFFVVQNTSGRYYTRAGAFSFNKDKTLVN
                                                                                                                                                                                                                                                                                                                                                                                                                              124 PSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQS
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                                                                                                                            Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Flagellar hock protein Figs.
Name=flgE; ORFNames=TDE2768;
Name=flgE; ORFNames=TDE2768;
Bacteria; Spirochaetes; Spirochaetaceae; Treponema.
                                                                                                                            91,
                                                       26.8%; Score 693.5; DB 2; Length 419; 34.9%; Pred. No. 3.7e-34; rive 70; Mismatches 166; Indels 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paulsen I.T.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017255; AAS13285.1;
GO; GO:00092888; C:flagellum (sensu Bacteria); IEA.
GO; GO:0003774; F:motor activity; IEA.
44051 MW; 3148770150C5C6EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TFAG-GVTAPQPIFFDLGV------
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                                                                                    Best Local Similarity 34.9
Matches 175, Conservative
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RESULT 9
Q6MHY9
          SKARAKARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 ARVPGEVNA--WRATVNVDPTNADATATRVGIGT-TDGVQNSFIVRFDNNGHLASVT--D 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 SQGPNQAGMGAQVGSVRIIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 TQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQL-----DFNDPTVAKSPAKTSTALNA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 VVNLGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 DGAPSSTGSKTFEYLVAMNPSEDGSAAS----GTDSAGLLMSGTMTFSSNGELKNMTAFT 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 TAGNVT------AGAP-VOISYNVVGANPDE------AGAP-TRHTFD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 TDIGKLPSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQ 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 VNLGE-----IGTSKNTITQFSDKSTTKAYEQDGYTLGYLENFRIDQSGIITGVYSNGV 367
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STRAIN=ATCC 3540S / DSM 14222;
STRAIN=ATCC 3540S / DSM 14222;
SubMed=15064399;
Seshadri R., Wydrs G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J., Durkin S.A.,
Daugherty S.C., Shetty J., Shvartsbeyn A., Gebregeorgis E., Geer K.,
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Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Treponema.
NCBI_TaxID=158;
                                                                                                                                                                                                                                                                                                                                                              67;
                                                                                                                                                                                                                                                                                                           DB 2; Length 463;
                                                                                                                                                                                                                                                                                                     23.0%; Score 595.5; DB 2; Length 32.2%; Pred. No. 3.9e-28; cive 73; Mismatches 210; Indels
                                                                                                                                                                                                                                                          463 AA; 49574 MW; E872E4C726F6C733 CRC64;
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0001539; P:ciliary/flagellar motility; IEA.
InterPro; IPR010930; DUF1078.
InterPro; IPR011491; Flag.
InterPro; IPR01444; Flag.bb_rod.
Pfam; PF06429; DUF1078; 1.
Pfam; PF00460; Flg.bb_rod; 1.
Pfam; PF00460; Flg.bb_rod; 1.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
04-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Flagalar hook protein FlgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467 SREMVNMIIIQRGFQMNSKSVTTADTMLQKALELKR 502
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les 166; Conservative
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AAS13285;
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AAS13285
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61 GWNPKEVGLGMMVASIDTIFTQGALQTTGVNTDLAIQGNGFFILKDGEKTFYTRAGAFGI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 VVNLGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYF
Tsegaye G., Malek J.A., Ayodeji B., Shatsman S., McLeod M.P., Smaje D., Howell J.K., Pal S., Amin A., Vashisth P., McNeill T.Z., Xiang Q., Sodergren B., Baca E., Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.; Riber C.M., Paulsen I.T.; "Comparison of the genome of the oral pathogen Treponema denticola with other spirochete genomes"; Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).

EMBL; AE017255, AAS13285.1; -.
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Bubbed=1475216;

Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
Sockett R.B., Schuster S.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=F1gE; OrderedLocusNames=Bd3395;
Bdellovibrio bacteriovorus.
Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
Bdellovibrionaceae; Bdellovibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                               23.0%; Score 595.5; DB 2; Length 32.2%; Pred. No. 3.9e-28; ive 73; Mismatches 210; Indels
                                                                                                                                                                                                                                                                                                                                                            463 AA, 49574 MW; E872E4C726F6C733 CRC64;
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SEQUENCE FROM N.A.
STRAIN-HDIOO / DSM 50701 / ATCC 15356 / NCIB 9529;
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Sockett R.E., Schuster S.C.;
"A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a genomic perspective.",
Science 303:689-622(2004).
EMBL; BX842655; CAE78193.1; -.
SRQUENCE 427 AA; 45943 MW; C74DA82F2E0FC003 CRC64;
             Lambert C., Evans K.J., Goesmann A., Meyer F.,
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  of Bdellovibrio bacteriovorus from
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STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
PubMed=14752164;
Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
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Badellovibrio bacteria, Deltaproteobacteria, Bdellovibrionales,
                                                                                                                                                                                                                                                                                                                                        Indels 119;
                                                                                                                                                                                                                                                                                          22.4%; Score 579.5; DB 2; Length 427; 30.6%; Pred. No. 3.3e-27; 1ve 73; Mismatches 171; Indels 119
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               genodic perspective.";
Science 303:689-692(2004).
EMBL; BR42655; CAE78193:1, -
InterPro; IPR01491; PlaE.
InterPro; IPR014491; PlaE.
InterPro; IPR014491; PlaE.
Ffam; PF06429; DUF1078; 1.
Pfam; PF06429; DUF1078; 1.
Pfam; PF07559; FlaE; 1.
Pfam; PF07659; FlaE; 1.
Complete processes: FLAGELLA BB_ROD; 1.
Complete 427 AA; 45943 NW; C74DA82F;
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predator unmasked: life cycle
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                                                                                                                                                                                                                                                                                                                                  160; Conservative
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                                                                                                                                                  61 QAGMGAQVGSVRIIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGF
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                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treponema phagedenis.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
Query Match 22.4%; Score 579.5; DB 2; Length 427; Best Local Similarity 30.6%; Pred. No. 3.3e-27; Matches 160; Conservative 73; Mismatches 171; Indels 119;
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05-JUL-2004 (Rel. 44, Last annotation update)
Flagellar hock protein flgs.
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1 17:08:09 2004 MON NOW MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083; MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083; Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L., Baket S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Ibather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).

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MEDLINE=22137863; PubMed=12142430;
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Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
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Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
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between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). 11; 310 HTFNINLGE-----IGTSRNTITQFAERSTIKAYQQDGYAMGYLENFKIDQSGIITGVY 363 SNSQVVDFYNIPLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETS 462 115 116 TODGFLNDPSGFTLMGSRISNNPNIKKETLEPIQL-----DFNDPTVAKSPAKTSTA 167 121 DRÖGTLVNPAN----GMRVQ---GWMAEDIEGQQIINTSDQTEDLIIPIGQKIDAKATTD 173 174 VAYACNLDKRLPELPEGANQADILRSTW-------ATDFNVYDTFGEQHKLQ 218 VYFDGAPSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGT-----MTFSSNGELKNM 282 TAFTPTGSATKDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASA 342 T--DIAGNVT-----APAGQVLVQASYNVVGA--------NPDEGGAPTR 309 343 AAIGTDIGKLPSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKY 402 LNAVVNIGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDIT 227 1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKOOOVVFODLFSQDLAIGS----TG 56 SQGPNQAGMGAQVGSVRTIFTQGAFEFGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRF Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; 75; Length 463; 21.9%; Score 567.5; DB 1; Length ilarity 31.2%; Pred. No. 2e-26; Conservative 66; Mismatches 217; Indels 463 AA; 49527 MW; 960548C364CA35BC CRC64; Q8ZFBS; Q74UV4; Q7CHX9; 01-MR-2002 (TrENBLrel. 20, Created) 01-MR-2002 (TrENBLrel. 20, Last sequence update) 01-MR-2002 (TrENBLrel. 20, Last sequence update) 01-OCT-2004 (TrENBLrel. 28, Last annotation update) Flagellar hook protein Flag (Hook protein) Name-flgE; Synonyms-Fla FV, flak, flgE1; OrderedLocusNames-FP1591, YPO1802, Y2507; EMBL, U04619; AAA73467.1; -.
InterPro; IPR010930; DUF1078.
InterPro; IPR001444; Flag_bb_rod.
Pfam; PP06429; DUF1078; 1.
PROSITE; PS00588; FLAGELLA_BB_ROD; 1. PRT; Enterobacteriaceae; Yersinia. NCBI_TaxID=632; PRELIMINARY; al Similarity 162; Conserva [1] SEQUENCE FROM N.A. Yersinia pestis. Flagellum. SEQUENCE 61 168 228 219 283 403 Query Match Best Local 8 RESULT 12
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A SONG Y., TONG Z., Wang L., Han Y., Oin H., Wang J., Li S., Guo Z.,

HAN Y., Pang X., Zhai J., Chen F., Oin H., Wang J., Huang P.,

Yang R.;

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EMBL; AJ414150; CAC90619.1; -.

EMBL; AJ414150; CAC90619.1; -.

EMBL; AG0219; AG0219.

EMBL; AG0219; AG0219.

REST, AG0219; AG0219.

REST, AG0219; AG0219.

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CO; GO:0003774; F:moror activity; IEA.

CO; GO:0003774; F:moror activity; IEA.

CO; GO:000198; F:structural molecule activity; IEA.

CO; GO:000198; F:structural molecule activity; IEA.

RO; GO:000198; F:structural molecule activity; IEA.

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Best Local Similarity 29.1%; Pred. No. 7.2e-26;
Matches 145; Conservative 74; Mismatches 196;
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RA Haske D.A., Verjovski-Almeida S., Hartskeerl R.A.,

RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,

RA Gottinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H.,

RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.T.,

RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.T.,

RA Goes-Neto A., Sommer B. G.M., Lemos M.V.F., Marino C.L., Nunes I.R.,

RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,

RA Siqueira W.J., Sommer D., Tsai S.M., Sohpson A.J.G., Ferro J.A.,

RA Gomargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;

R. Comparative genomics of two Leptospira interrogans serovars reveals

R. T. Comparative genomics of two Leptospira interrogans serovars reveals

R. InterPro; IPRO11491; FlaE.

DR EMBL, ABO17291; ABS697951;

DR FEAN; PFOGA429; DUF1078;

R. Ther Pro; IPRO11444; Flag_bb_rod.

BR Ffam; PFOGA59; FlaE; 1.

BR Pfam; PFOGA69; FlaB; 1.

BR Pfam; PROSIEF; PSOGS88; FLAGELLA_BB_ROD; UNKNOWN_1.

KW Complete proteome.
                                 LRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMN 483
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Name=flgE; OrderedLocusNames=LIC11188;
Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363
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                                                                                                                <u>:</u>
                                                                           364 NSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSEDG
                                                                                                                                                                                   LRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=91001 / Biovar Mediaevalis; Song Y., Tong Z., Wang J., Zhou Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z., Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P., Yang R.; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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24-WAR-2004 (TrEMBLrel. 27, Last sequence update)
04-WAY-2004 (TrEMBLrel. 27, Last annotation update)
Flagellar hook protein FlgE.
FLGEL OR YPIS91.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               428 AA.
PRT;
                                                                                                                                                                                                                                                                                                                        411 AQTIKTQDQILQTLVSLR 428
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Flagella.
SEQUENCE 428 AA; 44875 M7
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PubMed=1502012.

Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B., PubMed=150202.

Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B., Andrews M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H., Coutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H., Coutinho E.S., Ferro M.I.T., Furlan J.R., Gamberini M., Giglioti B.A., Goldman G.H., Goldman M.H.S., Harakava R., Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura B.T., Adeonimo S.M.B., Jongueira G.G., Resis M.S., Schriefer A., Goldman P., Setubal J.C., Van Slupson A.J.G., Ferro J.A., Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A., Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A., Comparative genomics of two Leptospira interrogans serovars reveals novel insights into physiology and pathogenesis.";

N. Bacceriol. 186:2164-2172 (2004).

B. BRBL, AEONISSI, AAS, 50349 MW; 7EDDSAA84709F64F CRC64;
121 DKNGYYVNPANGLKVQGWNSRLDDKGNKYINSAASIE-DIIIFVYSKEFARATSQIDFKS 179
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                                                                                                                     329 KSQQNWWAGAPASAAAIGTDIGKLPSWWPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLV
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                                                                                                                                                                                                                                                                                                                                         290 DSMNSGKLNAKVSFRIPGNPALQNPDLNLGB-AGWVNGITQFSSDF------
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21.3%; Score 550; DB 2; Length 464;
Best Local Similarity 27.9%; Pred. No. 2.3e-25;
Matches 149; Conservative 84; Mismatches 199; Indels 102;
                                                                                                                                                                                               VYFDGAPSSTGSKTFEYLVAMNPSEDGSAASGTDSA-----
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Last annotation update)
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                 MEFYKVRDNTWKARLSMTDSTQLSVDVSGTGGQNTQLPGNTELEFGFTPDGKLVYVSDGV 289
                                                                      ----NGELKAMTAPTPTGS---ATKDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGI 328
                                                                                                                                                                                KSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLV 388
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STRAIN=256601 / Serogroup Icterchaemorrhagiae / Serovar lai;
MEDLINE=2259843; PubMed=12712204;
Zhang Y.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Jia J., Tu Y.-F.,
Jiang Y.-X., Kiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
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Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y.,
Sang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y.,
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Xu J.-G., Zhao G.-P.,
"Unique physiological and pathogenic features of Leptospira
interrogans revealed by whole-genome sequencing.";
Mature 422:888-89312003).
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                                                                                                                                                                                                                                                                                                                          389 DVTITSEGKLQGKYSNSQVVDFYNIPLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGT
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Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                          449 SNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMNSKSVTTADTMLQKALELKR
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21.3%; Score 550; DB 2; Length 464;
Best Local Similarity 27.9%; Pred. No. 2.3e-25;
Matches 149; Conservative 84; Mismatches 199; Indels 102;
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ROJ, GO.0009288; C.flagellum (sensu Bacteria); IEA.

ROJ, GO.000574; F.enctor activity; IEA.

ROJ, GO.000539; F.enctoural molecule activity; IEA.

ROJ, GO.001539; P.iciliary/flagellar motility; IEA.

RIMERPRO, IPRO1449; Flag.

RIMERPRO, IPRO1444; Flag.

R Pfam, PF06429; DURF1078.

R Pfam, PF00460; Flag.

R Pfam, PF00460; Flag.

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R Pfam; PF00460; Flag.

R Pfam; PF00460; Flag.

R Pfam; PF00460; Flag.

R Complete proteome; Flagellum.

R Complete proteome; Flagellum.

R SEQUENCE 464 AA; 50349 MW; 7EDDSAA84709F84F CRC64;
                                                                                                         01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 AA
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                                                                                                                                   228 VYFDGAPSSTGSKTFEYLVAMNPSEDGSAASGTDSA------GLLMSGTMTFSS---
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SEQUENCE FROM N.A.
MEDLINE=96345631; PubMed=8755894;
Limberger N.J., Slivtenski L.L., El-Afandi M.C.T., Dantuono L.A.;
Limberger N.J., Slivtenski L.L., and expression of the 5' region of the fla operon of Treponema plagedenis and Treponema pallidum.";
J. Bacteriol. 178:4628-4634(1996).
                                 Flagellar hook protein flgE.
Flagellar hook protein flgE.
Treponema pallidum.
Bacteria; Spirochaetes; Spirochaetaceae; Treponema.
NCBL_TaxID=160;
                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
 463 AA
 PRT;
STANDARD;
                                                                                                                                                                           SEQUENCE FROM N.A.
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Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R.J., Gwinn M.L., Hickey E.K., Clayton R.A., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D., Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M., Utterback T.R., McDonald L.A., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M., Weidman J.F., Smith H.O., Venter J.C.;

"Complete genome sequence of Treponema pallidum, the syphilis STRAIN=Nichols; MEDLINE=98332770; PubMed=9665876;

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). spirochete."; Science 281:375-388(1998). -!- SIMILARITY: Belongs to the flagella basal body rod proteins family.

0.8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	EMBL; U28119; AAB61251.1; - EMBL; AZ001244; AAC65692.1; - PIR; C71292; C71292. TIGR; TP0727; - InterPro; IPR0109330; DUP1078. InterPro; IPR01044; Flag_bb_rod. Pfam; PF06429; DUF1078; 1. Pfam; PF06429; PUF1078; 1. Pfam; PF06429; PIG_Bb_rod; 1. COMPLETE PS05889; FLAGELIA, BB_ROD; 1. COMPLETE PS060000; FLAGELIA, BB_ROD; 1. SEQUENCE 463 AA; 49178 MW; 947C4C413B36E7A8 CRC64;
QWE	Query Match 20.7%; Score 534.5; DB 1; Length 463; Best Local Similarity 28.1%; Pred. No. 2e-24; Matches 154; Conservative 80; Mismatches 183; Indels 131; Gaps 14;
ò	GMKTHSTGLGTVSNNIANANTIG
đ	
ò	FTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVH
q	61 GVNPKEVGLGVLIASIDTVHTQGALQTTGINTDVSIQGSGFFVLKSGEKTFFTRAGAFGV 120
ò	116 TQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTST 166
q	121 DNAGTLVNPANGMRVQGWAAQDVAGERLINSSAQTQDLVIPIGQKIDAQQTS 172
ò	- Z
qq	173 TVHYACNLDKRLPELAADANEADVRKSTWTTDFQVYDSFGQQHTL 217
à	227 TVYFDGAPSSTGSKTFEYLVAMNPSEDGSAASGT 260
đ	218 QINFSRVPGTNNGWQATVAVDPGTEVDTQTRVGVGTSDGAANTFIVNFDNFGHLASVT 275
ò	261 DSAGLLMSGTWTFSSNGELKNWTAFTPTGSATKDLNAWQPAPLVNGLPQFSANFVGAGIQ 320
qq	776 DTAGNVTGPTGQVLEASYDVVGA 299
ò	PSMMPIQISSGNSTARNGSS
qq	300NPDDAGQVTRHAFTINLGEIGTARNTITQFAERSTT 335
ò	375 RRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSEDGLRREGNNHYSA 434
g	336 KAYRODGYAMGYLENFKIDQSGVITGVYSNGVSQDIGQLALAGFANQGGLEKAGENTYVQ 395
ò	SREMVNMIIIQRGFQMNSKSVTT
QC	396 SNNSGIANISTSGVMGKGKLIAGTLEMSNVDLTDQFTDMIITQKGFQAGAKTIQTSDTML 455
ò	495 QKALELKR 502
q	. 456 DTVLSLKR 463
RESULT	TT 18

Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales, Nitrosomonadaceae, Nitrosomonas Last sequence update) 410 AA. Q82XG9 PRELIMINARY; PRT; Q82XG9, Q82XG9, Q1-JIN-2003 (TrEMBLrel. 24, Last seq. 01-JUN-2003 (TrEMBLrel. 24, Last seq. 01-JMR-2004 (TrEMBLrel. 25, Last annofelagella basal body rod protein. Name=flgE; OrderedLocusNames=NE0305; Nitrosomonas europaea 082XG9 AC AC B 08 DT 01 DT 0

NCBI_TaxID=915;

SEQUENCE FROM N.A.

us-10-009-823a-1.rup

Page

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116 TODGFLANDPSGFTLMGSRISNNPNIKKET--LEPIQLD--FN-DPTVAKSPAKTSTALNA 170
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                                                                                                                                                                                                                                                                    TRAINE-1992816; PubMed=11997336;

MEDLINE-21992816; PubMed=11997336;

MEDLINE-21992816; PubMed=11997336;

A Chen Y., Xu Y., Xu Y., Xu Y., Yung L., Dong W., Yang J.,

Chen Y., Xuu Y., Xu Y., Yung H.;

A complete sequence of the T. tengcongensis genome.";

Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan H., Chen R., Mang J., Yu J., Yang H.;

Tan H., Chen R., Mang J., Yu J., Yang H.;

Tan H., Chen R., Wang J., Yu J., Yang H.;

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Tan H., Chen R., Mang J., Yu J., Yang H.;

Tan H., Chen R., Mang J., Yu J., Yang H.;

The Cool 0003774; Fractural molecule activity; IEA.

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28.9%; Pred. No. 4e-24;
.ive 77; Mismatches 180; Indels 107; Gaps
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Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacter.
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                                                                                                                                                               NCBI_TaxID=119072;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                 ACTAINTE-2256410; PubMed=12700255;
WEDLINE-2256410; PubMed=12700255;
WHEDLINE-2256410; PubMed=12700255;
WHEDLINE-2256410; PubMed=12700255;
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Archarder Geneme sequence of the ammonia-oxidizing bacterium and
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Bacteriol. 185:2759-2773 (2003)

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Best Local Similarity 28.7%; Pred. No. 2.1e-24;
Matches 144; Conservative 84; Mismatches 169; Indels 104; Gaps
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01-UNM-2002 (TrEMBLrel. 21, Created)
01-UNM-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Flagellar basal body and hook proteins.
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STRAIN=ATCC 19718 / IFO 14298;
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RC STRAIN=ATCC 15692 / PAO1;

RX MEDILNE=2043737; PubMed=10984043;

RA STOVER C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Ackey M.J., Brinkman C.T., Erwin A.L., Minagle W.O., Kowalik D.J., Lagrou M., RA Garber R.L., Goltry D., Tolentino B., Westbrock-Wadman S., Yuan Y., RA Garber R.L., Goltry D., Tolentino B., Westbrock-Wadman S., Yuan Y., RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., RA Swith K.A., Salerer M.H., Hancock R.B.W., Lory S., Olson M.V.;

RA Reizer J., Salerer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

REMBL; AE004539; AAG04469.1; -.

BR PRIR; PR3310; R83510.

GO; GO:0005189; F:setructural molecule activity; IEA.

GO; GO:0005189; F:setructural molecule activity; IEA.

GO; GO:0005189; P:idiay/flagellar motility; IEA.

BR InterPro; IPR011491; PlaB.

BR InterPro; IPR011491; PlaB.

BR Pfam; PP06429; DUF1078; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 PSGFTLMGSRISNNPNIKKETLEPIQLD-FNDPTVAKSPAKTSTALNAVVNLGDSTDKTQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 SEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYF---DGAPSST-- 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTVTPF------DPSDAATYNSSSSLGIYDSQGNSHTMSQPFIKNEPDPNATPP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 PGFSIDATINVIQFSPA---TGNPPTP----GTGWIPAASD-CKTPPTYAWNCATGAASG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 IGTDIGKLPSMMPIQTSSGNSTARNGSSSTRRYS-----QDGYPQGDLVDVTITSE 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ATKDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKLQGKYSNSQVVDFYNIPLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLS 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 ---GSKTFEYLV-AMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKAMTAFTPTGS---
                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 527.5; DB 2; Length 462;
; Pred. No. 5.4e-24;
84; Mismatches 199; Indels 93,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48336 MW; 519616DABACE9C48 CRC64;
                                         01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Flagellar hook protein Flag.
Name=flgE; OrderedLocusNames=pA1080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF07559; FlaE; 1.
Pfam; PF00460; Flg bb rod; 1.
Complete proteome; Flagellum.
SEQUENCE 462 AA; 48336 MM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 150; Conservative
                                                                                                                                         Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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ACWAYA BERTHARY BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND BY AND 
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121 GONLTGYGVDATGKINTAVLTNLÓIPVND----LAPLATTNTÁFS--INL-DAAGTVPT- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 -----TIPFSATNSATFNESVSEGVYDGTGTSHMLTNYY--VRIAAGWDV 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 ----TQYGGGFNDTTVSQDGYATGRLASYSVGTDGTITGRYSNGRTSTLGQIAMINFKAP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 VGSVRIIFTQGAFEPGNSVTDLAIGGKGFFQV--TLEDKVHYTRAGNFRFTQDGFLNDPS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VTKVSQSFIQGNVTVTGNPLDIAINGIGFYRMVDASSGQVSYTRNGQFQIDKNGYIISAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 GFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSP-AKTSTALNAVVNLGDSTDKTQSE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 FEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATKDLNAWQPA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 PLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTS 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 DGLRREGNNHYSATLDSGGFEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQ 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 SGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSE 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 GATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 ANPYFALLESWKGNGTPPISTSN---YSYAQPWRVYDQQGNSHDITVYFDGAPSSTGSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=O6:H1 / CFT073 / ATCC 700928;
MEDLINE=2238234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 -----TGT----AGMSIANMDF-------TGT----TGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.4%; Pred. No. 1.6e-22; ive 85; Mismatches 168; Indels 110; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammagroteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                             19.4%; Score 502; DB 2; Length 401; 27.4%; Pred. No. 1.6e-22;
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005199; P:ciliary/flagellar motility; IEA.
InterPro; IPR011491; FlaE.
InterPro; IPR01144; Flag.
InterPro; IPR01144; Flag.
Ffam; PF06429; DUF1078; 1.
Ffam; PF06429; PIBE; 1.
Ffam; PF00460; Flag.
Ffam; PF00460; Flag.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Flagellar hook protein flgg.
Name=flgg; OrderedLocusNames=c1345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 ANAQTIKTEDTILÓTLVSMR 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 27.4
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GTNPKQVGLGMNVASIDTIHTQGAFQSTQKASDLGVSGNGFFILKEGKNLFYTRAGAFDV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 APASAAAIGTDIGKLPSMMPIQTSSG-----NSTARNGSSSTRRYSQDGYPQGDLVDV 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 IPITFNVLGANVGEVGEQQTVNLKLGTVGSYTDSITQFADSSSTKAIIQDGYGMGYMENY 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 TITSEGKLOGKYSNSQVVDFYNIPLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSN 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 EIDQNĞVIVGIYSNGIRRDLGKIALASFMNPGGLAKSGDTNFVETSNSGQVRIĞETĞLAG 390
                                                                                                                                                                                                                                                                                                                                                                                                                   56 SQGPNQAGMGAQVGSVRIIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 TODGFLNDPSGFTLMGSRISN--NPNIKKETLEPIQLDFND---PTVAKSPAKTSTALNA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 VVNLGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 ACNLDKRLPLIQEGANPADIARGTWVVNKS-------LYDSFGN---VSVL- 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 DGAPSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .--------<u>ELR-----</u>220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 ATKDINA---WQPAPLVNGLPQFSANFVGAGIQPLTLDF------GIKSQQNMWAG 337
                                                                                                                                                                                                                                                                                   1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGS----TG 55
                                                                                                                                                                                                                                                                                                                       Gaps
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 LGDIRSGVLEMANVDLAEQFTDMIVTQRGFQANAKTITTSDQLLQELVRLK 441
                                                                                                                                           19.7%; Score 509; DB 1; Length 442; ilarity 28.2%; Pred. No. 6.7e-23; Conservative 71; Mismatches 190; Indels 120;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
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Ralstonia solanacearum (Pseudomonas solanacearum).
           174 174 V -> I (in strain HB19).
192 192 N -> S (in strain HB19).
442 AA, 47389 MW, 561AC092B72C69BE CRC64;
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Last annotation update)
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GO; GO:0009288; C:flagellum (sensu Bacteria); IEA.
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01-MAR-2002 (TrEMBLrel. 20, Last sequ
01-MAR-2004 (TrEMBLrel. 26, Last anno
PROBABLE FLAGELLAR HOOK PROTEIN FLGE.
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MEDLINE=21681879; PubMed=11823852;
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                                                                                                                                       Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                             Matches 150;
                                        VARIANT
SEQUENCE
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              VARIANT
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70 SVRTIFTQGAFEPGNSVTDLAIGGKGFFQ-VTLEDKVHYTRAGNFRFTQDGFLNDPSGFT 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 LTGYPATGTPPTIQQGANPTNISIPNTLMA---AKTTTTASMQINL-NSSDSLPSV---- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 FALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSSTGSKTFEYLVAM 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 ----VKTGDNKWQVY--- 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 NPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATKD-----LNAWQPAPL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 --TQDSSDPTGTAEPAM----TLVFNANGVL-----TSDPTKDITTGAINGADPA-- 255
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                                                                                                                                                                                                                                                                          19.3%; Score 498; DB 2; Length 401;
28.7%; Pred. No. 2.8e-22;
ive 74; Mismatches 171; Indels 110; Gaps
                                                                                                                                                                                                                                                                                                                                                 41978 MW; F9689023E643510F CRC64;
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01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Flagellar hook protein flgs.
Name=flgE; Synonyms=flaK, fla FV;
OrderedLocushames=STM1177, STV1216, t1743;
Salmonella typhimurium, and
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                Homma M., Derosier D.J., McNab R.M., "Flagellar hook and hook-aesociated proteins of Salmonella typhimurium and their relationship to other axial components of the flagellum."; J. Mol. Biol. 213:819-832(1990).
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MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                            SPECIES-S typhimurium, STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K.; Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C.W., Mungall K.L., Benley S.D., Holden M.T.G., Sebalhia M., Baker S., Basham D., Brooks K., Chillingworth T., Connection P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltweil T., Mamlin N., Hague A., Hier T.T., Hollroyd S., Jagels K., Krogh A., Lareen T.S., Leather S., Moule S., O'Gaora P., Parry C., Whitehead S., Barrell B.G., Whitehead S., Barrell B.G., Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 185:2330-2337(2003).
-i- SIMILARITY: Belongs to the flagella basal body rod proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES=S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
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EMBL, AE008751, AAL20107.1; -.
EMBL, AE016840, AA069367.1; -.
EMBL, AE016840, AA069367.1; -.
EMBL, SE016840, AA069367.1; -.
PIR, S10365, S10365.
StyGene, SG10104; F1GB.
InterPro, IPR010430, DUF1078.
InterPro, IPR01044; F1G_bb_rod, Pfam, PF06429; DUF1078; 1.
PROSITE; PS00588; FLAGELIA_BB_ROD; 1.
PROSITE; PS00588; FLAGELIA_BB_ROD; 1.
COMPLETE PROCEOME; F1G_BB_ROD; 1.
SEQUENCE 402 AA, 42079 WW; ADB262981
                                                                                                            SPECIES=S.typhimurium;
MEDLINE=90294298; PubMed=2193164;
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                                                  NCBI_TaxID=602, 601;
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MEDLINE=21156231; PubMed=11258796;

Hayashi T. Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Mirata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterchemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. B:11-22(2001).

RR InterPro; IPR010491; Flag.

InterPro; IPR011491; Flag.

InterPro; IPR011491; Flag.

R InterPro; IPR011491; Flag.

R Pfam; PF06429; DUF1078; I.

R Pfam; PF06459; Plag. I.

R Pfam; PF06459; Plag. I.

R Pfam; PF004560; Rlg_bb_rod; I.

R PROSITE; PS00588; FLAGELIA_BB_ROD; I.
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28.7%; Pred. No. 2.8e-22;
.ive 76; Mismatches 167; Indels 114; Gaps
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Flagellar hook protein Flgs.
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Query Match
Best Local Similarity 28.7%
Matches 144; Conservative
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70 SVRTIFTQGAFEPGNSVTDLAIGGKGFFQ-VTLEDKVHYTRAGNFRFTQDGFLNDPSGFT 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 --TQDSSDPTGTAEPAM----KLVFNANGVLTSNPTENITTGA----INGAEPA---- 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 RNGSSSTRRYSQDGYPQGDLVDVTJTSEGKLQGKYSNSQVVDFYNIPLARFTSEDGLRRE 427
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SEQUENCE FROM N.A.

MEDLINE=21074933; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kikkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shoo Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Melor R.A., Blattner F.R.,
"Genome sequence of entrophagement of schwirtinia coli 0157:H7.",
Nature 409:529-533(2001).
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                           19.1%; Score 493; DB 2; Length 401;
28.7%; Pred. No. 5.6e-22;
ive 76; Mismatches 174; Indels 102;
                                    401 AA; 42014 MW; 453B39179717CB14 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annocation update)
Flagellar biosynthesis, book protein.
Name=flgE, OrderedLocusNames=z1714;
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                                                                                                                                   Best Local Similarity
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Flagellum.
SEQUENCE
                                                                                    Query Match
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D.J.,

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Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose Mau B., Shao Y.;
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                                                                                       MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                      Echobase; EB4017; -. Echobase; EG14269; flgE. InterPro; IPR010330; DUF1078. InterPro; IPR01444; Flag bb_rod.
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Best Local Similarity 28.8%
Matches 143; Conservative
                                                              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                       19.1%; Score 493; DB 2; Length 401; 28.7%; Pred. No. 5.6e-22; ive 76; Mismatches 174; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flagellar hook protein figs.
Name=flgs; Synonyms=flaK, fla FV; OrderedLocusNames=bl076;
Escherichia coli.
                                                                                           Pfam; PP00460; Flg bb rod; 1.
PROSITE; PS00588; FLAGELLA BB ROD; 1.
Complete proteome; Flagellum.
SEQUENCE 401 AA; 42014 MW; 453B39179717CB14 CRC64;
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEGO; GO:0005199; P:ciliary/flagellar motility; IEA.
InterPro; IPR011930; DUF1078.
InterPro; IPR011491; FlaE.
InterPro; IPR01444; Flag.bb_rod.
Pfam; PF06429; DUF1078; 1.
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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
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KTQDQILNTLVNLR 401
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------VIPFSASNADSYNKKGSVTVFDSQGNAHDMSVYF----VKTGDNNWQ-- 208
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                                                                                                                                                                                                                                                            Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
Yano M., Horiuchi T.,
Pano M., Boriuchi T.,
Dia sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
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Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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Pfam; PF00460; Flg_bb_rod; 1.
PROSITE; PS00588; FLAGELLA_BB_ROD; 1.
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296 VAAKNAINAVKSQTGIEAYLDGKQLRLENTNELDGDEKLKNIVVTQAGTGAFANFLDGDK 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 476 KFTHATHATSIDVIDSLGTKHAMRIEFYRSGGAEWNFRVIVPEPGELVGGSAARPNVFEG 535
                                                                                                                                         236 LYNEDGDALLLNENOGİWVSYKSAKMVKDILPSAENSTLELNGVKISFTNDSAVSRTSSL
           TST--ALNAVVNLGDSTDKTQSEANPYFALLESWK--GNGTPPISTSNYSYAQPMR----
                                                                                                                                                                                                                                                                                                                                                                                                          416 QYGMFEINNKDNKNVİKENLNIFVSGYSSDSVTNNVLFKNAMKGLNTASLIEGGASASSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 ASNRISMRANIANGRHADQTAA----VFALDSSAKTPSDGINPVYDSGTNLAQVAEDMGS
                                                                                                                                                                                        245 LVAMNPSEDGSAASG----TDSAGLLMSGTMTFSSNGELKN-----
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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OrderedLocusNames=lmc0697;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRFTQDGFLNDPSGFTLM-----GSRISNNPNIKKETLEPIQLDFNDPTVAKSPAK 163
                                                            326 SEGDNVWSATQSSGVALLGTAGTAGTGRFGTLTNGALBASNVDLSKELVNMIVAQRNYQSNAQ 385
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                                            REGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMNSK 485
275 VAT------TQNGYKPGDLVSYQINDDGTVVGNYSNEQTQLLGQIVLANFANNEGLA 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=99120557; PubMed=9923682; DOI=10.1038/16495; Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Urita Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-!- SIMILARITY: Belongs to the flagella basal body rod proteins
                                                                                                                                                                                                                                                                                                                                                                                                                    Namē-flgE; OrderedLocusNames-JHP0804;
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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18.8%; Score 485; DB 1; Length 718;
Best Local Similarity 25.0%; Pred. No. 3.8e-21;
Matches 181; Conservative 94; Mismatches 222; Indels 226;
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PIR, G71888, G71888.
InterPro: IPR010930; DUF1078.
InterPro: IPR010910; Flagellin IN.
InterPro: IPR01444; Flag_bb_rod.
Pfam, PF00429; DUF1078, 1.
Pfam; PF00460; Flagellin IN; 1.
PROSITE; PS00588; Flagellin IN; 1.
COMPICE PROCESSE; Flagellin BB. ROD; FALSE_NEG.
COMPICE PROCESSE; Flagellin BB.
COMPICE 718 AA; 76280 MW; DF6A0500D8EF481D
                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Flagellar hook protein flgs.
                                                                                                                                                                                                                                                                                          718 AA.
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386 TIKTQDQILNTLVNLR 401
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439

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SEQUENCE FROM "A. A.

SECUENTIAL ENGRAPOR NOTA"

A Glaser P. Frangeul L., Buchrieser B., Rusmiok C., Amend A.,

A Glaser P., Frangeul L., Buchrieser B., Chakraborty T.,

B Baquero F., Bernde P., Chakraborty T.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Densurget O.,

A Domann B., Dominguez-Bernal G., Duchaud E., Durrant L., Dussurget O.,

Entian K.-D., Feihi H., Garcia-del Portillo F., Garrido P.,

A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

A Jones L. M., Kaeft J., Kuhn M., Kunst F., Kurapkat G.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

A Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

"Comparative genomics of Listeria species.",

"Comparative Galselloss",

"RMBL, Alsollof, CAC98775.1, -.
Listeria monocytogenes.
Bacteria, Firmicutes; Bacillales; Listeriaceae; Listeria.
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Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
A Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
A Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlich G.A.,
Bayles D.O., Luchansky J.B., Fraser C.M.;
"Whole genome comparisons of serotype 4b and 1/2a strains of the food-
mone pathogen Listeria monocycogenes reveal new insights into the
core genome components of this species.";
L Nucleic Acids Res. 23.2386.2395(2004).
InterPro; IPR010930; DUF1078.
R InterPro; IPR010930; DUF1078.
R InterPro; IPR01444; Flag.
R InterPro; IPR01444; Flag.
R Pfam; PF06429; DUF1078;
R Pfam; PF06429; PURE; 1.
                                                                                                                                                                                                                                                                           Pfam; PF00460; Flg_bb_rod; 1.
PROSTITS, PS00588; FLAGELLA BB_ROD; 1.
Complete protecme; Flagellum.
SEQUENÇE 411 AA; 42820 MW; BS84C931539B461D CRC64;
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OrderedLocusNames=lin0705;
Listeria innocua.
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                                                                                                                                                                                                                                                                         Query Match 18.7%; Score 484.5; DB 2; Length 411;
Best Local Similarity 27.0%; Pred. No. 1.9e-21;
Matches 137; Conservative 77; Mismatches 188; Indels 105; Gaps
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PubMed=15115801; DOI=10.1093/nar/gkh562;
Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listeria monocytogenes (serotype 4b / strain F2365).
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                Listilist; LM00697; -..

Go; GO:000374; F:mocractivity; IEA.

Go; GO:000374; F:motra activity; IEA.

Go; GO:000159; F:motra activity; IEA.

Go; GO:000159; F:motra molecule activity; IEA.

Go; GO:000159; F:motray/flagellar motility; IEA.

InterPro; IPR01449; FlaE.

InterPro; IPR0144; FlaE.

Pfam; PF06429; DUF1078; I.

Pfam; PF06459; PlaE; I.

Pfam; PF06459; FlaE; I.

Pfam; PF06460; FlaE; I.

Pfam; PF06460; FlaE; I.

Pfam; PF06460; FlaE; I.

PFAFER: PF06460; FlaE; I.

PFAFER: PF06460; FlaE; I.

PFOFER: PF06460; FlaE; I.

PFOFER: PF06460; FlaE; I.
                                                                                                                                                                                                                                            411 AA; 42836 MW; 3272D338BB4E1A7C CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Flagellar hock protein FlgE, putative.
OrderedLocusNames=LMOf2365_0733;
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                                                      Gaps
18.7%; Score 484.5; DB 2; Length 411; 27.0%; Pred. No. 1.9e-21; tive 77; Mismatches 188; Indels 105;
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C STRAING—CITE 11262 / Serovar 6a;

MEDLINB=21537279; PubMed=11679669;

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

A Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez Bernal G., Duchaud E., Durant I., Dussurget O.,

A Brian K.D., Falih H., Garcia-del Portillo F., Garrido P.,

A Gautier I., Goobel W., Gonez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

A Madueno E., Matrournam A., Mata Vicente J., Ng E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Raquez Boland U.-A., Voss H., Wehland J., Cossart P.,

Science 224:849-852(2001).
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Best Local Similarity 27.0%; Pred. No. 1.9e-21;
Matches 137; Conservative 77; Mismatches 188; Indels
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Listilist; INN0705; -...
Listilist; INN0705; -...
InterPro: IPR011491; Flas.
InterPro: IPR011491; Flas.
InterPro: IPR01444; Flas.
Efam; PF06429; DUF1078; 1...
Pfam; PF06429; PIBZ; 1...
Pfam; PF00460; Flaz; 1...
Complete protecome: SEQUENCE 411 AA; 42836 MW; 3272D3388
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Listeria monocytogenes str. 4b F2365.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria;
Listeria monocytogenes.
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Matches 137; Conservative 77; Mismatches 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANPY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 GLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTSSGNS 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 TARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSEDGLR 425
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MEDLINE-22592274; PubMed=12704152;

MEDLINE-2559274; PubMed=12704152;

MEDLINE-2559274; PubMed=12704152;

MEDLINE-2559274; PubMed W.F., Pulmkett G. III, Rose D.J., Darling M., Pornnier G., Mayhaw G.F., Plunkett G. III, Rose D.J., Zhou S., May B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., And B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., C., Blattner P.R., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., C., Blattner P.R., Man B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., L. Lifect. Immun. 71:275-2786 (2003).

The Complete genome sequence and comparative genomics of Shigella (In Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infert. Infe
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Best Local Similarity 28.4%; Pred. No. 2.1e-21;
Matches 141; Conservative 77; Mismatches 173; Indels 105; Gaps
                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Flagellar hook protein FlgE.
Name-flgE; OrderedLocusNames=S1160;
Shigella flexneri.
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PROSITE; PS00588; FLAGELLA BB ROD; 1.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                      O7UCX0;
01-OCT-2003 (
01-OCT-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 FALLESWKGNGTPPISTSN---YSYAQPMRVYDQQGNSHDITVYFDGAPSSTGSKTFEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 SGLNAAATNLDVIGNNIANSATYGFKSGTASFADMFA-----GS----KVGLGVKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 LIGYPVIGTPPTIQQGANPINISIPNILMA---AKTITTASMQINL-NSSDPLPI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 105; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=301 / Serotype 2a, MEDLINE=22272406; PubMed=12384590; Jin W., Wang J., Liu H., Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J. Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                          01-JUN-2003 (TFEMBLrel. 24, Last sequence update)
01-MAR-2004 (TFEMBLrel. 26, Last annotation update)
11 gellar blosynthesis, hook protein.
Name-figgs, OrderedLocusNames-SF1080;
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.7%; Score 483.5; DB 2; 28.4%; Pred. No. 4e-21; tive 77; Mismatches 173;
                                                                                                                                   642 AA
                                                                                                                                                                                Created)
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387 TIKTQDQILNTRVNLR 402
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329 SPEGDNAWSETASSGQAVVGLAGTGSLGKLIGKSTESSNVDLSKELVSMIVAQRNYQSNA 388
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MEDLINE=22882897; PubMed=14500908;

Mandakumar R., Gross M., Raddatz G., Simon J., Lanz C., Klimmek O.,

Mandakumar R., Gross M., Rosinus A., Keller H., Jagtap P., Linke B.,

Mayer F., Lederer H., Schueter S.C.;

"Complete genome sequence and analysis of Wolinella succinogenes.";

"Complete genome sequence and analysis of Wolinella succinogenes.";

"Complete genome sequence and analysis of Wolinella succinogenes.";

"Complete genome sequence and analysis of Wolinella Succinogenes.";

"Complete genome sequence and analysis of Wolinella Succinogenes.";

"Complete genome sequence and analysis of Wolinella Succinogenes.";

"Complete genome sequence and analysis of Wolinella Succinogenes.";

"Complete genome sequence and analysis of Wolingenes.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAI----GSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MIRSLWSGVSGMQAHQVALDVEGNNIANVNTTGFKYSRANFSDMLSQVNRIATSPYGGLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTOVNIDANLTAGDITDKLGCMYALDSTSVTAADGIAARYDSAGN-----KIQMAE
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           RREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMNS
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Helicobacteraceae; Wolinella.
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                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                         716 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLAGELLAR HOOK PROTEIN.
Name=FLGE; OrderedLocusNames=WS1758;
                                                                                                                                                                                                                                                                                                                                                                                Created)
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Pfam; PF00460; Flg_bb_rod; 1.
Complete proteome; Flagellum.
SEQUENCE 716 AA; 74684 MW; 2
                                                                                                                             KSVTTADTMLQKALELK 501
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QTIKTQDSILQTLVSLR 405
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                    TARNGSSSTRRYSODGYPOGDLVDVTITSEGKLOGKYSNSQVVDFYNIPLARFTSEDGLR 425
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Bell K.S., Sebainia M., Pritchard L., Holden M., Hyman L.J.,
Holeva M.C., Thomson N.R., Bentley S.D., Churcher C., Mungall K.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Barrell B.G., Parkhill J., Toth I.K.;
Submitted (PEB-2004) to the EMBL/GenBank/DDBJ databases.
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--TGANNI
                                                                                                                                                                   426 REGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMNSK
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405 AA; 41910 MW; 687FB7C32380814B CRC64;
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01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flagellar hook protein.
Name=flgE; Synonyms=flak; ORFNames=ECA1705;
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     ---TESLSFLNS--------MQQN
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Best Local Similarity 28.6
Matches 142; Conservative
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STRAIN=ATCC 33913 / NCPPB 528;

MEDLINE=2202145; PubMed=12024217;

A Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

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Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Retubal J.C., Kitajima J.P.;
532 EGGRVTFGEDGGLTGMNPPTIQFNPKS------GA-SSPQRIDLDFG-----VSGTFQ
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                                                                                                                                                                                                      ------OPAPLVNGLPQPSANF
                                                                         -----TDSAGLLMSGTWT
                                                                                                                     352 DNSITAFRYAYTTASDADSTSRLFRTTEDLRALLQQDANNIKHGGGYVDSTGTNASVKVT
                                                                                                                                                                                                                                                                                                                    472 SASLMAAKHTATTDIVDSLGNKHTLTVTFRKVGPQEWSFSLHVPEPATFVNGSGERPNYF
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Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae, Xanthomonas.
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EMBL; AE01299; AAM1238-1; -.

EMBL; AE01299; AAM1238-1; -.

GO; GO:0009288; C:flagellum (sensu Bacteria); IEA.

GO; GO:000374; F:motor activity; IEA.

GO; GO:000189; F:structural molecule activity; IEA.

GO; GO:0001539; P:ciliary/flagellar motility; IEA.

InterPro; IPR010930; DUF1078.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 26, Last annotation update)
Flagellar biosynthesis, hook protein.
Name=flgE; OrderedLogusNames=XCC1949;
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SKTVTTSDQILNTLLQLKQ 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 IQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 SVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRFTQDGFLNDPSGFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 NPYFALLESWKGNGTPPISTSNYSYAQ-PMRVYDQQGNSHDITVYFDGAPSSTGSKTFFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 LVAMNPSE------DGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATKDLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 WOPAPLVNGLPOFSANFVGAGIOPLTLDFGIKSQONMWAGAPASAAAIGTDIGKLPSMMP
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STRAIN=306 / ATCC 13902 / XV 101;

MEDINE=22022145; PubMed=12024217;

MEDINE=22022145; PubMed=12024217;

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Cicarelli R.M.B., Couteinho L.L., Cursino-Santos J.R., El-Dorry H.,

Farla J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
                                                                                                                                                                                                                                                            Query Match
18.6%; Score 481; DB 2; Length 407;
Best Local Similarity 27.2%; Pred. No. 38-21;
Matches 137; Conservative 77; Mismatches 174; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonas axonopodis (pv. citri).
Bacteria; Forthomonadales;
Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=92829;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 ------TGAGV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8PL23 PRELIMINARY; PRT; 407 AA.
PRELIA:
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Flagilar biosynthesis hook protein.
Name=flgE; OrderedLocusNames=XAC1983;
InterPro; IPR011491; FlaE.
InterPro; IPR001444; Flag_bb_rod.
Pfam; PF0649; DUF1008; 1.
Pfam; PF0649; PlaB; 1.
PROM10; PF00460; FlaB; 1.
PROSITE; PS00588; FLAGELLA BB.ROD; 1.
COMPLETCEOME; Flagellum:
SEQUENCE 407 AA; 42710 MW; 307EB1287BE2B079 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 RNFQANSQMISTQDQVTQTIINIR 407
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Retaughieri E.F., Franco M.C., Greggio C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Rating E.C., Machada M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machada M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machada M.A., Chura V.K., Oliveira M.C., Oliveira V.R.,

Recira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.P.,

Spinola L.A.F., Takita M.A., Truffi D., Teai S.M., White F.F.,

Trindade Gos Santos M.Y., Truffi D., Tsai S.M., White F.F.,

Trindade Gos Santos M.Y., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.,

"Comparison of the genomes of two Xanthomonas pathogens with differing

those specificities ".

"Mature 417.459-463(2002).

"EMBL, AE011833; AAM36845.1; -.

"GO; GO:00029288; C:flagellum (sensu Bacteria); IEA.

"GO; GO:0001939; F:structural molecule activity; IEA.

"GO; GO:0001939; F:structural molecule activity; IEA.

"GO; GO:0001939; F:structural molecule activity; IEA.

"GO; GO:0001939; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:structural molecule activity; IEA.

"GO; GO:000599; P:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 SVRIIFIQGAFEPGNSVIDLAIGGKGFFQVILEDKVHYTRAGNFRFIQDGFLNDPSGFTL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 --QVFAPNPSGNGFDVGRLSDLOLLTTD----SPPKSTSTVNLAFTLPGNATAPTVTPF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 NPYFALLESWKGNGTPPISTSNYSYAQ-PMRVYDQQGNSHDITVYFDGAPSSTGSKTFEY 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 V-----DGAAVGAPTTLOFSDTGALTTPANGIIA-MDPFTPS------ 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 NGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTSSGN 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LIMMÖLNVTG 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 TGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGFNQAGMGAQVG 69
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ive 80; Mismatches 181; Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 407;
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PROSTITE; PS00588; FLAGELLA BB_ROD; 1.
Complete proteome; Flagellum.
SEQUENCE 407 AA; 42762 MW; 57E2E732E6069F9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.6%; Score 481; DB 2; 27.0%; Pred. No. 3e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 134; Conservative
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FLGE_HELPY
                     RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA RAARA 
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718 AA.

PRT;

FLGE HELPY STANDARD; FPSO610; 01-OCT-1996 (Rel. 34, Created)

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                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97394467; Pubwed=9522185; DOI=10.1038/41483;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Teleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
Dougherty B.A., Nelson K.B., Quackenbush J., Zhou L., Kirkness B.F.,
Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
Glodek A., Nokeney K., Fitzgerald L.M., Lee N., Adams M.D.,
Hickey B.K., Berg D.E., Goayne J.D., Utterback T.R., Peterson J.D.,
Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.;
Matth H.O., Fraser C.M., Wenter J.S., Borodovsky M., Karp P.D.,
Smith H.O., Fraser C.M., Wenter J.S.,
"The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: A flexible structure which links the flagellar filament to the drive apparatus in the basal body. Absence of the gene tadast to absence of the hook protein, lack of the flagellar filament and thus loss of mobility. Approximately wild-type levels of the flagellar subunits are still produced and accumulate mostly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Envelope.

MISCELLANBOUS: The N-terminal amino acid sequence was from strain CCUG 951; the DNA sequence was from strain CCUG 17874. Disruption and subcellular localization experiments were performed for both strains. The apparent DI for the hook protein was 5.1.

SIMILARITY: Belongs to the flagella basal body rod proteins
                                                                                                                                                                                                                                                                 O'Toole P.W., Kostrzynska M., Trust T.J.;
"Non-metile mutants of Helicobacter pylori and Helicobacter mustelae defective in flagellar hook production.";
Mol. Microbiol. 14:691-703(1994).
                                                                               Helicobacter pylori (Gampylobacter pylori).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
                                                                                                                                                                                                   AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLET FOLSON DIRECT PROTEIN Sequencing; Flagellum. CONFLICT 237 23 -> N (in Ref. 1). CONFLICT 253 259 C -> Y (in Ref. 1). CONFLICT 253 259 C -> Y (in Ref. 1). CONFLICT 373 374 DI -> NS (in Ref. 1). CONFLICT 413 414 SV -> TI (in Ref. 1). CONFLICT 413 414 SV -> TI (in Ref. 1). SEQUENCE 718 AA; 76206 MM; F36EB60684AD1333 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR010930; DUF1078.
InterPro; IPR010810; Flagellin IN.
InterPro: IPR001441; Flagellin IN.
Pfam; PF06429; DUF1078; 1.
Pfam; PF07156; Flagellin IN; 1.
Pfam; PF07156; Flagellin IN; 1.
PROSITE; PS00588; FLAGELLA_BB_ROD; FALSE_NEG.
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2004 (Rel. 65, Last annotation update)
Flagellar hook protein flgE.
Name=flgE, OrderedLocusNames=HP0870;
                                                                                                                                                                                                SEQUENCE FROM N.A., SEQUENCE OF 1-25, AND CHA
STRAIN≈CCUG 17874 / NCTC 11638, and CCUG 951;
PubMed≈7891557;
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PIR; F64628; F64628.
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695 / ATCC 700392;
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                                                                                                                                                          NCBI_TaxID=210;
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RXX
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                                                                                                                         113 FRFTQDGFLNDPSGFTLM-----GSRISNNPNIKKETLEPIQLDFNDPTVAKSPAK 163
                                                                                                                                       164 TST--ALNAVVNLGDSTDKTQSEANPYFALLESWK--GNGTPPISTSNYSYAQ----- 212
                                                                                                                                                                                                                                                                                                              415
                                                                                                                                                                                    180 ASNRISMRANLNAGRHADQTAA----IFALDSSAKTPSDGINPVYDSGTNLAQVAEDMGS 235
                                                                                                                                                                                                                      236 LCNEDGDALLIANENQGIWVSYKSAKWYKDILPSAENSTLEINGVKISFTNDSAVSRISSL 295
                                                                                                                                                                                                         -----PMRVYDQQG-----SSTGSKTFEY 244
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                                                                                   57 QGPN--QAGMGAQVGSVRIIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKV--HYTRAGN
                                           MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGS----IGS
                                                                1 MLRSLWSGVNGMQAHQIALDIESNNIANVNTTGFKYSRASFVDMLSQVKLIATAPYKNGL
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 26, Last sequence update)
Flagellar hook protein Flag.
Name-flag. 1 OrderedLocusNames=HH1704,
Helicobacter hepaticus.
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales;
Helicobacteraceae, Helicobacter.
    Query Match
Best Local Similarity 24.6%; Pred. No. 6.7e-21;
Matches 178; Conservative 96; Mismatches 223; Indels 226;
                                                                                                                                                                                                                                                LVAMNPSEDGSAASG----TDSAGLLMSGTWTFSSNGELKN-
                                                                                                                                                                                                                                                                                     282 -MTAF----TPTGSATKDIMAWQPAPLVNGLPOFSANFV---
                                                                                                                                                                                                                                                                                                                              DFG-----IKSQQNMW-----
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[1] SEQUENCE FROM N.A. NCBI_TaxID=32025;

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REDLINE=22709201; PubMed=12810954;
RA MEDLINE=22709201; PubMed=12810954;
RA Suerbaum S., Oscanhans C., Sterzabach T., Drescher B., Brandt P.,
RA Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
RA Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
RA Schuer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
RT Gonglete genome sequence of the carcinogenic bacterium
RT Helicobacter hepaticus."; Frosch M., Fox J.G.;
RT Helicobacter hepaticus."; Trosch M., Fox J.G.;
RD GO.0002189; C. Flagellum (sensu Bacteria); IEA.
DR GO; GO.0005198; F. Sentuctural molecule activity; IEA.
DR GO; GO.0005198; F. Sentuctural molecule activity; IEA.
DR GO; GO.0005199; P. Ciliary/flagellar motility; IEA.
DR GO; GO.0005199; P. Ciliary/flagellar motility; IEA.
DR InterPro; IPRO10491; Flag.
DR InterPro; IPRO10491; Flag.
DR InterPro; IPRO10491; Flag.
DR Fam.; PRO559; Flagellin IN.
DR Pfam.; PRO7559; Flagellin IN; I.
DR Pfam.; PRO7559; Flagellin IN; I.
DR Pfam.; PRO7560; Flagellin IN; I.
DR Pfam.; PRO766; Flagellin IN; I.
Commister arrorecame: Flagellum.
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Pred. No. 8.8e-21;
0; Mismatches 209;
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Conservative 90;
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SEQUENCE : 718 AA; 77099 MW;
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- Search completed: October 26, 2004, 09:09:00 Job time : 206 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame plus p2n model

October 31, 2004, 02:44:06; Search time 3026 Seconds (without alignments) 6045.190 Million cell updates/sec Run on:

US-10-009-823A-1 2586 1 MMGSLFIGATGMXTHSTGLG......NSKSVTTADTMLQKALELKR 502 Title: Perfect score: Sequence:

BLOSUM62 Scoring table:

0 0 0 0 0 0 0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

32822875 segs, 18219865908 residues

65645750 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST: * Database :

995 est1: 995 est2:: 995 est4:: 995 est4:: 995 est5:: 995 gss2:: 995 gss2::

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

-	Description	BH370667 AG-ND-165	BZ577315 msh2 5350	BZ556688 pacs1-60	BH795484 23H03LLIO	BZ563024 pacs2-164	CF891171 UI-CF-DU1	BZ577405 msh2_5391	CB065273 EST64954	CO423013 GGEZHT102
	ID	BH370667	BZ577315	BZ556688	BH795484	BZ563024	CF891171	BZ577405	CB065273	CO423013
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onerv	Length	11.4 729	891	1319	742	1105	752	895	565	868
Ouerv	Match	11.4	10.5	9.8	8.5	8.3	8.1	8.1	8.0	7.8
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ALIGNMENTS

GSS 10-DEC-2001 Other GSS8: AG-ND-165N21.TR
Contact: Brendan V Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
Thy Institute for Genomic Research
Thy 2 Medical Center Dr., Rockville, ND 20850, USA
This 301 838 9543
Eax: 301 838 3543
Eaxi: 101 910 ftusefirgr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
P.H. Collins and sequenced by The Institute for Genomic Research Anopheles.

1 (bases i to 729)
Hong Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J., Ren, C., Huff, E.R., Carlile, J.L., Black, K., Zhang, H.-B., Gardher, M.J. and Collins, F.H.
Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African malaria mosquito Anopheles gambiae
Mol. Genet. Genomics 268 (6), 720-728 (2003) Anopheles gambiae (African malaria mosquito) Anopheles gambiae Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; AG-ND-165M21.TF ND-TAM Anopheles gambiae genomic clone AG-ND-165M21, genomic survey sequence. linear DNA 729 bp BH370667.1 GI:17316792 GSS. VERSION KEYWORDS SOURCE ORGANISM RESULT 1 BH370667/c DEFINITION JOURNAL MEDLINE PUBMED COMMENT REFERENCE AUTHORS ACCESSION TITLE

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Percent Similarity:
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(TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas A?M 13-2123, USA using a HindIII Seq primer: M13 For Class: BAC ends.
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                                                                                                                                                                                                                    /db_xref="taxon:7165"
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/clone lib="ND-TAM"
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Conservative:
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/organism="Anopheles gambiae"
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891 bp DNA linear GSS 17-DEC-2002 msh2 5350.x1 msh Pseudomonas aeruginosa genomic clone msh2_5350, pseconic survey sequence.
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Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Spencer, D.H., Raymond, C.K., Smith, B.E., Sims, B.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Mhole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
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487 ValThrThrAlaAspThrMetLeuGlnLysAlaLeuGluLeuLys
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/strain="MSH"
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Mismatches:
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University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066657244
Email: craymond@u.washington.edu
Class: shotgun:
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pacs2-164_405.s1 pacs2-164 Pseudomonas aeruginosa genomic clone
pacs2-164_405, genomic survey sequence.
BZ563024_405, genomic survey sequence.
BZ563024.1 GI:27186093
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                                                              316 GlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsnMetTrp 335
                                                                                                                                       336 AlaGlyAlaProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLysLeuProSerMet 355
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Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadacea; Pseudomonas.
1 (bases 1 to 1105).
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, T.L., Kaul, R. and Olsen, M.V.
Mhole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
                                                                                      577 GTTGGTGATCAATTAATGTATACAAGAGCAGGTGCTTTTAAACTTAATCAGGATGGGACT
                                                                                                                                                                                                                                                                                                            631 ACAGGTAATCCTCTAAATATGGCTATTGAAGGCAAAGGGTTTTCACAAGTA-----TTG
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Box 352145, Seattle, WA 98105-2145, 1
Tel: 2062216954
Exa: 2066897244
Email: craymond@u.washington.edu
                           US-10-009-823A-1 (1-502) x BH795484 (1-742)
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801 AACAGCGTGCTGGACCTGCCCATCAACGGCAACGGCTTCTTCGTCACCAGCAAACAACGG 860
                                                                                                                                                                                        ------GluThr 144
                                                                                                                                                                                                                                                           145 LeuGluProlleGlnLeuAspPheAsn-----AspProThrValAlaLysSerPro 161
                                                                                                                                                                                                                                                                                                                                 162 AlaLysThrSerThrAlaLeuAsnAlaValValAsnLeuGlyAspSerThrAspLysThr 181
                                                                                                                                                                                                                                                                                                                                                                                                                    201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deltaproteobacteria; Desulfovibrionales;
                                   104 LysValHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAsp
                                                                                                           124 ProSerGlyPheThrLeuMetGlySerArglleSerAsnAsnProAsnIleLysLys---
                                                                                                                                           920 CACAACCGTTACCNGCTGCAGGGCTTTGCGTCNGGCCGAACGGCCAGTTGCAGAACNGGT
                                                              182 GlnSerGluAlaAsnProTyrPheAlaLeuLeuGluSerTrpLysGlyAsnGlyThrPro
                                                                                                                                                                                                                                                                                                                                                             1091 GGCCGTACCTAAACTGGTCTC-----TTGGTTGGGATT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zhang, O
Department of PathoBiology
University of Minnesota
1971 Commonwealth Ave. St. Paul, MN 55108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      742
62
33
87
12
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/organism="Lawsonia intracellularis"

/mol_type="genomic DNA"

/db_xref="taxon:29546"

/clone_lib="Lawsonia library"

/note="Vector: pUC18; Site_1: Smal"
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Matches:
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Gaps:
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Bacteria, Proteobacteria; Delt.
Desulfovibrionaceae; Lawsonia.

(bases I to 742)
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BH795484
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shotgun.
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Email: qing@ahc.um
Class: shotgun.
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Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayd by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cf.html
Seq primer: MI3 FORWARD
POLYA=No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 ProlleGlnThr-----SerSerGlyAsnSerThrAlaArgAsnGlySerSer 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 TACCGCAACCCGCCCACCGACGGTTACGCCACCGGTCAAATCACCGGGCTGAAATC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 ThrSerGluGlyLysLeuGlnGlyLysTyrSerAsnSerGlnValValAspPheTyrAsn 412
                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 75.
Bonaldo, M.F., Lemnon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866
Fax: 319 356 7171
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Conservative:
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                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
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209.00
50.00%
31.08%
8.08%
               sapiens (human)
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                                                                                                                                                                                                                                                    University of Iowa
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                                                                                                                                                                                                                                                                                                                                                362 rGlyAsnSerThr-----AlaArgAsnGlySerSerSerFrThrArgArgTyrSerGlnAs 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 pGlyTyrProGlnGlyAspLeuValAspValThrIleThrSerGluGly-LysLeuGlnG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 ThrMetThrPheSerSerAsnGlyGlu-----LeuLysAsnMetThrAlaPheThr 286
                                                                                                                                                                                                                                                                                                                                                                                               287 ProThrGlySerAlaThrLysAspLeuAsnAlaTrpGlnProAlaProLeuValAsnGly 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 LeuProGlnPheSerAlaAsnPheValGlyAlaGlyIleGlnProLeuThrLeuAspPhe 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           912 TTGTTACCGTTTTCG-----GTGTCCTCGGGA-----CCCAGAGATCTTAACCCC 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 Gly---IleLysSerGlnGlnAsnMetTrpAlaGlyAlaProAlaSerAlaAlaIle 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ACATTG 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 GlyThrAspIleGlyLysLeuProSer-MetMet------ProIleGlnThrSerSe 362
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             /db_xref="taxon:287"
/clone="pac82-164_405"
/clone_lib="pac82-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library."
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Matches:
Conservative:
Mismatches:
Indels:
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strain="2-164"
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214.00
47.03%
32.63%
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Best Local Similarity:
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94

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CB065273 565 bp mRNA linear EST 21-JAN-2003 EST644954 HOGA Medicago truncatula cDNA clone HOGA-1C13, mRNA
       233 ATGTTATCGGCACTGTGGGTCAGCAAGACCGGTCTGTCCGCCCAGGACATGAACCTGACC 292
                                                                                                                                               95 GlyPhePheGlnValThrLeuGluAspLys---ValHisTyrThrArgAlaGlyAsnPhe 113
                                          ThrValSerAsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValVal 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                               41 PheGlnAspLeuPheSerGlnAspLeuAlaIleGlySerThrGlySerGlnGlyProAsn 60
                                                               61 GlnAlaGlyMetGlyAlaGlnValGlySer---ValArgThrIlePheThrGlnGlyAla
                                                                                                                                                                                                                                                     80 PheGluProGlyAsnSerValThr-------AspLeuAlaileGlyGlyLys
                                                                                                                                                                                                                                                                                                                                                    Table 1 (Dasses 1 to 565)

Hahn, M.G., Ojanen-Reuhs, T., Samac, D., Town, C.D., Van Utterback, T., Cho, J. and Fraser, C.M.

ESTS from roots of Medicago truncatula treated with oligogalacturonides of DP 6-20
Unpublished (2001)
Contact: Michael G. Hahn
Complex Carbohydrate Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR sequence name: MTWAA19TK
More information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
1. .565
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220 Riverbend Road, Athens, GA 30602-4712,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medicago truncatula (barrel medic)
Medicago truncatula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 706-542-4457
Fax: 706-542-4412
Email: hahn@ccrc.uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB065273.1 GI:27810851
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
CB065273
                                          21
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AUTHORS
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128 GACGGCAGCGGTGTGTTGTTCGCCACTTTCAGCAACCAGCGAAGGCCATCGGCCAG 187
                                                    IleProheuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyr 432
                                                                                                                       433 SerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGly 452
                                                                                                                                                                                          453 LysLeuSerValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMetValAsn 472
                                                                                             247
                                                                                                                                                          248 AAAGAAACCTTCGCGTCGGCCAGCCGGGTTTTGATACCCCCGCAAGTCGGGACCCTGGGT 307
                                                                                                                                                                                                                    308 TCGATCGTGGCCAACTCCCTGGAGAACTCCAACGTCAACCTGACCAACGTGGTGGAC 367
                                                                                                                                                                                                                                                               473 MetilelleGlnArgGlyPheGlnMetAsnSerLysSerValThrThrAlaAspThr 492
                                                                                                                                                                                                                                                                                   368 CTGATCAGGCCCAGAGCAACTATCAGGCGAAGGCAAGACCATCTCCACCAAAGGACC 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                        BZ577405 895 bp DNA linear GSS 17-DBC-20
msh2_5391.x1 msh Pseudomonas aeruginosa genomic clone msh2_5391,
genomic survey sequence.
BZ577405
                                                                              Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonadaceae; Pseudomonae.

(Dases 1 to 855)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="msh2_5391"
/clone_lib="msh"
/note="Emvironmental isolate. Whole genomic shotgun
library."
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/mol_type="genomic DNA"
/strain="MSH"
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Matches:
Conservative:
Mismatches:
Indels:
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Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 2066857244
Email: craymond@u.washington.edu
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                                                                                                                                                                                                                                                                                                                                                          ATCATGCAGACCATCATTCAGATG 451
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|one="msh2_5391"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Washington
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38.10%
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BZ577405
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Town, C.D., Van Aken, S.,

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/clone_lib="HGGA"
//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xho1: cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
                                                                                                                                                                                                      /dev_stage="24 hours after treatment in the dark at 26 with 0.5 mg/ml oligogalacturonides (DP 6-20) in the presence of 100 ug/ml Gentamicin"
                                                                                                      /db_xref="taxon:3880"
/clone="HGGA-1C13"
/tissue_type="3 day old seedling roots"
/organism="Medicago truncatula"
/mol type="mRNA"
/cultivar="A17"
                                                                                                                                                                                                                                                                                                             'lab host="XLOLR"
```

/downer="GEZEHT102100"
/tissue_type="pituitary and hypothalamus"
/tissue_type="pituitary and hypothalamus"
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/clone_lib="HT1"
/clone_lib="HT1"
/clone_lib="HT1"
/clone_lib="HT1"
/clone_lib="HT1"
/clone_lib="WetCor: pSPORTI; Site_1: NotI; Site_2: Sall; This cond. Invariant of the superScript Plasmid System with Gareway Tecnology kit (Invitrogen), following manufacture's protocols. Plasmid DNA was purified using a modified alkaline lysis method. Sequencing reactions were conducted using the kit Big Dye Terminator Cycle Sequencing Ready Reaction (Applied Biosystems) according to the manufacturer's recommendations. Clones were sequenced by the 5' end with T' primer. Sequencing reactions were analyzed on ABI Prism 3100 Genetic Analyzer (Applied Biosystems). The quality and clustering of the ESTS were analyzed using the softwares Phred/Cap3. Only EST sequences with Phred quality greater than 20 and at least 150 bp were considered for clustering."

DRIGIN

/mol_type="mRNA" /db_xref="taxon:9031"

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CO423013 898 bp mRNA linear EST 02-UUL-2004 GGEZHT1021A02, GRINA sequence.
                                                                                                                                                                                                                                                                                                                    242
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excised
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                                                                                                                                                                                                              46 ------SerginAspLeuAlaIleGlySerThrGlySerGlnGlyProAsn---
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 ThrLeuGluAsp --- LysValHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAsp
                                                                                                                                                                                                6 PhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGlyThrValSerAsnAsn
extracts. Plasmids containing cDNA inserts were excisuerom the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."
                                                                            Length:
Matches:
Conservative:
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Indels:
Gaps:
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CO423013.1 GI:49639261
                                                                           2.75e-11
206.50
52.67%
35.88%
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Best Local Similarity:
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                                                                                                                                   Query Match:
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CO423013
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ORIGIN

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pacs1-60 645.s1 pacs1-60 Pseudomonas aeruginosa genomic clone pacs1-60-645, genomic survey sequence.

BZS57649.1 GI:27170747
GSS.
                                                                                                                                                                                                                                                                                                                                 84 AsnSerValThrAspLeuAlalleGlyGlyLysGlyPhePhe---GlnValThrLeuGlu 102
                                                                                                                                                                                                                                                                                                                                                          656 GGCGCCACGCTGGACATGGCGATCCAGGCGCGGCTTCTTCGTGCAGAAGGGCCAGCGAC 715
                                                                                                                                                                                                                                                                                                                                                                                   103 AsplysvalHisTyrThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsn 122
                                                                                                                                                                                                                                                                                                835
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                                                                                                                                                                                                                                                     595
                                                                                                                      4 SerLeuPhelleGlyAlaThrGlyMetLysThrHisSerThrGlyLeuGlyThrValSer 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                        123 AspProSerGlyPheThr---LeuMetGlySerArgIleSerAsnAsnProAsnIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                        551 ATCTACGCG-------GCGTCCAAGCTGGCACCGGCCAGAACAGCATCGGC
                                                                                                                                                                         24 AsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnValValPheGlnAsp
                                                                                                                                                                                                                              44 LeuPheSerGlnAspLeuAlaIleGlySerThrGlySerGlnGlyProAsnGlnAlaGly
        889
70
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                               Conservative:
Mismatches:
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        Length:
Matches:
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     2.47e-10
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases I to 1988)
Silva,C.S., Jorge, B.C., Patricio, M., Ledur, M.C. and Coutinho, L.L. Discovery of new genes expressed in the chicken pituitary and

Gallus gallus (chicken)

Gallus gallus

ORGANISM

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Contact: Clarissa S. Silva Laboratory of Animal Biotecnology, Dep. of Animal Production ESALQ - University of Sac Paulo Av. Padua Diss, 11, Piracicaba, SP, 13418-900, Brazil Tel: 55 19 3429 4434 Fax: 55 19 3429 4285

Unpublished (2004)

JOURNAL

hypothalamus

AUTHORS TITLE

REFERENCE

Email: cssilva@esalq.usp.br and llcoutin@esalq.usp.br PCR PRimers

.898
 /organism="Gallus gallus"

Location/Qualifiers

BACKWARD:

source

FEATURES

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604 ATCCTCAACACGCTGGTTAACTTACGC 578
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                                                                                                                                         CL660824.1 GI:50146561
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44.94%
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CL660824
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                      /mol type="genomic DNA"
/mol type="genomic DNA"
/strain="1-60"
/db.xref="xaxon:287"
/clone="pacs1-60 645"
/clone="pacs1-60"
/note="clinical isolate 1-60 Whole genomic shotgun
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Matches:
Conservative:
Mismatches:
Indels:
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University of Washington
Box 352456, Seattle, WA 98105-2145, USA
Tel: 2062516594
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
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/organism="Pseudomonas
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CL660824 GSS 09-JUL-2004 PRI0138a.B21 (849) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
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/db_xref="taxon:54126"
/clone_ilb="Mixed stage fosmid library of P. pacificus
/astrain="California"
/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda, Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

(Contact: Sommer, R.J.

AppaDB: an AcedB database for the nematode satellite organism puristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 LysLeuSerValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMetValAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433 SerAlaThrLeuAspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Class: fosmid ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-009-823A-1 (1-502) x CL660824 (1-849)
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/unce_Tructor: DSPORTI; Site_1: NotI; Site_2: SalI; This cond.

/note=Tructor: DSPORTI; Site_1: NotI; Site_2: SalI; This cond.

CDNA library was constructed with the SuperScript Plasmid System with Gateway Tecnology kit (Invitrogen), following manufacture's profocols. Plasmid DNA was purified using a modified alkaline lysis method. Sequencing reactions were conducted using the kit Big Dye Terminator Cycle conducted using the kit Big Dye Terminator Cycle Sequencing Ready Reaction (Applied Biosystems) according to the manufacturer's recommendations. Clones were sequenced by the S. and with IT? primer: Sequencing reactions were analyzed on ABI Prism 3100 Genetic Analyzer (Applied Biosystems). The quality and clustering of the ESTS were analyzed using the softwares Phred/Cap3. Only EST sequences with Phred quality greater than 20 and at least 150 bp were considered for clustering."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CO421506 758 bp mRNA linear EST 02-JUL-2004 GGEZHC1025H08.g HC1 Gallus gallus cDNA clone GGEZHC1025H08, mRNA sequence.
                                                                                                                                                        136 LeuaspserglyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSer 455
                                                                                                                                                                                      456 ValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMetValAsnMetIlelle 475
--ccgcctcccAGGTGATCGC-----AACCTGCAAACC 393
                                                                                             EST.

Gallus gallus (chicken)

Gallus gallus

Gallus gallus

Gallus gallus

Auesi, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

I (bases I to 788)

Silva, C.S., Jorge, E.C., Patricio, M., Ledur, M.C. and Coutinho, L.L.

Discovery of new genes expressed in the chicken pituitary and
                                                                                                                                                                                                                                                                                                                                            416 AlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyrSerAlaThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2004)
Contact: Clarissa S. Silva
Laboratory of Animal Biotecnology, Dep. of Animal Production
Laboratory of Animal Biotecnology, Dep. of Animal Production
Laboratory of Animal Biotecnology, Dep. of Animal Production
Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil
Tel: 55 19 3429 4434
Fax: 55 19 3429 4285
Email: cssilva@esalq.usp.br and llcoutin@esalq.usp.br
PCR PRimers
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organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pituitary a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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CO421506.1 GI:49637754
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                        355 GGCAAC---
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                           UCZUZE'') B24 bp mRNA linear EST 21-JUN-2004 or splbn 13E13 M13 Reverse Sheep spleen\brain pSportl library Ovis colos colos Oa_splbn_13E13 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 TrpGlnProAlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAla 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 GlylleGlnProLeuThrLeuAspPheGlylleLysSerGlnGlnAsnMetTrpAlaGly 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 AlaProAlaSerAlaAlaIleGlyThr------AspIleGlyLysLeuPro 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 SerMetMetProlleGlnThrSerSerGlyAsnSerThrAlaArgAsnGlySer---- 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------SerSerThrArgArgTyrSerGlnAspGly----- 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 GACGCCAATGGCCAGGTCGTGACCGCCAACGGTTTCGCGCTGGAGCCGGCGATTGTGGTG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TyrProGlnGlyAspLeuValAspValThrileThrSerGlu 395
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                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 CGGATTCCCGGGTCGACCCGGAATTGCCGTCGGGCCTGCAACTGGGTACCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .824
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/mol_type="mRNA"
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Conservative:
Mismatches:
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Gossner, A. and Hopkins, J.

Govine spleen\Land nona library

Unpublished (2004)

Contact: J Hopkins

Veterinary Biomedical Sciences

Veterinary Biomedical Sciences

Vinversity of Edinburgh

Summerhall Square, Edinburgh

Summerhall Square, Edinburgh

Flate: 13 row: E column: 13

Seq primer: M13 reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13_Reversor
High quality sequence stop: 548.
Location/Qualifiers
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DB:
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 761)
Hopwood, P.A., Zhang, F., Lowden, S., Talbot, R., Burt, D., Archibald, A.
                                                                                                                                             318
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                                                                                                                                                                                                                                                                     339 ProAlaSerAlaAlaIleGlyThrAspIleGlyLysLeuProSerMetProIle 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                456 ValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMetValAsnMetIlelle 475
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                                                                                                                                        299 GlnProAlaProLeuValAsnGlyLeuProGlnPheSerAlaAsnPheValGlyAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476 CAAAGCACCCTGGAAACGTCCAACGTCAGCACGTTGAAGAAGATGGTCAACATGATCACC
                                                                                                                                                                       --- CTGGGTACCGGT
                                                                                                                                                                                                       319 IleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsnMetTrpAlaGlyAla
                                                                                                                                                                                                                                       44 GIGGCCAICGIIGGCACTCAGAAGAACTICAGCGCCGGIAACTIGCAGCAAACCGGCCAG
                                                                                                                                                                                                                                                                                                 104 CCGCTGGACTTGGCGGTCAACGGTAAG-----GGTTTCTTCCAGATCCTGCAGCCGGAC
                                                                                                                                                                                                                                                                                                                                  -----SerSerGlyAsnSerThr
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| GGCACCACCTACACCCGCGACGGTACGTTCCACCTGGACGCCAATGGCCAGGTCGTG
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                                                                                                                                                              2 CAGGACAGCGAATTGCCGTCGGGCCTGCAA-----
                                                                                                            US-10-009-823A-1 (1-502) x CO421506 (1-758)
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EST.
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              197.50
41.10%
29.68%
7.64%
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                             Percent Similarity:
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CO423511 766 bp mRNA linear EST 02-JUL-2004
GGEZHT1017H04,g HT1 Gallus gallus cDNA clone GGEZHT1017H04, mRNA
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Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM
Sequencing was performed by ARK genomics. This clone is available
from ARK-Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS,
UK. See www.ark-genomics.org or contact info@arkgenomics.org.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryoda, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 766)
Silva.C.S., Jorge, E.C., Patricio, M., Ledur, M.C. and Coutinho, L.L.
Discovery of new genes expressed in the chicken pituitary and
hypothalamus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 GGCGAATGCGTTAAGTTCACCATCGGTCGTGATGGCGTGGTCAGCGTAACCCAAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluaspGlyLeuargargGluGlyasnasnHisTyrSeralaThrLeuaspSerGlyGly
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Laboratory of Animal Biotecnology, Dep. of Animal Production
ESALQ University of Sac Paulo
Av. Padua Dias, II. Piracicaba, SP, 13418-900, Brazil
Tel: 55 19 3429 4434
                                                                                                                                                                                                                                minus unstimulated
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                                                                                                                                                                                                                                                                                                                       761
22
44
7
                                                                                           1.761
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/clone_lib="forward - stimulated mi
                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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CO423511.1 GI:49639759
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Gallus gallus
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CN823216 870 bp mRNA linear EST 02-JUN-2004 Oa splbn 04023 Ml3reverse Sheep spleen\brain pSportl library Ovis aries cDNA clone Oa_splbn_04023 5', mRNA sequence.
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                                                                       156 ValAsnGlnLeuGluThrSerAsnValAspMetSerArgGluMetValAsnMetIleIle 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 AsnAsnIleAlaAsnAlaAsnThrIleGlyTyrLysGlnGlnGlnValValPheGlnAsp 43
63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Caprinae, Ovis.
                                                                                                                                                                                                     493 AACAACATCGCCAACGTCGCGACCACCGGCTTCAAATCGTCCCGTGCCGAATTCTCGGAT
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                                                                                                                                                                        476 IleGlnArgGlyPheGlnMetAsnSerLysSerValThrThrhlaAspThrMetLeu
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Matches:
Conservative:
Mismatches:
Indels:
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Veterinary Biomedical Sciences
Vaterinary Biomedical Sciences
University of Edinburgh, EH9 10H.
Summerhall Square, Edinburgh, EH9 10H.
Email: j.hopkins@ed.ac.uk
Email: j.hopkins@ed.ac.uk
Seq primer: Ml3reverse
High quality sequence start: 7
High quality sequence stop: 548.
Location/Qualifiers
1. .870
/organism="Ovis aries"
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Gossner,A. and Hopkins,J.
Ovine spleen\brain cDNA library
Unpublished (2004)
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190.50
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Ovis aries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 IleGlnProLeuThrLeuAspPheGlyIleLysSerGlnGlnAsnMetTrpAlaGlyAla 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 GTGGCCATCGTTGGCACTCAGAAGAACTTCAGCGCCGGTAACTTGCAGCAAACCGGCCAG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProAlaSerAlaAlaAlaIleGlyThrAspIleGlyLysLeuProSerMetMetProIle 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SerSerSerThrArg 375
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             Fax: 55 19 3429 4285
Email: cssilva@esalq.usp.br and llcoutin@esalq.usp.br
PCR PRimers
BACKMARD: T7.
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Matches:
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                                                                                                            Location/Qualifiers
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197.50
41.10%
29.68%
7.64%
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Best Local Similarity:
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11brary is GGCTGTAGGC. TAG_SEQ=None found" Alignment Scores:	Qy 357 ProlleGlnThrSerSerGlyAsnSerThralaArgAsnGlySerSer 372 CAL	Qy 472 snWetlleIleIleGlnArgGlyPheGlnWetAsnSerLysSerValThrThrAlaAspT 492 :::::	FEATURES Location/Qualifiers source 1661 / organism="Acyrthosiphon pisum"
	RESULT 17 CB854175 LOCUS LOCASION CB854175.1 G1:30044552 REYWORDS EST. CB854175.1 G1:30044552 REYWORDS EST. CB854175.1 G1:30044552 REYWORDS EST. CB854175.1 G1:30044552 REYWORDS EST. CB854175.1 G1:30044552 REPERENCE LOCASION MARMAIA; BUTHERIA; Primates; Catarrhin; Hominidae; Homo. REFERENCE LOCASES 1 to 650) AUTHORS Bonaldo, M. F., Lennon, G. and Soares, M.B. TITLE AUTHORS LOCUS JOURNAL Genome Res. 6 (9), 791-806 (1996) REPERENCE PUBMED COMMENT MCCTAY, PB MCCTAY, LA MCCTAY, LA MCCTAY, LA MCCTAY, LA MCCTAY, LA MCCTAY, LA MCCTAY, LA MCCTAY, LA MCCTAY, LA MCCAY LAB CORTACT LOCAS LOCATION	Tel: 319 356 4866 Fax: 319 356 4710 Email: paul-mccrayeliowa.edu Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research (www.open.bookystems.com). Seq primer: M13 FORWARD Seq primer: M13 FORWARD PEATURES 1650 Cocation/Qualifiers 1650 Cocation/Qualifiers 1650 Cocation/Qualifiers About Stage="Repairs" Cocation/Qualifiers About Stage="Repairs" Cocation/Qualifiers About Stage="Repairs" Cocation/Qualifiers About Stage="Repairs" Cocation/Qualifiers About Stage="Repairs" Cocation/Qualifiers About Stage="Repairs" Cocation/Qualifiers About Stage="Repairs" Cocation/Qualifiers About Stage="Repairs Cocation About Stage="Repairs Cocation About Stage="Repairs Cocation About Stage="Repairs Cocation About Stage="Repairs Cocation About Stage="Repairs Cocation About Stage="Repairs Cocation About Stage="Repairs Cocation About Stage="Repairs Cocation About Stages Cocation About Stages Cocation About States Cocation About States Cocation About States Cocation About States Cocation About States Cocation About States Cocation About States Cocation About States Cocation About States Cocation About States Cocation About States Cocation About States Cocation About States Cocation About States Cocation About States Cocation About States About States About States About States About States About States About States About States About States About States About States About States About States About States About States About States About S	used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this

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                                                                                           /clone libe Acyrthosiphon pisum, Pea Aphid"
//clone libe Acyrthosiphon pisum colonies. Library by Srini
//mote="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
//mote="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
//wholy Acyrthosiphon pisum colonies. Library by Srini
//wholy Acyrthosiphon pisum colonies. Library by Srini
//wholy and Evolutionary Biology, Princeton University,
//whole State I Face Tarace There score of 20 or better.
//whole Sequencing of Clones by Dr. PM Dang, US. Horricultural
//whole Research Lab, Ft. Pierce, FL. (772) 462-5940."
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260 AATATTCAAGGTATGTATCTAACTGGACTTAATACATCTTGTTCAAAAAGTGATTTTAAT 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 LeuPheSerGlnAspLeuAlalleGlySerThrGlySerGlnGlyProAsnGlnAlaGly
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30
30
27
6
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Conservative:
Mismatches:
Indels:
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BP562788 RAFL14 Arabidopsis thaliana CDNA clone RAFL14-76-G17 5',
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 566)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramateu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
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                                                                                                                                                                                                                                                                                                                                                                             Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3.1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: meski@rtc.riken.go.jp
Plaase viait our web site (http://pfgweb.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..566 / organism="Arabidopsis thaliana" / nol type="ManA" / mol type="RakNa" / db xref="taxon:3702" / clone="RakIJ4-76-G17" / tissue type="root" / lab host="DH109" / clone lib="RakIJ4" / note="Site_1: BamH1; Site_2: Sall"
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                                             sequence.
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                                           mRNA
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JOURNAL
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Schistosoma mansom.

Schistosoma mansom.

Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigeidida; Schistosomatoidea; Schistosoma.

1. (bases 1 to 436)

Strigeidida; S., DeMarco, R., Martins, B.A.L., Guimaraes, P.E.M., Ojopi, E.P.B., Paquola, A.C.M., Plazza, J.P., Nishiyama, M.Y. Jr., Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F., Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L., Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A., Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A., Sa.R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T., Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C.C. and Dias-Netco, B.

Transcriptome analysis of the accelomate human parasite Schistosoma
                                                                                                                                                                                                                                                                                                         CD119187

MEI-0052U-V172-E05-U.B MEI-0052 Schistosoma mansoni cDNA clone
MEI-0052U-V172-E05.B, mRNA sequence.
                                     473 MetilelleGlnArgGlyPheGlnMetAsnSerLysSerValThrThrAlaAspThr 492
                                                                   182 ATGATCGTCGCGCAGCGCTTCTATCAGGCCAACGCGCAGACCATCAAGACGCAGGATGCC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
plate: MEl-0052U-V172 row: 5 column: E.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
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/organism="Schistosoma mansoni"
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                                                                                                                                                                              242 ATCCTGCAAACCCTGCTCAACCTGCGT 268
                                                                                                                                           493 MetLeuGlnLysAlaLeuGluLeuLys 501
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Departemento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l. .436
organism="Schistosoma mansoni"
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                                                                                                                                      CD119056.1 GI:34657168
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Schistosoma mansoni
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413 IleProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyr 432

Match: 6.67%	us-10-009-823A-1 (1-502) x AIO57966 (1-	216 ValTyrAspGlnGlnGlyAsnSerH	516 GTTTTGACAGTGGGTAATGTTC 236 SerThrGlySerLysThrPheGluT	468 AAGACCGGGATAATAACTGGCAG- 256 AlaalaSerGlyThrAspSerAlaG		276 AsnGlyGluLeuLysAsnMetThrA	375 AATGGCACATTAGTGGATG	296 AsnAlaTrpGlnProAlaProLeuV	316 GlyAlaGlyIleGlnProLeuThrL	282 AACTCC	336 AlaGlyAlaProAlaSerAlaAlaA	265	MetProlleG		376 ArgTyrSerGlnAspGlyTyrProG	237ACCCAGAACGGNAC-AAAC			TATOPICATIONICATION OF THE PROPERTY OF THE PRO)		23		CD444534 ION EL01N0442D08 ON CD444654	N CD444654.1 GI:31360297 DS EST. Zea mays	Σ	Spermatophyta; Magnollophyt clade; Panicoideae; Andropo NCE 1 (bases 1 to 715)		
Query !	UB:	8	8 &	g 8	7 A	ò	đ	Å 43	ò	ga	à	ପ୍ପ	λo	q 	Å,	요 :	÷ ÷	·	ŝ t	3 8	Š	RESULT	CD444654	DEFINITION ACCESSION	VERSION KEYWORDS SOURCE	ORGANISM	REFEREN	AUTHORS	TITLE
	z Giltertejeracetifigalaalecetagggeerjecaggeeraalggeeraalggeeraalggeeraal 433 SeralaThrLeuaapSerGlyGlyProGluPheGlyLeuProGlyThrSerasnTyrGly 452		453 LysbeuSerValAsnGlnbeuGluThrSerAsnValAspMetSerArgGluMetValAsn 472 	473 MetilelleileGlnArgGlyPheGlnMetAsnSerLysSerValThrThrAlaAspThr 492 ::	MetLeuGlnLysAlaLeuGluLeuLys 501	::: 242 ATCCTGCAAACCCTGCTCAACCTGCGT 268		AI057966 SWOVL3CAN21B (SAW94WL-OVL	MKNA Sequence. MAS/96/ AINS/96/6 1 GT.3331R32	BATCS COST CT. 5051004	Onchocerca volvulus Onchocerca volvulus Eukarvota: Metazoa: Nematoda: Chromadorea: Spirurida: Filarioidea:	dae; Onchocerca.	Nailliams, S.A., Lu, W., Lizotte-Waniewski, M. and Laney, S.J. Genes expressed in infective third stage larvae of Onchocerca		even A. Willia arasitology	Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science Center, Smith	COllege, Morthampton, FA, Olues, USA Tel: 413585386 Energy Angersase	Fax: 413553/60 Email: genome@smith.edu	seq primer: pbidescript sk. Location/Qualifiers	/organism="Onchocerca volvulus"	/mol type="mkna" /strain="Signary Leone" /dr vene="mkna"	/ wxt= 'caxon:exez" /clone="SWOYISONZIBO3" /lab host="XI]-Blue MRP"	/clone lib="Onchocerca volvulus infective larva cDNA	(SAWWHLOVUL) /note="Vector: lambda Unizap XR; Site 1: EcoR I; Site 2: Xho I; Cutaneous filarial nematode parasite of humans.	mkNA was prepared from third stage infective larvae of Onchocerca volvulus isolated from mosquitoes 10 days after infection and converted to down a stranded chow using	reverse transcriptase and oligo (dr) followed by RNase H and DNApol 1. The library had 1.8 x 1085 independent	recombinants and average insert size was you base bairs. The library was constructed by Wenhong Iu. The library is available from Dr. 8 A. Williams, email genome@emith.edu."		scores:
i	9 &	QQ	\$ 65	<i>₹</i> 3	ò	рр	RESULT 22 AI057966/c	LOCUS	ACCESSION	KEYWORDS	SOURCE	a CNG CARD C	AUTHORS TITLE	JOURNAL	COMMENT				FEATURES	omos								ORIGIN	Alignment Scores

Length: Matches: Conservative: Mismatches:

1.03e-07 172.50 39.57% 27.23%

Percent Similarity: Best Local Similarity:

Score:

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715 bp mRNA linear EST 03-JUN-2003
4 Zea mays cDNA, mRNA sequence.
                                                                                         HisaspileThrValTyrPheAspGlyAlaProSer 235
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yta; Liliopsida; Poales; Poaceae; PACCAD
pogoneae; Zea.
                                                                                                                  regrecearregegaaraararegeaacegegaarr 322
                                                                                                                                                                                                                                                                                                                                                                                                                      AshSerThrAlaArgAsnGlySerSerSerThrArg 375
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                                                                                                                                                                     JTyrLeuValAlaMetAsnProSerGluAspGlySer 255
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                                                                                                                                                                                                                                              AGIYLeuLeuMetSerGlyThrMetThrPheSerSer 275
                                                                                                                                                                                                                                                                                                                        ralaPheThrProThrGlySerAlaThrLysAspLeu 295
                                                                                                                                                                                                                                                                                                                                                                                               WalAsnGlyLeuProGlnPheSerAlaAsnPheVal 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rLeuAspPheGly1leLysSerGInGlnAsnMetTrp 335
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Indels:
Gaps:
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CF886932 692 bp mRNA linear EST 03-NOV-2003 UI-CF-DU1-aas-f-05-18-UI-IB UI-CF-DU1 Homo sapiens cDNA clone
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67 GGGACGGGAAACTTTGGCACCTGACCAACGTGCGCTGGAAGGGTCCAACGTCGATCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA 2024 University of Iowa Fax: 319 356 7171

Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 692)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Xhol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447 GlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMet
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190 Frelinghuysen Rd., Piscataway, NJ 08854, USA Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.
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97044477
                                                                                      Location/Qualifiers
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CF886932/c
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/clone="Ul-CF-DUI-aas-f-05-18-UI"
/tissue_type="Primary Lung Epithelial Cells"
/dev_tage="Addit"
/lab_host="DH10B [Life Technologies) (TI phage resistant)"
/clone_lib="Ul-CF-DUI"
/lote="Organ: Lung; Vector: PT73-pec (Pharmacia) with a modified polylinker; Site=1: EcoR I; Site=2: Not I;
/U-CF-DUI is a normalized cDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)lab tail. The sequence tag for this
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Clone Distribution: Distribution information can be found http://genome.uiowa.edu/distribution/cf.html
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                             Location/Qualifiers
                                         Seq primer: M13 REVERSE
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1208 bp DNA linear GSS 17-DEC-2002
pacs1-60 645.82 pacs1-60 Pseudomonas aeruginosa genomic clone
BZS57650 BZS57650.1 GI:27170751
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                                                                                                -- ValValAsp-PheTy 411
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Whole-cenome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
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Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1208)
       360 ThrSerSerGlyAsnSerThrAlaArgAsnGlySerSerSerThrArgArgTyrSerGln
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---ACCACCAGTACTCCACCGCGTTCGCCCAGAGCAACCCGATC-------CAG
                                                                         380 AspGlyTyrProGlnGlyAspLeuValAspValThrIleThrSerGluGlyLysLeuGln
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/clone="pacs1-60 645"
/clone_lib="pacs1-60"
/note="clinical isolate_1-60 Whole genomic shotgun
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University of Washington
University of Washington
University Seattle, WA 98105-2145, US
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
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                                                                                                                                                  400 GlyLysTyrSerAsnSerGln--------
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/strain="1-60"
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1158)
2 pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1158)
2 pencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Whole-Genome-Sequence variation among multiple isolates of psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                   /clone="pacs1-60_658"
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/note=clinical isolate 1-60 Whole genomic shotgun
library."
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192
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Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
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/strain="1-60"
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Email: craymond@u.washington.edu
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161.50
39.88%
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/tissue_type- /dev_stage="" /dev_stage="" /dys_after po //otone_libe-" /note="Vecton Xho!; Immatun after pollin after pollin plants. At b isolated pod in liquid nit extraction. o The CDNA was Vector from S Gold packagir	ignment Scores: ed. No.: creet Similarity: st Local Similarity ery Match: -10-009-823A-1 (1-5	1	Oy 187 ProtyrPhealaLeuLeuGl Db 254TyrSerTy Cy 207 ASBTyrSerTy Db 233 AATGCGGATAGCTATAACAA. Oy 224 HisAspileThrValTyrPh Db 173 CATGACATGGCGTCTACTTY. Oy 244 TyrLeuValAlaMetAsBPX.	125 264 80 SULT 28 822668 CUS FINITION OA
Score: Percent Similarity:	Oy 409 AspPheTyrAsnIleProLeuAlaArgPheThrSerGluAspGlyLeuArgArgGluGly 428 bb 354 GGCAACATCCAGGCCGCCGACTTCATCAACCCGGCCGCTTCAGGCCATCGGC 301 Oy 429 AsnAsnHisTyrSerAlaThr-LeuAspSerGlyGlyPro-GluPheGlyLeuProGlyT 448 Db 300 AACAACCTGCAGAACGGCGCCCACAGGCGCGCGCGCGATCGGGC 241 Oy 448 hrSerAsnTyrGlyLysLeuSerValAsnGlnLeuGluThrSerAsnValAspMatSerA 468 1:::::	180 AGGAGTGGTGAACATGATCACCAGGGGCCTACGAGTGATGACTCCAAGGTCATCT 488 hrThralaAspThrMetLeu 494 120 CCACCGCGACCAGATGATGATGATGACTCTTTTTTTTTT	rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; REFERENCE Médicago. 1 (bases 1 to 554) AUTHORS Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., CLO,J. and Fraser, C.M. TITLE ESTS from developing reproductive tissues of Medicago truncatula JOURNAL Unpublished (2001) COMMENT CONTact: Michael A. Grusak USDA/ARS Children's Nutrition Research Center Baylor College of Medicine 1100 Bates Street, Houston, TX 77030-2600, USA Tel: 713-798-7044 Fax: 713-798-7078	Enail: mgrusak@bcm.tmc.edu Enail: mgrusak@bcm.tmc.edu Enail: mgrusak@bcm.tmc.edu TIGR sequence name: MTOBD44TX More information is available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gtg gAT CC). FEATURES 1. c554 /organism="Medicago truncatula" /organism="Medicago truncatula" /organism="Medicago truncatula" /cultivar="A17" /db_xref="taxon:3880" /clone="pGGPOD-11G16"

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ector: pBluescript SK-; Site 1: EcoRI; Site 2: macure pods, ranging in age from 15 to 30 days lination, were collected from greenhouse-grown At harvest, seeds were removed from pods and pod walls were collected and immediately frozen distrogen. Pod walls were pooled for mRNA, was directionally ligated into the Unizap XR rom Stratagene and packaged using dispack III kaging extracts. Plasmids containing cDNA inserts is aged from the recombinant lambda-Zap phage using the helper phage and propogated in XLOIR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heArgPheThrGlnAspGlyPheLeuAsnAspProSerGly 126
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TT------GTGAAGACCGGGATAATAACTGGCAG 126
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be="immature pod walls"
"Immature pods, ranging in age from 15 to 30
pollination"
"GPOD"
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TTAAGCTGGATGAAAACCGTAACCTGGTGAATATGCAAGGT
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CACTGGAATTTAATGCTAATGGCACATTA 45
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Conservative:
Mismatches:
Indels:
Gaps:
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musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   651 GGGGGCACGCTGGACATGGCGATCCAGGGCGCGGCTTCTTCGTGCAGAGGGCAGCGAC 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           486 AACAACATCGCCAACGTCGCGACCACCGGCTTCAAGTCGTCCCGTGCCGAATTCTCGGAT 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              591 AACGGCGTAAACCTGGCGGCAGTGCCCCAGCAGTTCACCCCAGGGTGACGTCAACAACAGC 650
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                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 MetGlyAlaGlnValGlySerValArgThrIlePheThrGlnGlyAlaPheGluProGly 83
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                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9940"
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Matches:
Conservative:
Mismatches:
Indels:
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Veterinary Blomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, EH9 1QH.
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High quality sequence start: 7
High quality sequence stop: 549.
Location/Qualifiers
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Gosener, A. and Hopkins, J.
Ovine spleen\brain cDNA library
Unpublished (2004)
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                                                                                                                                                                                                                                                                       Email: j.hopkins@ed.ac.uk
Plate: 02 row: E column: 20
                  CN822868.1 GI:47950937
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HTC; CAP trapper.
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154.00
44.43$
. 34.82$
5.96$
                                                 Ovis aries (sheep)
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Query Match:
                                                                    Ovis aries
 CN822868
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subrraction of cap-trapper-selected cDNAs to genere full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Ktubna, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yaliwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Sequencing pipeline with 384 multicapillary sequence analysis (RISA) system—384 format genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation 6 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 305?)
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                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Nature 409, 685-690 (2001)
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                                                                                                                                                  Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                            878 TTGGGAAGGACAGAGAAACAGCAAGAACCTGTTACTTCTACTTCTCTGGTGTTTGGG
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1406 ACAGGAGCCAGCATAATAGTGTCTTTTTGGGGTTTTTGGGGCTACAACCACGTCA
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SAPATSSGGIFGSSTSSSNPPVAAFVFGQASNPVSSSAFGNAAESSTSGSLLFPQES
EPATTSSTAPAASPFVFGTGASSNSYSSGFTFGATTFSSSSSFYGTGHSAFSASP
GFANQTPTFGGSGGASQAPVPFSFGSISSTALFAATTGSSPSPPIFGTVSSSSQPPVF
GQQPSQSAFGSGTANASSVPOFGSSTTNFNFTNNPSGVFTFGASPSTPAASAQPSGG
GVFSPSQSAFGSGTANASSVPOFGSSTTNFNFTNNPSGVFTFGASPSTPAASAQPSGG
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/dev_stage="9.5 days embryo"
<1. -2002
                                                                                                                                                                                                                                                                                                                                                                        /note="unnamed protein product; nucleoporin homolog
[Rattus norvegicus] (PIR|A44345, evidence: FASTY, 92.8%ID,
45.4%length, match=1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSSGLSQTLTSTGNPKFGDQGGFKLGTSSDSGSTVTMNTNFKFSKPTGDFKFGVLSDS
KPBEVKNDNKNDNFQFGSSSGLTNPASSAPFQPGVSTLGQQEKKEELPKSSPAGFSFA
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                            organism="Mus musculus"
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URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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/note="putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon start=2
protein id="B
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31.66%
22.72%
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Best Local Similarity:
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                                                  FEATURES
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1590 bp DNA linear GSS 16-DEC-2003
VIRTUAL TRANSCRIPT, partial sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.

(base) 1 to 159;

Clark, A.G. (Janowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Rerriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M. And Cargill, M. Anders, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Cargill, P. Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.D. and Adams, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ThrGlyMetLygThrHisSerThrGlyLeuGlyThrValSerAsnAsnIleAlaAsnAla 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 AsnThrileGlyTyrLysGlnGlnGlnValValPheGlnAspLeuPheSerGlnAspLeu 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 ServalArgThrilePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAspLeu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Mang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission Cargill, M. Burect Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Snockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 AlalleGlySerThrGlySerGlnGlyProAsnGlnAlaGlyMetGlyAlaGlnValGly
   185 TACGAAATGAACTCCAAGGTCATCCAGGCCGCGGACGAGATG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 302 (5652), 1960-1963 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="CDSN"
/locus_tag="HCM4723"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cocation/Qualifiers
                                                                                                                                                                                                                         genomic survey sequence.
                                                                                                                                                                                       Homo sapiens CDSN gene,
                                                                                                                                                                                                                                                                              AY412935.1 GI:39768900
                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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Best Local Similarity:
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                                                                                                                                                                                       DEFINITION
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                                                                                          RESULT 31
AY412935
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AUTHORS
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REFERENCE
AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                   AZS77776 374 bp DNA linear GSS 08-DEC-2000 14f11 Shot-gun genomic library of Rhizobium strain ANU265 Rhizobium sp. NGR234 genomic clone 14f11, genomic survey sequence. AZS77776
                                                                                                                                     1904 TCATTTACA------GTGGGGTCAAATGGGAAAATATGTTCTCTTCC--- 1948
1847 GCAGCCTCAGCCCTCAGGTTCAGGGGTCTTTTCATTCAGCCAGTCTCCA---GCA 1903
                                                                                          417 ArgPheThrSerGluAspGlyLeuArgArgGluGlyAsnAsnHisTyrSerAlaThrLeu 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420 SergluAspGlyLeuArgArgGluGlyAsnAsnHisTyrSerAlaThrLeuAspSerGly 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440 GlyProGluPheGlyLeuProGlyThrSerAsnTyrGlyLysLeuSerValAsnGlnLeu 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 GAACCGATCGTCGGCACGCCGGTCCCGGCTTCGCGCAGATCAAGCAGGCTATCTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 GluThrSerAsnValAspMetSerArgGluMetValAsnMetIleIleIleGlnArgGly 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Shot-gun genomic library.of Rhizobium strain ANU265"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 GAATCCTCCAACGTCGATCCGGTCAAGAAATCACCGACCTGATCTCGGCCCAGGGGCGCC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: M13; derivative strain of NGR234 cured of pNGR234a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. Chemin de 1'Imperatrice, Chambesy/Geneva 1292, Switzerland Tel: +44(0)1603450000
Fax: +44(0)1603450045
Enail: virginie.viprey@bbsrc.ac.uk
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium sp. NGR234
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Virginie Viprey
Laboratoire de Biologie Moleculaire des Plantes Superieures
University of Geneva
                                                                                                                                                                                                                                                                              ------GGAACTICAGTTTCTGGTGGC 1969
                                                                                                                                                                                                               437 AspSerGlyGlyProGluPheGlyLeuProGlyThrSerAsnTyrGlyLys 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 374)
Viprey, V., Rosenthal, A., Broughton, W.J. and Perret, X. Genetic snapshots of the Rhizobium species NGR234 genome Genome Biol. 1 (6), RESEARCH0014 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 PheGlnMetAsnSerLysSerValThrThrAlaAspThrMet 493
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="ANU265"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ577776.1 GI:11604390
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138.00
56.76%
37.84%
5.34%
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
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                                                                                                                                                                                                                                                                                                                                           RESULT 30
AZ577776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
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KEYWORDS
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Oy 412 nIleProLeuAlaArgPheThrSerGluAsp		TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios nonneutral evolution from human-chimp-mouse orthologous JOURNAL Science 302 (5622), 1960-1963 (2003) PUBMED 14671302 REFERENCE 2 (Dases 1 to 4428) AUTHORS Clark,A.G. (Janowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Adams,M.D. and Cargill,M. TITLE Direct Submission JOURNAL Submitted (16.NOV-2003) Celera Genomics, 45 West Gude Drive,	COMMENT This sequence was made by sequencing genomic exons and ordering FEATURES them based on alignment: FEATURES Location/Qualifiers Location/Qualifier	Alignment Scores:	Oy 16 SerThrGlyLeuGlyThrValSerAsnAsnIleAlaAsnThrIleGlyTyrLys 35
100ThrLeuGluAspLysVall 406 AGCAGCAGCTCTCACTGGGAAGCAGCGGCTCTCACTGGGAAGCAGCAGCTCT 108 ThrArgAlaGlyAsnPheArgPheThrGlnAspGlyPheLeuAsnAspProSer:	Oy 159 sSerProAlaLysThrSerThrAlaLeuAsnAlaValValAsnLeuGlyAspSerThr 178	236 822 253 253 882 273 273	Qy 293 sAspLeuAsnalaTrpGlnProAlaProLeuValAsnGlyLeuProGlnPhe 310	Qy 332 nAsnMetTrpalaGlyAlaProalaSerAlaAlaIleGlyThrAspIleGlyLysle 352 : :	1254 Trcccacacccrgcrcccaccadd

	1312 GGTGGGTTCACATTTGGTAAGTGGGCTCCTTCTTTGCCATCTTCCTCAAGTTTGTT 3231 131 GlySerArg	196 LysGlyAsnGlyThrProProlle	284 AlapheThrProThrGlySerAlaThrLySASpLeuAsnAlTrGGLOGGCGA 3879 284 AlapheThrProThrGlySerAlaThrLySASpLeuAsnAlaTrgGln 299 3880 GCATTGGTGCTAACCGACGTTTGGACAAAGTCAAGGTGCCAGGCCAG
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0y 44 LeuPheSerGlnAspLeuAlaileGlySerThrGlyBerGlnGlyProAsnGlnAlaGly 63	AY416870 LOCUS DEFINITION Mus musculus NUP153 gene, VIRTUAL TRANSCRIPT, partial sequence, ACCESSION AY416870 AY	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Ferriera, S., Wang, G., Zheng, X.H., White, T Adams, M.D. and Cargill, M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA This sequence was made by sequencing geno them based on alignment. Location/Qualifiers 1. 4355 / organism="Wub musculus" / mol_type="genomic DNA" / db xref="wavn:10090" / gene="NUP153" / locus_tag="HCM6034" Scores: 0.0388 Length: milarity: 33.75\$ Conservative:	ty: -502) -502) -1

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4089 376 4140	TyrserginaspgiyTyrProginglyaspLeuvalaspvalThrileThrSerglugly 396	LysLeuGlnGlyLysTyrSerAsnSerGlnValValAspPheTyrAsnIleProLeuAla 416	•	CN762396 374 bp mRNA linear EST 20-MAY-2004 IDOAAAAB01RM1 ApMS Acyrthosiphon pisum cDNA clone IDOAAA4AB01 5', CN762396	Pterygota; Aphidiformes;	Aphidoidea; Aphididee; Macrosiphini; Acyrthosiphon. I (bases I to 374) Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B., Stern,D., Tagu,D. and Wincker,P. An expressed sequence tags database for the pea aphid Acyrthosiphon	, varkes to bhen fedex Prance	Tel: +33.2.23.48.51.65 Fax: +33.2.23.48.51.50 Risk of contamination by bacterial sequences from obligatory Risk of contamination by bacterial sequences were Subchneral or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope PCR PRimers	ChdGAAACAGCTATGACC row: B column: 1. Location/Qualifiers 1. 374 //organism="Raythosiphon pisum"	/cultivar="developmentstage" /cultivar="developmentstage" /db xref="taxon:1702" /clone="1D0AAA4AB01" /tissue_type="whole insect" /tissue_type="whole insect" /tissue_type="whole insect" /lab_host="Xil-Blue" /lab_host="Xil-Blue" /clone_lib="ApMS" /
4054 GGACAGCAGCCTAGTCA 357 ProlleGlnThrSerSe ::::	377 TyrSerGlnAspGlyTy ::: 4141 AACTTCACAAACAATAA	397 LysLeuGlnGlyLysTy ::: 4201 GCAGCCTCAGCCCAGCC	417 ArgPheThr 419 4258 TCATTTACA 4266	CN762396 IDOAAAABO1RM1 ADMS MRNA sequence.	CN762396.1 GI:47536319 EST. Acyrthosiphon pisum (pea aphid) Acyrthosiphon pisum Eukaryota, Metazoa, Arthropoda, Neoptera, Paraneoptera, Hemipte	Aphidoidea; Aphidid 1 (bases 1 to 374) Hunter, W., Martines Stern, D., Tagu, D. a An expressed sequen	Unpublished (2004) Contact: D. Tagu INRA Rennes	Tel: 433.2.23.48.51 Fax: 433.2.23.48.51 Fax: 433.2.23.48.51 Risk of contaminati (Buchnera) or facul obtained in the fra Genomics in collabo PCR PRIMETS	FORWARD: (Plate: 4	/culfivar/ /db_xref= /clone=[t] /tissue_[t] /dev_stagg /lab_hostagg /lab_hostagg /lab_hostagg /sample nar Sample nar Sample nar Sample nar Scology & Soil cond: Harvestring under non and both library or library or
Db 40 Qy 3 Db 40	Cy 3 Db 41	Oy 3	Oy 4	RESULT 35 CN762396/C LOCUS DEFINITION	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL		FEATURES SOURCE	

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EST.

Chlamydomonas reinhardtii

MISM Chlamydomonas reinhardtii

Elwaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.

Chlamydomonadaceae; Chlamydomonas.

Chlamydomonadaceae; Chlamydomonas.

NCE 1 (bases 1 to 348)

ORS Grossmant, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., Mrobernott, J.P., Silflow, C., Stern, D. and Surzycki, R.

Analyses of the Chlamydomonas reinhardtii Genome: A Model,

Unpublished (2000)

Contact: Charles Hauser

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG857482 348 bp mRNA linear EST 29-MAY-2001 1024052B06.x1 C. reinhardtii CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence. BS857482 BS857482 BS857482 BS857482. GI:14238666 BST.
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Mismatches:
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        1. No.: 0.00119
:e: 132.00
:ent Similarity: 62.50$
: Local Similarity: 42.19$
:y Match: 5.10$
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ORIGIN

Alignment Scores:

MEDLINE 20530913 PUBMED 11076861 REFERENCE 4 AUTHORS THE RIKEN GENOM FANTOM CONSOLLITIE JOURNAL Nature 409, 685 REFERENCE 5		Katoh,H., Kawai Koya.S., Kuriha Nakamura.M., Sui Okazaki,Y., Sui Sano,H., Sasaki Sogabe,Y., Taga Takeda,Y., Taga	Muramatsu,M. an TITLE Direct Submissi JOURNAL Submitted (16-A, Physical and Ch Exploration Res RIKEN Vokohama Kanagawa 230-00 URL:http://genou	Pax:81-45-503-9; COMMENT CDNA library was Encyclopedia Pra Genomic Science Division of Exp prepare mouse t: prepare mouse t:	UKL:http://fantc URL:http://fantc FEATURES 1.0catid Source 1.177 /mol_ty /strain	/db_xxx//db_xxx//db_xxx//db_xxx//dlone//dlon	putative polyA_signal 1703 polyA_site 1723 ORIGIN note="	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:: DB: US-10-009-823A-1 (1-502) x A
	eAlaAsnAla 29 ::: TCGCCAACTCC 127 erGlnAspLeu 49 CC 178	31nvalGly .:: &&>TGCC fhraspLeu	GTCTGGACGTT 271 alHisTyrThr 108	HTC 03-APR-2004 full-length rin 98, full	Buteleostomi; Murinae: Mus.		ibata,K., ishizaki,Y. ed cDNAs to ery of new genes	1., Carninci, P.,), H., Itoh, M., T., Harada, A., Kashiwagi, K., Watahiki, M., S., Kawai, J., Shizaki, Y., 14-format
1.2 Length: 348 50 Matches: 34 7% Conservative: 15 Mismatches: 43 8% Indels: 13 Gaps: 3	823A-1 (1-502) x BG857482 (1-348) ThrGlyMetLysThrHisSerThrGlyLeuGlyThrValSerAsnAsnIleAlaAsnAla 1	AlalleGlySerThrGlySerGlnGlyProAsnGlnAlaGlyMetGlyAlaGlnValGly	GGTATCACTCAGGACTTTACCGATGGCACCACCACCACCGGGCGAGGTCTGGACGTT Ala11eGlyGlyLysGlyPhePheGlnValThrLeuGluAspLysValHisTyrThr	J46 1723 bp mRNA linear RCB-1283 B16 melanoma cDNA, RIKEN clone:G430037K05 product:nucleopo	GI:26105674 GI:26105674 Tolouse mouse) fetacag Chordata, Craniata, Vertebrata, Buteleostomi, fetacag Chordata, Sciurocnathi, Muridae; Musinae: Musinae	dayashizaki,Y. full-length cDNA cloning 33, 19-44 (1999)	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new gonome Res. 10 (10), 1617-1630 (2000)	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Hazada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwaj, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Oheda, Y., Ishkawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system384-format sequencing pipeline with 384 multicapillary sequencer
Scores: 0.0012 131.50 milarity: 46.67% Similarity: 32.38%	10 ThrGlyMetLysThrHisSer' 10 ThrGlyMetLysThrHisSer' 11:	50 AlaileGlySerTh 179 70 SerValArgThril ::		AKO89973 Mus musculus skin enriched library,	AK089973 AK089973.1 G1:26105674 AK089973.1 G1:26105674 HTC; CAP trapper. Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chorda Mammalia; Eutheria; Rodenta	l Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999) 10349636	Carninci, P., Shih Itoh, M., Konno, H Normalization and prepare full-leng Genome Res. 10 (20499374	Shibata,K., Itoh, Konno,H., Akiyama Sumi,N., Ishii,Y. Yamamoto,R., Mate Fujiwake,S., Inou Yoneda,Y., Ishikk Okazaki,Y., Muran RIKEN integrated sequencing pipeli Genome Res. 10 (1
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	US-10-009-823A-1 Qy 10 Thn Db 68 AGG Qy 30 Asr Db 128 GCC		8 & 8 & 8 8 & 8 & 8	SULT 37 089973 CUS FINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE	AUTHORS TITLE JOURNAL MEDLINE PUBMED	AUTHORS AUTHORS TITLE JOURNAL

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Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Carninci, P., Furuno, M., Hanagaki, T., Hirozane, W., Hirozane, T., Hirozane, T., Cotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kando, S., Konno, H., Kouda, M., Cawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nasuyama, T., Miyazaki, A., Muraca, M., Ohsato, M., Satoh, R., Satoh, H., Sakai, K., Ohno, M., Ohsato, Sato, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sakai, D., Shibata, K., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tamaka, T., Toya, T., Yasunishi, A., and Hayashizaki, Y.
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me Exploration Research Group Phase II Team and the
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notation of a full-length mouse cDNA collection
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324 bp DNA linear GSS 08-DEC-2000 t-gun genomic library of Rhizobium strain ANU265 Rhizobium 4 genomic clone 14el0, genomic survey sequence.
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                                                                                                                                              -----GlyAlaProAlaSerAlaAlaAlaIleGl
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ire de Biologie Moleculaire des Plantes Superieures
y of Geneva
y of Geneva
de l'Imperatrice, Chambesy/Geneva 1292, Switzerland
(0)1603450000
(0)1603450045
irginie, viprey@bbsrc.ac.uk
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sp. NGR234
Proteobacteria; Alphaproteobacteria; Rhizobiales;
eae; Rhizobium/Agrobacterium group; Rhizobium.
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, Rosenthal,A., Broughton,W.J. and Perret,X.
mapshors of the Rhizobium species NGR234 genome
ol. 1 (6), RESEARCH0014 (2000)
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	Fred. No.: 0.00224 Length: 324 Score: 128.50 Matches: 41 Percent Similarity: 50.94% Conservative: 13 Best Local Similarity: 38.68% Mismatches: 41 Query Match: 4.97% Indels: 11 DB: 8 Gaps: 5 US-10-009-823A-1 (1-502) x AZ577764 (1-324)	10 ThrGlyMetLysThrHisSerThrGlyLeuGlyThrValSerAsnAsn1leAla	AACATCGCGAP PheSerGlnAs		50 AlaileGlySerThrGlySerGlnGlyProAsnGlnAlaGlyMetGlyAlaGlnValGly	Db 191 CTGCCCTCGAGCAACGGCTCCTACAÀCTCCGGCĠĠĠĠTAGAGACC 147 Qy 70 SerValArgThrilePheThrGlnGlyAlaPheGluProGlyAsnSerValThrAsp 88		Qy 89 LeuhlaileGlyGlyDhePheGlnValThrLeuGluAspLySValHisTyr 107	108	Db 26 ACGCGGCGGTGCNTTC 9	AY416868 LOCUS AY416868 4428 bp DNA linear GSS 17-DEC-2003 DEFINITION Home carriers with the carriers	genomic survey sequence. ON AY416868	VEKSLON AY416868.1 GI:39772828 KEYWORDS GSS. SOURCE OFCANTSM Homo sapiens (human)		Leark, J. Jandowski, S., Nleeson, K., Thomas, P., Kejariwe Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B. Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J. Adams, M.D. and Cargill, M.		, Thomas,P., Kejariwa P. I., F. M. Thomas		TITLE Direct Submission JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockwille Mn 20050 193		FEATURES LOCATION/Qualifiers 1442	/nol_type="genomic DNA" /db_xref="taxon:9606" gene <1>4128	uəb/

103 422 115 482

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-----AspGlyPheLeuAsn 122
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111 ::: |||
483 TCTCAACTGCTTAGCCCTGGAGCCAGTGATCGTGGTGCCCAACGAGACCCATACCTTCAT
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library."
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20
20
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53
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Matches:
Conservative:
Mismatches:
Indels:
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msh2_5352.xl msh Pseudomonas aeruginosa genomic clone msh2_5352,
genomic survey sequence.
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TTTGGACAGCAACCTAGT------CAGTCTGCATTTGGCTCTGGAACAACTCCT 4167
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                                      3919 GGAACTGGACCCTCAGCACCATCTGCCAGCATTTGGTGCTAACCAGACCCAACA 3978
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                                                                                                                                    309 GlnPheSerAlaAsnPheValGlyAlaGlyIleGlnProLeuThrLeuAspPheGlyIle 328
                                                                                                                                                                                                                                                                 349 IleGlyLysLeuProSerMetProIleGlnThrSerSerGlyAsnSerThrAlaArg 368
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Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales;
Pseudomonadaceas, Pseudomonas.
1 (bases 1 to 867)
                                                                        289 GlySerAlaThrLysAspLeuAsnAlaTrpGlnProAlaProLeuValAsnGlyLeuPro
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Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates
Psedomas aeruginosa library
J. Bacteriol. (2002) In press
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        442 GluPheGlyLeuProGlyThrSerAsnTyrGlyLys 453
             -----IysAsnMetThrAlaPhe
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Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
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Fax: 2066857244
Email: craymond@u.washington.edu
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Location/Qualifiers
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

October 26, 2004, 09:04:16 ; Search time 40 Seconds (without alignments) 1207.520 Million cell updates/sec Run on:

US-10-009-823A-1 2586 Title: Perfect score:

1 MMGSLFIGATGMKTHSTGLG......NSKSVTTADTMLQKALELKR Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79: * 1: pir1: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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flagellar hook protein FlgE [imported] - Yersinia pestis (strain CO92)
C;Species: Versinia pestis
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG0219
R;Parkhill, J.; Wreen, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
Asrkhill, J.; Wreen, B.W.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I; Nature 413, 233-527, 2001
A;Accession: AG0219
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AG0219
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1428 <KUR>
A;Accession: WIPROT:QB2FBB; GB:ALS90842; PIDN:CAC90619.1; PID:g15979825; GSPDB:GR
C;Genetics:
A;Gene: f1gE

83; Gaps 21.6%; Score 557.5; DB 2; Length 428; 29.1%; Pred. No. 2.16-27; Live 74; Mismatches 196; Indels 83; Query Match Best Local Similarity 29.19 Matches 145; Conservative

11;

70 SVRIIFIQGAFEPGNSVTDLAIGGKGFFQVTLEDK---VHYTRAGNFRFTQDGFLNDPSG 126 127 FTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEAN 186 170 306 GLP--QFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSMMPIQTSSG 363 246 VAMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKNMTAFTPTGSATKDLNAWQPAPLVN 305 364 NSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLOGKYSNSQVVDFYNIPLARFTSEDG 423 10 TGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVG 187 PYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITV-YFDGAPSSTGSKTFEYL 278 GAPAOSFALINVAGS------KQQN-----KQQN----g ઠે 원 Š 셤 g ઠે $\stackrel{>}{\circ}$ a ઠે ď ઠે

296 -----TGADSIVAQNOTGYAAGEFTGFQINSDGSVVGTYSNQOTQLLGQIVWNNFSNPEG 350

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flagellar hook protein FigE PA1080 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Sacession: F83510
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, ..., Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Tele: Complete ganome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc, A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Residues: 1-462 <STO>
A;Cross-references: UNIPROT:0914P9; GB:AE004539; GB:AE004091; NID:g9946985; PIDN:AAG04465; A;Genetics:
A;Genetics:
A;Gene: flgE; PA1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 PSGFTLMGSRISNNPNIKKETLEPIQLD-FNDPTVAKSPAKTSTALNAVVNLGDSTDKTQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 SLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SFNIGLSGIQAASSGLNVTGNNIANAGTVGFKQSRAEFADVYAASV-LGS----GSNPQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 527.5; DB 2
Pred. No. 1.7e-25;
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Best Local Similarity 28.58
Matches 150; Conservative
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A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0727
                                                                                                                                                                                                                   Cibate: 24-Jul-1998 #sequence_reviein (figE) - syphilis spirochete
CiSpecies: Treponema pallidum subsp. pallidum (syphilis spirochete)
CiSpecies: Treponema pallidum subsp. pallidum (syphilis spirochete)
CiSpecies: Treponema pallidum subsp. pallidum (syphilis spirochete)
CiAccession: C71292
RiFraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, Isson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, Cthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: C71292
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                      LRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMN 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DNAGTLVNPANGMRVQGWMAQDVAĞERLINSSAQTQDLVIPIG-----QKIDAQQTS 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 TVYFDGAPSSTGSKTFEYLVAMNP-----SEDGSA-----ASGT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | : | | ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSAGLIMSGTWTFSSNGELKNWTAFTPTGSATKDLNAWQPAPLVNGLPQFSANFVGAGIQ 320
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Best Local Similarity 28.1%; Pred. No. 6.2e-26;
Matches 154; Conservative 80; Mismatches 183; Indels 131; Gaps
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Vugt,
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: C70135
C;Accession: C70135
C;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
                                                                                                                                                              217 IPENSWIMKVLIDGVNPLDPSNKTP-----MSFNVTFDASGQMISVRA--PDGSTSG 266
                                                                                                                                                                                                                                                                                                                                                                     PGFSIDATTNVIQFSPA---TGNPPTP----GTGWIPAASD-GKTPPTYAWNGATGAASG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------TIQYSTAFAQSNPIQDGYTTGQLAGIEIDDT 356
PTVTPF------DPSDAATYNSSSSLGIYDSQGNSHTMSQFFIKNEPDPNATPP
                                                                                                                 ---GSKTFEYLV-AMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGS---
                                                                                                                                                                                                                                                                               ----ATKDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAA
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Nature 390, 580-586, 1997
Ajauthors: Smith, H.O.; Venter, J.C.
Ajauthors: Smith, H.O.; Venter, J.C.
Ajauthors: Smith, H.O.; Venter, J.C.
Ajauthors: Smith, H.O.; Venter, J.C.
Ajauthors: Sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
Ajacession: G70135
Ajacession: G70135
Ajacession: G70135
Ajacession: G70135
Ajacession: Totalianary; nucleic acid sequence not shown; translation not shown
Ajmolecule type: DNA
Ajacsiques: 1-442 < KLEP
Ajacession: G70135
Ajaces-references: UNIPROT: Q44767; GB: ABC001137; GB: ABC000783; NID: G2688160; PIDN: AAC6666
Ajacerimental source: strain B31
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                                                                                                                                                                                                                                                                              SQGPNQAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFRF 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.7%; Score 509; DB 2; Length 442; 28.2%; Pred. No. 2.3e-24; iive 71; Mismatches 190; Indels 120;
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                                                                                                                                                                             Best Local Similarity 28.23
Matches 150, Conservative
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A;Map position: 23 min
C;Keywords: basal body; flagellum
F;2-403/Product: flagellar hook protein #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.3%; Score 498; DB 2; L
ilarity 28.7%; Pred. No. 9.5e-24;
Conservative 76; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: protein
A,Residues: 2-5 <JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 144; Conserv
RESULT 5
ABG640
flagellar hook protein FlgE [imported] - Salmonella enterica subsp. enterica serovar Typ
flagellar hook protein FlgE [imported] - Salmonella enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Dacesoion: Abg640
C;Accession: Abg640
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connetron, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Atthors: Parry, C.; Qualil, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Atthors: Parry, C.; Qualil, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Reference number: AB0502; MUD:21534947; PMID:11677608
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-403 cPAR>
A;Coss-references: GB:AL513382; PIDN:CAD08301.1; PID:g16502347; GSPDB:GN00176
C;Genetics:
A;Gene: STY1216
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14;
                                                                                                                                                                                   70 SVRTIFTQGAFEPGNSVTDLAIGGKGFFQ-VTLEDKVHYTRAGNFRFTQDGFLNDPSGFT 128
                                                                                                                                                                                                                             56 GIIQDFTDGTTTNTGRGLDVAISQNGFFRLVDSNGSVFYSRNGQFKLDENRNLVNMQGMQ 115
                                                                                                                                                                                                                                                                             129 LMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDSTDKTQSEANPY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 VAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELK----NWTAFTPTGSATKDLNAWQP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 GANNIVATN------QNGYKPGDLVSYQINNDGTVVGNYSNEQEQVLGQIVLANFAN 322
                                                                                                                     189 FALLESWKGNGTPPISTS---NYSYAQPMRVYDQQGNSHDITVYFDGAPSSTGSKTFEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 SSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------PESVSDADSYNKKGTVTVYDSQGNAHDMNVYP-----VKTKDNEWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 APLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLPSNMPIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGF
                                                                                         10 TGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 114;
Query Match
19.3%; Score 498; DB 2; L
Best Local Similarity 28.7%; Pred. No. 9.5e-24;
Matches 144; Conservative, 76; Mismatches 167;
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Salmonella typhimurium and their A; Accession: S1036
A; Molecule type: DNA
A; Residues: 1-403
A; Residues: 1-403
A; Conserved to MIPROT:P16322; EMBL:X51737; NID:g47671; PIDN:CAA36022.1;
A; Cross-references: UNIPROT:P16322; EMBL:X51737; NID:g47671; PIDN:CAA36022.1;
B; Mol. Biol. 212, 377-387, 1990
A; Title: Stoichiometric analysis of the flagellar hook-(basal-body) complex of A; Reference number: S15353; MUID:90204563; PMID:2181149

complex of Salmonella PID:947673

Gaps 114; Indels

14;

Qy 189 FALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSSTGSKTFEYLVAM 248 168NAFDASNADSNADSKALSGCHADMSVFVKTGDNNWQVY 211 QY 249 NPSEDGSAAGTDSAGLLMSGTMTFSSNGEL-KUMTAFTPTGSATKDLNAWQPAPLVNGL 307 212TQDSSDPTGTAEPAMKLVFNANGVLTSNPTENITTGA 185 QY 308 PQFSANFVGAGIQPLTLDFGIKSQQNWWAGAPASAAAIGTDIGKLPSMMPIQTSSGNSTA 367	QY 428 GNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVMIIIQRGFQMJSKSV 487	RESULT 8 BB5501 C.Species: Excherichia coli (strain 0157:H7, substicage) C.Species: Excherichia coli (strain 0157:H7, substicage) C.Species: Excherichia coli (strain 0157:H7, substicage) C.Species: Excherichia coli (strain 0157:H7, substicage) C.Species: Excherichia coli (strain 0157:H7, substicage) R. Petria, N. T.; Plundet III, G.; Burland, V.; Mau, B.; Glasner, J. D.; Rose, D. J.; Maybew, Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 Nature 5201 Nature
QY 10 TGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGAQVG 69 1	QY 246 VAMUPSEDGSAASGTDSAGLIMSGTWIFSSNGELKNWTAFTPTGSATKDLNAWQP 300 Db 210 VYTHDSSDPAATAPTTASTTLKFNENGILESGGTVNITTGTLNGATA 256 QY 301 APLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNWWAGAPASAAAIGTDIGKLPSMMPIQT 360 Db 257ATFSLSFLNSMQQN	99 31 SCRUSTARNGESSTRRYSQUEGOUGHUNDTESERGACKERSQUUDTWIPLARERS 220 1

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Giggellar hook protein - Helicobacter pylori (strain J99)

Giggellar hook protein - Helicobacter pylori

Giggellar hook protein - Helicobacter pylori

Giggellar hook protein - Helicobacter pylori

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A;Experimental source: strain J99
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OGPN--QAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKV--HYTRAGN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRFTQDGFLNDPSGFTLM-----GSRISNNPNIKKETLEFIQLDFNDPTVAKSPAK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 LYNEDGDALLLNENQGIWVSYKSAKMVKDILPSAENSTLEINGVKISFTNDSAVSRTSSL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----AGAPASAA 343
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416 QYGMFEINNKDNKNVIKENLNIFFVSGYSSDSVTNNVLFKNAMKGLNTASLIEGGASASSS 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GAGIQPLTL 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
18.8%; Score 485; DB 2; Length 716
Best Local Similarity 25.0%; Pred. No. 1.4e-22;
Matches 181; Conservative 94; Mismatches 222; Indels
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A;Molecule type: DNA
A;Residues: 1-402 <BLAT>
A;Ecross-references: UNIPROT:P75917; GB:AE000208; GB:U00096; NID:gl787308; PIDN:AAC74160.
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V.; Riley, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMNSK 485
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                                                      T-----TQNGYKPGDLVSYQINDDGTVVGNYSNEQTQLLGQIVLANFANNEGLASE 327
                                                                                                                                                                           GNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMNSKSV 487
                                                                                                                                                                                                                        RESULT 9
A64851
C19861ar hook protein flgE - Escherichia coli (strain K-12)
C19pedies: Escherichia coli
C19pedies: Escherichia coli
C19pedies: Bscherichia coli
C29bedies: Bscherichia coli
C3pedies: Bscherichia coli
C3pate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C3pate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C3pate: R5Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; F.R.; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; F. Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64705; MuID:97426617; PMID:9278503
A; Reference number: A644051
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A;Gene: fig8; fla_FV
C;Keywords: basal body; flagellum
F;2-402/Product: flagellar hook protein flgE #status predicted <MAT>
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Cipate: 27-Nov-2001
Rights: P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
Jonninguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entjan, K.D.; Fsihi, H.;
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
A;Authors: Kreft, T.; Sinnes, N.; Tisteria species
A;Title: Comparative genomics of Listeria species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                          A;Molecule_type: DNA.
A;Residues: 1-411 <GLA>
A;Residues: 1-411 <GLA>
A;Cross-references: UNIPROT:092DV7; GB:AL592022; PIDN:CAC95937.1; PID:g16413157; GSPDB:GR.
B;Xperimental source: strain Clip11262
C;Genetics:
A;Gene: lin0705
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                               flagellar hook protein FlgE homolog lin0705 [imported] - Listeria innocua (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TNPMSFGSGSKIGAILTDYTAGSPTSTGRNKDAALQGRGFFIAGDNAGGNIVYTRDGSFA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.7%; Score 484.5; DB 2; Length 411; 27.0%; Pred. No. 6.8e-23; ative 77; Mismatches 188; Indels 105.
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Best Local Similarity 27.09
Matches 137; Conservative
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A; Status: preliminary
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A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo697
                                                                                                                                                                                                                     - Listeria monocytogenes (strain
656 QALIGAANTGRRGSISGSKLESSNVDLSRSLINLIVVQRGFQANSKAVTTSDQILNTLLN 715
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                                                                                                                                                                                                              flagellar hook protein FlgE homolog lmo0697 [imported] - Listeria monocytoge
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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18.7%; Score 484.5; DB 2;
Best Local Similarity 27.0%; Pred. No. 6.8e-23;
Matches 137; Conservative 77; Mismatches 188;
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LKQ 718
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RESULT

thors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. tle: The complete genome sequence of the gastric pathogen Helicobacter pylori. Ference number: A64520; MUID:97394467; PMID:9252185	. & .Q	348DIGKLPSMMP
atus: preliminary; nucleic acid sequence not shown; translation not shown lecule type: DNA sidues: 1-718 <tom></tom>	<i>₹</i> 6	380 DGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSEDGLRREGNNHYSATLDSG 439
	& 8	440 GPEFGLPGTSNYGKLSVNQLETSNVDMSREMVNMIIIQRGFQMNSKSVTTADTMLQKALE 499 656 OALIGAANTGRRGSISGSKLESSNVDLSRSLTNLIVVQRGFQANSKAVTTSDQILNTLLN 715
lecsacule type: DNA lectle type: DNA sidues: 1-105,'N',107-236,'Y',238-258,'P',260-372,'NS',375-412,'TI',415-508,'D',510- coss-references: EMB:U09549,'NID:9600723, PIDN:AAA92803.1; PID:9600725 pperimental source: CCUG 17874; NCTC 11637 Toole, P.W.; Kostrzynska, M.; Trust, T.J.	oy Oy	
ae defective i	RESULT 1 E70460	4 hook nootein Blab - Amitex aeclicis
,238-258,'P',260-372,'NS',375-412,'TI',415-508,'E 11637	C; Specie C; Date: C; Access R; Decker	18. Aquifex acolicus 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004 1. B70460 # P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
the nucleic acid sequence is shown in 6-25 <020>	V. Nature 3 A;Title: A;Refere	
: CCUG 915	A; Access A; Status A; Molecu	
<pre>ywords: flagellum tery Match</pre>	A,Residu A,Cross- A,Experi C,Geneti A,Gene:	A,Residues: 1-482 <aqf> A,Residues: 1-482 <aqf> A,Cross-references: UNIPROT:067711; GB:AE000760; NID:g2984138; PIDN:AAC07675.1; PID:g2984 A,Experimental source: strain VF5 C,Genetics: A,Gene: flgE</aqf></aqf>
SNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGS 56	Query Match Best Local Matches 14	/ Match Local Similarity 27.6%; Pred. No. 1e-19; hes 143; Conservative 94; Mismatches 204; Indels 78; Gaps 23;
57 QGPNQAGMGAQVGSVRTIFTQGAFEPGNSVTDLALGGKGFFQVTLEDKVHYTRAGN 112	oy Oy	1 MYGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQ 57 : :
113 PRFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAK 163	cy GP	58 GPNQAGMGAQVGSVRIIFTQGAFEPGNSVIDLAIGGKGFFQVILEDKVHYTRAGNFRF 115
164 TSTALMAVVNLGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQ 212 :-	55 dg	116 TQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVV 172
213PWRVYDQQGNSHDITVYFDGAPSSTGSKTFEY 244 236 LCNEDGDALLINENQGIWVSYKSAKMVKDILPSAENSTLEINGVKISFTNDSAVSRISSL 295	දු පු	173 NLGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPWRVYDQQGNSHDITVYFDG 232
245 LVAMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKN	S Q	233 APSSTGSKTFE-YLVAMNPSEDGSAASGTDSAGL-LMSGTWIFSSNGELKNWIA 284 220VKTGTNQWKVYFLASLKERYINVDWNGD-DDKTDIVFLDLENDQVHIADNGTFSTLP7 276
282 -MTAFTPTGSATKDINAWQPAPLVNGLPQFSANFVGAGIQPLTL 324	çy Op	285 FTPTGSATKDLNAWOPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQON 333 277 FASKTLE-FDPSTGKLVYIPGGDIVQDTANQKFYLEVDLTPESGPSEIN 324
325 DFGIKSQQNMW	& 4	334 WWAGAPASAAAIGTDIGKLPSWMPIQTSSGNSTARNGSSSTRRYSQDGYPQ 384
344 347 :: 476 KFTHATHATSIDVIDSLGTKHAMRIEFYRSGGAEWNFRVIVPEPGELVGGSAARPNVFEG 535	& 음 .	385 GDLVDVTITSE-GKLQGKYSNSQVVDFYNIPLARFTSEDGLRREGNNHYSATLDSGGPEF 443 - -

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C;Species: Versinia pestis
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probable flagellar hook protein flgE [imported] - Yersinia pestis (strain CO92)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 NDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLGDS-TDK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 SVSVFN------PTNEKSYNFTTTSTVYDSLGREHAVAHYF--VKSTTPPA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 VNGQGMKLQGYPADAAGNIQAGIISDLKIN-----NAGVPAKASEQLDFMANLNASVTAP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLAR 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 TQLSQGFTTTRNKS------DGYTSGVKNAERIESDGSVYATFSNGERVLQGKVVLAN 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATKDLNA 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 MGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQV--TLEDKVHYTRAGNFRFTQDGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SFSIANTALNAHTEQLNTISNNIANSATKGFKASRTEFSSMYAQSQPLGVAVS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSST---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 418; DB 2; Le
Pred. No. 9.5e-19;
5; Mismatches 196;
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RNYQASTKIISTNDSMMNALFQV 412
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28.6%; Pre-
tive 65; 1
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Best Local Similarity 28.6'
Matches 144; Conservative
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                                                                                                                                                                                      A Status: preliminary
A Molecule type: DNA
A Molecules: 1-545 «PAR»
A Cross-references: UNIPROT: Q9PJ68; GB:AL139074; GB:AL111168; NID:G6967505; PIDN:CAB7253
A Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: flgE; Cj0043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
16.5%; Score 426.5; DB 2; Length 545;
Best Local Similarity 26.5%; Pred. No. 4.2e-19;
Matches 155; Conservative 84; Mismatches 224; Indels 121; Gaps
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flagellar hook chain protein Cj1729c [imported] - Campylobacter jejuni (strain NCTC 11168 C;Species: Campylobacter jejuni (strain NCTC 11168 C;Species: Campylobacter jejuni (strain NCTC 11168 C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: E81271 C;W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell Nature 403, 665-668, 2000 A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ajstatus: preliminary
AjMolecule type: DNA
AjResidues: 1-865 cPAR>
AjCross-references: UNIRROT:09PLU9; GB:AL1139079; GB:AL111168; NID:g6968971; PIDN:CAB73711:
AjExperimental source: gerotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
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                                                                              121
                                                                                                                              58 VOAAKVAQOFHEGSSIYTNNPLDLRIAGTGFFAVAKDRLVPQQNELTRNGAFHLDKNSFM 117
                                                                                                                                                                                                                                                                                                                                                                                                237 TGSKTFEYLVAMNPSE-----DGSAASGTDSAGLLMSGTWTFSSNGELKNWTAFTPTGS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 ATKDLNAWQP---APLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407
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                                                                                                                                                                                                                          172 LKDP----ALFDI----TDP---ETYNRTISSTIYDSMGQPYKLTTYYLKDMNQ
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                                                                                                                                                                                      122 NDPSGFTLMGSRISNNP---NIKKETLEPIQL--DFNDPTVAKSPAKTSTALNAVVNLGD
                                                                                                                                                                                                                                                                                           177 STDKTQSEANPYFALLESWKGNCTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGAPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 DIGKLPSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  215 ANTWQTYYTVTDKTGEKPINVVGGDAASPIGHVG----HTMRFNNDGTLSS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|:|:| || || ||::: | |::: | | |::: | QELVDLISAQRNFQANSRALEVHNGLQQNILQIR 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 REMYNMIIIQRGFOMNSKSVTTADTMLQKALELK 501
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A,Gene: flgE2; Cj1729c
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D82106
flagellar hook protein FIGE VC2197 [imported] - Vibrio cholerae (strain N16961 serogroug C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vemter, J.C.; Frager, C.M.
I, R.R.; Mekhalanos, J.J.; Venter, J.C.; Frager, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Accession: D82106
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Accession: D82106
A; Stetus: preliminary
A; Molecule type: DNA
A; Residues: 1-434 - KHINA
A; Residues: 1-434 - KHINA
A; Residues: 1-434 - KHINA
A; Residues: 1-434 - KHINA
A; Residues: Lource: serogroup O1; strain N16961; biotype E1 Tor
C; Genetics:
A; Gene: VC2197
A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 QVGSVRIIFIQGAFEPGNSVIDLAIGGKGFFQ-VILEDKVHYTRAGNFRFIQDGFLNDPS 125
                                                                                                                                                                                                                                                                                                                                                                                        115 GMYLTGLNTSCSKSDFNN----RSNLEPINL--KONSNILKNKPTSEIMLKAFLNRNTESK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSAT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 PSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYN 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------TGTIEQSNSDVSWEEHSQNGYPQGNLKTFDIVTNGEIIGTYCNQKQQTIGQ 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPLARFISEDGLRREGNNHYSATLDSGGPEFGL-PGTSNYGKLSVNQLETSNVDMSREMV 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --IYNKEGKKEDITVSFN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 -KKETNKWIVN--VESNDSDDKETIKN-----SFDLTFNDDGELTSDNVFNITSKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- DSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPWRVYDQQGNSHDITVYFDG
                                                                                                                                                                                                                                              7 IGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPNQAGMGA
                                                                                                                                                                                                                                                                                                 IAISGLLANNDYMEIISNNIANASTIGYKSRKPLFFDMFSHSFYSNTTN-----GYGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFTLMGSRIS-----NNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLG----
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25.7%; Pred. No. 7.5e-17;
tive 69; Mismatches 213; Indels 100;
                                                                                                                                                                                            Indels 121;
                                                                                                                                      16.0%; Score 413.5; DB 2; 25.7%; Pred. No. 1.8e-18; ive 73; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----YENITLNL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NMIIIQRGFQMNSKSVTTADTMLQKALELK 501
  A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
GGenetics:
A;Gene: f1gE; BU340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 SSVDNSDNKLSKPEDYMTYIS--
                                                                                                                                   Query Match
Best Local Similarity 25.7%
Matches 131; Conservative
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bb 6 AMLAGVSGLIANSSALAAISDNIAJVVIVGFKRSTSNFSTLVTSGNKNQTYSA 58 Qy 64 MGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLEDKVHYTRAGNFFFT 116 Db 59 GGVKAOTHOFISGOGLTGSTTSNLDISISGAGFFVTTEKPERLIATDTRSFTRAGSFQLD 118	117 QDGFINDPSGFTLMGSRISNNPNIK 14	Qy 142 KETLEPIQLDFNDPTVAKSPAKTSTALNAVVNLG-DSTDKTQSEANPYFALLESWKG 197	OY 198 NGTPPISTSNYSYAQPM	QY 215RVYDQGNSHDITVYFDGAPSSTGSKTFEYLVAMNP 250 298 ADDAEVVAGKLYDPSTWSMSDYAKDNSKGVRPDFEVQIPLSDSKGGQRTVTLSMLKGPGP 357	QY 251SEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATKDLNAWQPAP 302 :: : :	QY 303 LVNGLPQFSANFVGAGIQPLTLDFGIKSQQNWWAGAPASAAAIGTDIGKLFSMMPIQTSS 362 1	QY 363 GNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLARFTSED 422	QY 423 GLRREGNNHYSATLDSGGPEFGLPGTSNYQKLSVNQLETSNYDMSREWVNMIIQRGFQM 482 	Qy 483 NSKSVTTADTWLQKALELKR 502		
	200	Qy 222TF- 242 	Qy 243PSED 253 STATE	Qy 254 GSAAS-GTDSAGLLMSGTMTFSSNGELKNM	OY 283 299 Db 540 TADGHFAISNANEQSTVPPNAINGVGNATTIDPKNMSFNITAYSNKQGTVSTNDAFTAIF 599	OY 300PAPLVNGLPQFSANFVGAGI	Qy 334 MWAGAPASAAAIGTDIGKLPSWMPIQISSGN 364 :	Qy 365 STARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNIPLA 416	QY 417 RFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMYNMII 476 :	477 ORGFOMNSKSVTTADTMLOKALELKR 502	

6 GGWNPRQVQLGNQLSNQLSNNPHIGGSLQSPTNRSELDGIGSDGFFQVQDGDTFTYTRSGNPY 115 115 FTQGFLMDPSGTTLMGSRISNNPHIKGETLEDIGLDFNDFTVAKSPAKTSTALMAVVUL 13 126 FDQGG 127 FDQGG 128 SSTGSKTFFLVANDPEDGAAGTDSGLLDSPARATOROGGNSHDITVYDSARYDD 13 129 SSTGSKTFFLVANDPEDGAAGTDSGLLDSPARATOROGGNSHDITVYDSARYDD 13 129 STGSKTFFLVANDPEDGAAGTDSGLLDFGLKSGDNWAGAPASAAGITDSGLLSS 35 129 STGSKTFFLVANDPEDGAAGTDSGLLDFGLKSGDNWAGAPASAAGITDSGLLSS 35 120 TATAGASTSGLASANITALSSNSGAGTDSGLTANGARATTDGLLSS 35 121 TATAGASTSGLASANITALSSNSGAGTDSGLASANITALSTFTGSANITA
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Db 272 DOVSGVPOALVIDLSOMTOPSAKFTPGTAVINGNPSOIKDVRIGKGIVVAVYODGG 329	Db 504 RIGILAFINDQGLRKIGGNLYEMQEGTINGENRPLSGNPILGWDEEGKLKFGKIRHKYLE 563
407 VVDFYNIPLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSYNQLETERNYDM 46 .	Qy 461 ISNVDMSREWVNMIIIQRGFQMNSKSVTTADIMLQKALELKR 502
Cy 467 SREMVNMIIIQRGFQMNSKSVTTADTWLQKALELKR 502 : : : : 1 Db 390 ASELTDMIESQRIYTANSKVFQTGSDLMDVLINLKR 425	RESULT 25 G71881 probable flagellar basal-body/rod/hookprotein - Helicobacter pylori (strain J99) C,Species: Helicobacter pylori
RESULT 24 D64633 [lagellar hook - Helicobacter pylori (strain 26695) [species: Helicobacter pylori C;Species: Helicobacter pylori C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004 C;Accession: D64633	A; Variety: strain J99 C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 C; Accession: G71881 R; Alm, R.A.; Ling, L.S.L.; Motr, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; ires, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; INature 397, 176-180, 1999 A; Title: Geometre equence comparison of two unrelated isolates of the human gastric patho
Pererson, S., Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Mature 388, 539-547, 1997. A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.	A, Accession: G71881 A, Status: preliminary A, Molecule type: DRNA A, Residues: 1-65 < ARNA A, Residues: 1-65 < ARNA A, Cross-references: UNIPROT: Q9ZKUI, GB: AE001513; GB: AE001439; NID: G4155407; PIDN: AAD06422 A, Experimental source: strain J99
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-605 <tom> A;Residues: 1-605 <tom> A;Cross-references: UNIPROT:025566; GB:AE000600; GB:AE000511; NID:g2314042; PIDN:AAD0795</tom></tom>	ć
Query Match 13.7%; Score 354.5; DB 2; Length 605; Best Local Similarity 23.5%; Pred. No. 1.5e-14; Matches 151; Conservative 82; Mismatches 232; Indels 177; Gaps 22;	MACCHES 148; CONSELVATIVE 85; MISMACCHES 224; INCELS 191; GADS 1 MAGSIFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPN : : : : :
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QY 105 VHYTRAGNERFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQL 150	120 NFLTRAGNFARDADGYLVTFEGYYVYGIDLKKIKDGTLNSTARDEDIEKLHGNTLSFLQ1 151DFNDP
CY 151NDP 155 DD 180 PQDLTYQPVLSTKVNISVNLAPKDHLKGVQDFFLADKGEIIKERPLAQDINALANNDNEP 239	180 PQDLTYQPVLSTKVNISVNLNPKDHLKGYQDFFLNDKGEIIKERFLNQDINALANDDNEP 156 TVAKSPAKTSTALNAVVNLGDSTDKTQSBANPYFA :
Qy 156 TVAKSPAKTSTALNAVVNLGDSTDKTQSEANPYFA 190	240 IDAITNRKLNVSIQKENGRKEDFVFTYGDAEKGENQFKTLGDLQKLLKEKTGLDLN 191 LLESWKGNGTPPISTSNYSYAQPWRVYDQQG-NSHDITVYFDQAPSSTGSKTF ::
QY 191 LLESWKGNGTPPISTSNYSYAQPWRVYDQQGNSHD-ITVYFDGAPSSTGSKTFEYLVAMN 249	OD 296 LIKBEKUARSPFULLEIANPSETFIAFSLEGGIAUKUGLMANQMELKKOISKUSVAIRIF 355 QY 243 EYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATKDLNA 297 OF VALUE OF THE STATE OF THE
CY 250 PSEDGSAASGIDSAGLLMSGIMTFSSNGELKNWTAFITPIGSATKDLNAWQPAPLV 304	298 WQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAA
Qy 305NGLPQFSANFVGAGIQPLTLDFGIKSQQNNWAGAPASAAAIGTDIGK 351	DVIITSEGKLQGKYSN 40
QY 352 LPSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFY 411	405 SQVVDFYNIPLARFTSEDGLRREGNMHYSATLDSGGPEFGLFGTSNYGK
CY 412 NIPLARFISEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLE 460	DD 497 GVVEFVARIGILAFTNDÜGLKKIGGNLIEMQEGTINGENKFLÖGNFILGMDEEGKLKFGK 556 QY 454 LSVNQLETSNVDMSREMVAMIIIQRGFQMNSKSVTTADIMLQKALELKR 502

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A; Residues: 1-149,'S', 151-264 <ALB>
A; Residues: 1-149,'S', 151-264 <ALB>
A; Accession: 34450.2
A; Accession: 34450.2
A; Residues: 1-264 <AL2>
A; Residues: 1-264 <AL2>
A; Residues: 1-264 <AL2>
A; Cross-references: RMEL: X56049; NID: 939904; PIDN: CAA39528.1; PID: 939912
B; Cross-references: RMEL: X56049; NID: 939904; PIDN: CAA39528.1; PID: 939912
A; Title: Gene-protein relationships in the flagellar hook-basal body complex of EA; A; Reference number: JG0019; MUID: 91285431; PMID: 1905667
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
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A;Cross-references: GB:M54966; NID:g142918; PIDN:AAA22444.1;
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Superfamily: rod protein flgF
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GGenetics:
A;Genetics:
A;Gene: BMEII0159
A;Map position: II
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AB3529
flagalar hook protein flgB [imported] - Brucella melitensis (strain 16M)
flagacies: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3229
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, F.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
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G69622
Ispace and the protein flgs - Bacillus subtilis
NiAlternate names: flagellar hook-basal body protein flgg
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69622; I42365; S14502; JG0023
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13.4%; Score 347; DB 2; Length 396;
Best Local Similarity 25.6%; Pred. No. 2.4e-14;
Matches 130; Conservative 67; Mismatches 191; Indels 120;
                                                               605
                                 -----LVSG-GNVAVNLGAYGGOTLNLNL-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-396 <KUR>
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Db 233 ITAQRAYEFNSRVIQTADEMLRTATNVKR 261	RESULT 29 C70372 flagellar hook basal body protein flgG - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004 C;Accession: C70372 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove	Nature 392, 353-358, 1998 A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300; MUID:98196666; PMID:9537320 A,Accession: C70372 A,Status: preliminary: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-262 <aqf> A,Cross-references: UNIPROT:067006; GB:AE000709; NID:g2983373; PIDN:AAC06963.1; PID:g2983</aqf>	A; Gene: IlgG2 C; Description: located in the distal rod C; Superfamily: rod protein flgF C; Keywords: basal body; flagellum	Query Match 12.0%; Score 311; DB 2; Length 262; Best Local Similarity 21.2%; Pred. No. 2.3e-12; Matches 108; Conservative 45; Mismatches 102; Indels 254; Gaps 9; Qy MMGSLPIGATGMKTHSTGGTGVSNNINTGYRQQVVFQDLAIGSTGS 56	GMTAQQTNLDVISHNMANVNTVGYKKMRATFQL GAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFF	Db 61 RSPSGFQIGLGTYVSDTYGIFTQGNLTKTDNQLDIAIQGDGFFKIVLPDGTIAYTRNGQF 120	Qy 114 RFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVN 173 	QY 174 LGDSTDKTQSEANPYPALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGA 233	QY 234 PSSTGSKTPEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKAMTAFTPTGSATK 293 Db , 143 142	Qy 294 DLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGTDIGKLP 353	354 SMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNI 150	414 PLARFTSEDGLRREGNNYSATLDSGGPEFGLPGTSNYGKLSYNQLETSNYDMSREMYNM	Qy 474 IIIQRGFQMNSKSVTTADTMLQKALELKR 502 : Db 234 IIAQRAYEFVTKGIQAADEMLSQAANLRR 262	RESULT 30 H83510 flagellar basal-body rod protein FlgG PA1082 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Qy 356 MPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFVNIPL 415	416 ARFTSEDGLEREGNNHYSATLDSG-GPEFGLPGTSNYGKLSVNQLETSNYDMSREMVNNI 474 416 ARFTSEDGLEREGNNHYSATLDSG-GPEFGLPGTSNYGKLSVNQLETSNYDMSREMVNNI 474 177 VIPANSPGLPKIGSNLYRESIANSGTASAANQPGDGGTGALKKSGFLEMSNYDLTDEFTEMI 236 475 IIQRGPQNNSKSVTTADTMLQKALELKR 502 1	SULT 28 243 agellar basal-body rod protein FlgG - Thermotoga maritima (strain MSB8) Species: Thermotoga maritima Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 Accession: B7243 Relson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey rett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;	fer between Archaea and Bacteria from genome seq 6; PMID:10360571	A;Molecule type: DNA A;Residues: 1-261 -ARN» A;Cross-references: UNIPROT:Q9XIM8; GB:AE001800; GB:AE000512; NID:g4982090; PIDN:AAD3660 A;Experimental source: strain MSB8 C;Genetics: A;Genetics: TM1542	C;Superfamily: rod protein flgF Query Match Door 12.6%; Score 325.5; DB 2; Length 261;		QY 1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPN 60	QY 61 QAGMGAQVG-SVRIIFTQGAFBPGNSVTDLAIGGKGFFQVTLED-KVHYTRAGNF 113	QY 114 RFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVNN 173 : : Db 121 KMDSEG	CY 174 LGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGA 233	234 PSSTGSKTFEYLVANNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATK	DLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIXSQQNMWAGAPASAAAIGTDIGKLP	QY 354 SMMPIQTSSGNSTARNGSSSTRRYSQDGVPQDLVDVTITSEGKLQGKYSNSQVVDFYNI 413 Db 152TI 172	OY 414 PLARETSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSRENVNM 473

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C; Accession: H83510
R; Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradanan, S.J.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A; Accession: H83510
A; Accession: H83510
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-261 < STO>
A; Residues: 1-261 < STO>
A; Residues: 1-261 < STO>
A; Residues: Logi < STO>
A; Status: preliminary
A; Residues: Logi < STO>
A; Coss-references: UNIPROT: Q914P7; GB: AE004539; GB: AE004091; NID: 99946985; PIDN: AAG0447
A; Experimental source: strain PA01
C; Genetics:
A; Superfamily: rod protein flgF
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E, Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res 8, 11-22, 2001
A; Tille: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and g A; Reference number: A99629; MuID:2115621; PMID:11258796
A; Accession: H90810
A; Accession: H90810
A; Residues: 1-260 cHAY>
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; Pred. No. 4e-12;
46; Mismatches 93; Indels 254;
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Best Local Similarity 21.6%;
Matches 108; Conservative 4
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A;Cross-references: UNIPROT:P75939; GB:BA000007; PIDN:BAB34879.1; PID:g13360920; GSPDB:GP.A;Experimental source: strain O157:H7, substrain RIMD 0509952
Ggenetics:
A;Gene: ECs1456
C;Superfamily: rod protein f1gF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ខ
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White Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grocheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; FMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            flagellar basal body rod protein flgG [similarity] - Escherichia coli (strain 0157:H7,
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                                                                                                                                                                                                                                                                                                                                                                                                                   111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFRFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAV 171
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C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                QAGM--GAQVGS-VRTIFT----QGAFEPGNSVTDLAIGGKGFFQVTLED-KVHYTRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 OTTLPSGLOIGTGVRPVATERLHSOGNLSQTNNSKDVAIKGOGFFOVMLPDGSSAYTRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----QPAITIPA----
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                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                            tch
al Similarity 21.4%; Pred. No. 7e-12;
109; Conservative 44; Mismatches 98; Indels 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.7%; Score 303; DB 2; Length 260; ilarity 21.4%; Pred. No. 7e-12; Conservative 44; Mismatches 98; Indels 2
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C,Superfamily: rod protein flgF
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Best Local Similarity
Matches 109; Conserv
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Matches 109; Conserv
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A,Molecule type: DNA
A,Residues: 1-260 <ST
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	Db 167 166 Qy 352 LPSNMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFY 411 Db 167PVQVGQLN 174 Qy 412 NIPLARFTSEDGLRREGNNHYSATLDSGGPEFGLPGTSNYGKLSVNQLETSNVDMSREMV 471 Db 175LTTPNNDTGLESIGENLYIETQSSGAPNESTPGLNGAGLLYQGYVETSNVNVAEELV 231 Qy 472 NMIIQRGPQMNSKSVTTADTMLQKALEL 500 Db 232 NMIQVQRAYEINSKAVSTTDQMLQKLTQL 260 RESULT 36 RESULT 36 E97165
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Naturburs: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Fitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Fitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Accession: AD0640 A; Accession: AD0640 A; Accession: AD0640 A; Residues: 1-260 cPAR> A; Residues: 1-260 cPAR> A; Residues: 1-260 cPAR> A; Residues: GB: AL513382; PIDN: CAD08303.1; PID: gl6502349; GSPDB: GN00176 C; Genetics: C; Genetics: CA; CA; CA; CA; CA; CA; CA; CA; CA; CA;	
Query Match 11.6%; Score 301; DB 2; Length 260; Best Local Similarity 21.4%; Pred. No. 9.4e-12; Matches 109; Conservative 43; Mismatches 99; Indels 258; Gaps 10; MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQVVFQDLFSQDLAIGSTGSQGPN 60 MMSSLMIAKTGLDAQQTNMDVIANNIANVSTNGFKRQRAVFEDLLYQ-TIRQPGAQSSE 58 MISSLMIAKTGLDAQQTNMDVIANNIANVSTNGFKRQRAVFEDLLYQ-TIRQPGAQSSE 58 61 QAGM-GAQVGS-VRIIFTQQAFEPGNSVTDLAIGGKGFFQVTLEDKVH-YTRAG 111	NDPSGFTLMGSRI. TADGRKVLGYSM SSEANPYFALLES STANPYFALLES FEYLVAMNPSEDG
	Db 197TMAGSDENAATTIAAEGGDDLNKSIVAAVDKNPSGGGTATIKKGDVAFÜDÄN 248 CY TMTESENGELKKMTAETPTGSATKOLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDF 326 Db 249 DVDLAADNRYLHTLKIPPTVTKVTATRD

	RESULT 38 C97426 flagellar basal-body rod protein flgG (distal rod protein) [imported] - Agrobacterium tun C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;bactes 30-59p-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 C;Accession: C97426
RESULT 37 AC2644 [lagellar basal-body rod protein [imported] - Agrobacterium tumefaciens (strain C58, Dup C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004	R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUID:21608551; PMID:11743194
C; Accession: AC2544 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001	A;Status: preliminary A;Molecule type: DNA. A;Residues: 1-262 <kur> A;Creferences: UNIPROT:Q44338; GB:AE007869; PIDN:AAK86364.1; PID:g15155490; GSPDB:GN. C:Genetics:</kur>
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W. A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CSB. A; Reference number, BSS577, MITTID: 216,08550, ENTI-11743102	A;Gene: AGR C_972 A;Map position: circular chromosome C;Superfamily: rod protein flgf
A; Accession: AC2644 A; Status: preliminary A; Molecule type: DNA	Ouery Match 11.2%; Score 290.5; DB 2; Length 262; Best Local Similarity 21.5%; Pred. No. 4.3e-11; Matches 109; Conservative 44; Mismatches 86; Indels 267; Gaps 12;
A, Tross-references: UNIPROT:Q44338; GB:AE008688; PIDN:AAL41569.1; PID:g17738903; GSPDB:G A, Experimental source: strain C58 (Dupont) C, Genetics:	Qy 2 MGSLFIGATGWTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQG-PN 60
A;Gene: flgG A;Map position: circular chromosome C;Superfamily: rod protein flgF	Qy 61 QAGMGAQVGSVRIIFTQG-AFEPGNSVTDLAIGGKGFFQVTLED-KVHY 107
Query Match 11.2%; Score 290.5; DB 2; Length 262; Best Local Similarity 21.5%; Pred. No. 4.3e-11; Matches 109; Conservative 44; Mismatches 86; Indels 267; Gaps 12;	108 TRAGNER FTODGELNDESGETLMGSRISHIELGNAL-LYALILGGGRILEAGNOSILL 108 TRAGNER FTODGELNDESGETLMGSRISHNPNIKKETLEPIQLDFNDFTVAKSPAKTSTA 110
QY 2 MGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSGG-PN 60 :	168 LNAVVNLGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDIT
Qy 61 QAGMGAQVGSVRIIFTQG-AFEPGNSVTDLAIGGKGFFQVTLED-KVHY 107 	145DAQDIT. 228 VYFDGAPSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTP ;
Qy 108 TRAGNFRFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTA 167	Db 151 I 151 Qy 288 TGSATKDINAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWAGAPASAAAIGT 347
QY 168 LNAVVNLGDSTDKTQSBANPYPALLESWKGNGTPPISTSNYSYAQPWRVYDQQGNSHDIT 227	Db 152 151 Qy 348 DIGKLPSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQV 407
228 VYFDGAPSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTWTFSSNGELKNWTAFTP 2	DD 152 TRTGQVTRIGNADFTQLG
288 TGSATKDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNYWAGAPASAAAIGT 3	Db 172QLTIANFANEAGLKPLGDNLFSQTPASGAPVVGVPDDPSYGYVKQSYLEGSNVDAV 227 Qy 468 REMVAMIIQRGFQMNSKSVTTADTM 493
Db 152 151 Qy 348 DIGKLPSMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQV 407 Db 152 151	Db 228 KBITDLITAQRAYEMNSKVITTADEM 253
408 VDFYNIPLARFTSEDGIRREGNNHYSATLDSGOPEFGLPGTSNYGKLSVNQLETSNVDMS 467 108 VDFYNIPLARFTSEDGIRREGNNHYSATLDSGOPEFGLPGTSNYGKLSVNQLETSNVDMS 467	F71801 flagellar basal-body, rod protein (distal rod protein) - Helicobacter pylori (strain J99) C;Species: Helicobacter pylori
468 REMVNMIIIQRGFÇMUSKSVTTADTM 493 1 :: :	C.Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 C.Accession: F71801 R.Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; I Nature 397, 176-180, 1999

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C;Species: Helicobacter mustelae
C;Species: Helicobacter mustelae
C;Species: Helicobacter mustelae
C;Species: Helicobacter mustelae
C;Species: Helicobacter mustelae
C;Accession: S61455; S6144
R;O'Toole, P.W.; Kostrzynska, M.; Trust, T.J.
Mol. Microbiol. 14, 691-703, 1994
A;Title: Non-mortile mutants of Helicobacter pylori and Helicobacter mustelae defective is
A;Reference number: S61442; MUID:95198543; PMID:7891557
A;Accession: S61444
A;Residues: 1-41;420-454 <OTO>
A;Experimental source: strain 4298
A;Accession: S61444
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 31-39,'S','41-420 <OWO>
A;Experimental source: BMB:109548
A;Experimental source: strain 4298
A;Experimental source: strain 4298
A;Experimental source: strain 4298
A,Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A,Reference number: A71800, MUID:99120557; PMID:9923682
A,Accesion: F71801
A,Accesion: F71801
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-262 cARN>
A,Esperimental type: DNA
A,Experimental source: strain J99
A,Experimental source: strain J99
A,Experimental source: strain J99
C,Senerics:
A,Generics:
C,Superfamily: rod protein flgF
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                                                                                                                                                                                                                                                                                                                                                                                                             61 LSPDGMEVGLGVRPSAITKMFSQGSPKETENNLDIAITGKGFFQVQLPDGTTAYTRSGNF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VDGT 156
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                                                                                                                                                                                                                                                                                                                                                                                 -----QAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLED-KVHYTRAGNF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFTQDGFLNDPSGFTLMGSRISNNPNIKKETLEPIQLDFNDPTVAKSPAKTSTALNAVVN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGDSTDKTQSEANPYFALLESWKGNGTPPISTSNYSYAQPMRVYDQQGNSHDITVYFDGA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 PSSTGSKTFEYLVAMNPSEDGSAASGTDSAGLLMSGTMTFSSNGELKNMTAFTPTGSATK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DINAWOPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNWWAGAPASAAAIGTDIGKLP 353
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                                                                                                                                                                                                                                                                                                                                1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAIGSTGSQGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 SMMPIQTSSGNSTARNGSSSTRRYSQDGYPQGDLVDVTITSEGKLQGKYSNSQVVDFYNI
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                               11.1%; Score 288; DB 2; Length 262;
llarity 21.0%; Pred. No. 6.18-11;
Conservative 39; Mismatches 109; Indels 254;
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Best Local Similarity
Matches 107; Conserva
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the nucleotide sequence was submitted to the EMBL Data Library, May 1994
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                                                                                                                                                                                                                                                                                                  55 GSGGPNQAGMGAQVGSVRTIFTQGAFEPGNSVTDLAIGGKGFFQVTLE--DKVHYTRAGN 112
                                                                                                                                                                                                                                                                                                                             61 GGQNDVSVGLGVNVNSTTKVFSQGSTQNTDVKTDLAIBGDGFFIISPDRGKTQNFTRDGE 120
                                                                                                                                                                                                                                                                                                                                                                                                                           164 TST--ALNAVVNLGDSTDKTQSEANPYFALLESWKG--NGTPPISTSNYSYAQPMR---- 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451
                                                                                                                                                                                                                                                                                                                                                                                               FRFTQDGFLNDPSGFTLMG-----SRISNNPNIKKETLEPIQLDFNDPTVAKSPAK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 -MTAF-----TPTGSATKDLNAWQPAPLVNGLPQFSANFVGAGIQPLTLDFGIKSQQNMWA 336
                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 ASSNISLRANIANAGRHVDQV---AN-VFGLGSTTKTPVDGINPIYDSHDNLTQKAEDFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 VAAQNAINALKQXTGVEAFVDNGMLRLQNKNNMDGDAEVKNIRITADGTGAFANFIEGDS
                                                                                                                                                                                                                                            --SSGNSTARNGSSSTRRYS
                                                                                                                                                                                                         1 MMGSLFIGATGMKTHSTGLGTVSNNIANANTIGYKQQQVVFQDLFSQDLAI----GST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 VYDQQGN-----SHDITVYFDGAPSSTGSKTFEYLVAMNPSEDGSAASGTDS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403 ---DSTASVSVKFNKY-GMLEIQNKDNGDELKQDLNIFVSGYSSENST-NNGS----E
                                                                                                                                                                  Gaps
                                                                                                                   11.1%; Score 287.5; DB 2; Length 454; 25.7%; Pred. No. 1.5e-10; ive 59; Mismatches 169; Indels 131;
                                                                                                                 Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 DITAFRYRYTTSASPDSGTGOFRTTEDLRALIQYDANLIKDPSQAYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AGLLMSGTMTFSSNG-------ELKN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 GAPASAAAIGTDIGKLPSMMPIQT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 October 26, 2004, 09:10:16
                                                                                                                                                                  Conservative
                                                                                                                                         Similarity
    A,Note: the nucleotide
C,Genetics:
A,Gene: flgE
C,Keywords: flagellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDG 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed:
Job time : 48 secs
                                                                                                                   Query Match
Best Local Simi
Matches 124;
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